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(54) Title: **CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS, RESISTANCE AND TOLERANCE PROTEINS**

(57) Abstract: Isolated nucleic acid molecules, designated SRT nucleic acid molecules, which encode novel SRT proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SRT nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated SRT proteins, mutated SRT proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of SRT genes in this organism.

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**CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
RESISTANCE AND TOLERANCE PROTEINS**

Related Applications

5 This application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial No. 60/142692, filed July 1, 1999, and also to U.S. Provisional Patent Application Serial No. 60/151214, filed August 27, 1999. This application also claims priority to German Patent Application No. 19930429.7, filed July 1, 1999, German Patent Application No. 19931413.6, filed July 8, 1999, German Patent Application No. 19931457.8, filed July 8, 1999, German Patent Application No. 19931541.8, filed July 8, 1999, German Patent Application No. 19932209.0, filed July 9, 1999, German Patent Application No. 19932230.9, filed July 9, 1999, German Patent Application No. 19932914.1, filed July 14, 1999, German Patent Application No. 19940764.9, filed August 27, 1999, and 15 German Patent Application No. 19941382.7, filed August 31, 1999. The entire contents of all of the aforementioned applications are hereby expressly incorporated herein in their entirety by this reference.

Background of the Invention

20 Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic 25 compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through large-scale culture of bacteria developed to produce and secrete large quantities of a particular desired molecule. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have 30 been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as stress, resistance and tolerance (SRT) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The SRT nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the SRT nucleic acids of the invention, or modification of the sequence of the SRT nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The SRT nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The SRT nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms.

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Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The SRT proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, permitting *C. glutamicum* to survive in a setting which is either chemically or environmentally hazardous to this microorganism. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (e.g., *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals, through the ability of these proteins to permit growth and multiplication of *C. glutamicum* (and also continuous production of one or more fine chemicals) under circumstances which would normally impede growth of the organism, such as those conditions frequently encountered during large-scale fermentative growth. For example, by overexpressing or engineering a heat-shock induced protease molecule such that it is optimized in activity, one may increase the ability of the bacterium to degrade incorrectly folded proteins when the bacterium is challenged with high temperatures. By having fewer misfolded (and possibly misregulated or nonfunctional) proteins to interfere with normal reaction mechanisms in the cell, the cell is increased in its ability to function normally in such a culture, which should in turn provide increased viability. This overall increase in number of cells having greater viability and activity in the culture should also result in an increase in yield, production, and/or efficiency of production of one or more desired fine chemicals, due at least to the relatively greater number of cells producing these chemicals in the culture.

This invention provides novel SRT nucleic acid molecules which encode SRT proteins which are capable of, for example, permitting *C. glutamicum* to survive in a setting which is either chemically or environmentally hazardous to this microorganism. Nucleic acid molecules encoding an SRT protein are referred to herein as SRT nucleic acid molecules. In a preferred embodiment, the SRT protein participates in metabolic pathways permitting *C. glutamicum* to survive in a setting which is either chemically or

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environmentally hazardous to this microorganism. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an SRT protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of SRT-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8....). The preferred SRT proteins of the present invention also preferably possess at least one of the SRT activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an SRT activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or

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more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected from those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown the corresponding odd-numbered
5 SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....)).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an SRT fusion protein) which includes
10 a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and has the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism, or possesses one or more of the activities set forth in Table 1, and which
15 also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-
20 numbered SEQ ID NO in the Sequence Listing). Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* SRT protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression
25 vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an SRT protein by culturing the host cell in a suitable medium. The SRT protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered
30 microorganism in which an SRT gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by the introduction of a nucleic acid molecule of the invention encoding wild-type or mutated SRT sequence as

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a transgene. In another embodiment, an endogenous SRT gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered SRT gene. In another embodiment, an endogenous or introduced SRT gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SRT protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of a SRT gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SRT gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 304)) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated SRT protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated SRT protein or portion thereof possesses the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism. In another preferred embodiment, the isolated SRT protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism.

The invention also provides an isolated preparation of an SRT protein. In preferred embodiments, the SRT protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein

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which is substantially homologous to an entire amino acid sequence of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing). In yet another embodiment, the protein is at least about 50%,
5 preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated SRT protein comprises an amino acid sequence which is at least about 50% or more homologous to
10 one of the amino acid sequences of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to improve the survival rate of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated SRT protein can comprise an amino acid sequence
15 which is encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred
20 that the preferred forms of SRT proteins also have one or more of the SRT bioactivities described herein.

The SRT polypeptide, or a biologically active portion thereof, can be operatively linked to a non-SRT polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the SRT protein alone. In
25 other preferred embodiments, this fusion protein results in increased yields, production, and/or efficiency of production of a desired fine chemical from *C. glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates the production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which
30 modulate the activity of an SRT protein, either by interacting with the protein itself or a substrate or binding partner of the SRT protein, or by modulating the transcription or translation of an SRT nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an SRT nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining
5 a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an SRT nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

10 Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates SRT protein activity or SRT nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated in resistance to one or more
15 toxic chemicals or in resistance to one or more environmental stresses, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates SRT protein activity can be an agent which stimulates SRT protein activity or SRT nucleic acid expression. Examples of agents which stimulate SRT protein activity or SRT nucleic acid expression include small
20 molecules, active SRT proteins, and nucleic acids encoding SRT proteins that have been introduced into the cell. Examples of agents which inhibit SRT activity or expression include small molecules, and antisense SRT nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant SRT
25 gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred
30 embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides SRT nucleic acid and protein molecules which are involved in the survival of *C. glutamicum* upon exposure of this microorganism to chemical or environmental hazards. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, since these SRT proteins provide a means for continued growth and multiplication of *C. glutamicum* in the presence of toxic chemicals or hazardous environmental conditions, such as may be encountered during large-scale fermentative growth. By increasing the growth rate or at least maintaining normal growth in the face of poor, if not toxic, conditions, one may increase the yield, production, and/or efficiency of production of one or more fine chemicals from such a culture, at least due to the relatively greater number of cells producing the fine chemical in the culture. Aspects of the invention are further explicated below.

15 I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in

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Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

5 A. *Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the
10 nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids
15 have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways
20 to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are
25 interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout
30 the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in

both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be
5 useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of
10 producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-
15 step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase.
20 Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-
step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction
25 catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine
30 from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of

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the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them.

5 Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount
10 of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although
15 they are readily synthesized by other organisms, such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other
20 processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins
25 may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such
30 molecules are vitamins, antioxidants, and also certain lipids (e.g., polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (e.g., pyridoxine, pyridoxamine, pyridoxal-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- β -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives

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of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

- 5 Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are
- 10 also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

- The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-
- 15 scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

20 *C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses*

- Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic
- 25 structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or
- 30 their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are

nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

- Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.
- The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell.

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Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α, α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Resistance to Damage from Chemicals, Environmental Stress, and Antibiotics

Production of fine chemicals is typically performed by large-scale culture of bacteria developed to produce and secrete large quantities of these molecules. However, this type of large-scale fermentation results in the subjection of the microorganisms to stresses of various kinds. These stresses include environmental stress and chemical stress.

A. Resistance to Environmental Stress

Examples of environmental stresses typically encountered in large-scale fermentative culture include mechanical stress, heat stress, stress due to limited oxygen, stress due to oxygen radicals, pH stress, and osmotic stress. The stirring mechanism used in most large-scale fermentors to ensure aeration of the culture produces heat, thus increasing the temperature of the culture. Increases in temperature induce the well-characterized heat shock response, in which a set of proteins are expressed which not

only aid in the survival of the bacterium in the face of high temperatures, but also increase survival in response to a number of other environmental stresses (see Neidhardt, F.C., *et al.*, eds. (1996) *E. coli* and *Salmonella*. ASM Press: Washington, D.C., p. 1382-1399; Wosten, M. M. (1998) *FEMS Microbiology Reviews* 22(3): 127-50; 5 Bahl, H. *et al.* (1995) *FEMS Microbiology Reviews* 17(3): 341-348; Zimmerman, J.L., Cohill, P.R. (1991) *New Biologist* 3(7): 641-650; Samali, A., and Orrenius, S. (1998) *Cell. Stress Chaperones* 3(4): 228-236, and references contained therein from each of these citations). Regulation of the heat shock response in bacteria is facilitated by specific sigma factors and other cellular regulators of gene expression (Hecker, M., 10 Volker, U (1998). *Molecular Microbiology* 29(5): 1129-1136). One of the largest problems that the cell encounters when exposed to high temperature is that protein folding is impaired; nascent proteins have sufficient kinetic energy in high temperature circumstances that it is difficult for the growing polypeptide chain to remain in a stable conformation long enough to fold properly. Thus, two of the key types of proteins 15 expressed during the heat shock response consist of chaperones (proteins which assist in the folding or unfolding of other proteins – see, *e.g.*, Fink, A.L. (1999) *Physiol. Rev.* 79(2): 425-449), and proteases, which can destroy any improperly folded proteins. Examples of chaperones expressed during the heat shock response include GroEL and DNAK; proteases known to be expressed during this cellular reaction to heat shock 20 include Lon, FtsH, and ClpB.

Other environmental stresses besides heat may also provoke a stress response. Though the fermentor stirring process is meant to introduce oxygen into the culture, oxygen may remain in limited supply, particularly when the culture is advanced in growth and the oxygen needs of the culture are thereby increased; an insufficient supply 25 of oxygen is another stress for the microorganism. Cells in fermentor cultures are also subjected to a number of osmotic stresses, particularly when nutrients are added to the culture, resulting in a high extracellular and low intracellular concentration of these molecules. Further, the large quantities of the desired molecules produced by these organisms in culture may contribute to osmotic stress of the bacteria. Lastly, aerobic 30 metabolism such as that used by *C. glutamicum* results in carbon dioxide as a waste product; secretion of this molecule may acidify the culture medium due to conversion of this molecule to carboxylic acid. Thus, bacteria in culture are also frequently subjected

to acidic pH stress. The converse may also be true – when high levels of basic waste molecules such as ammonium are present in the culture medium, the bacteria in culture may be subjected to basic pH stress as well.

To combat such environmental stresses, bacteria have elegant gene systems which are expressed upon exposure to one or more stresses, such as the aforementioned heat shock system. Genes expressed in response to osmotic stress, for example, encode proteins capable of transporting or synthesizing compatible solutes such that osmotic intake or export of a particular molecule is slowed to manageable levels. Other examples of stress-induced bacterial proteins are those involved in trehalose biosynthesis, those encoding enzymes involved in ppGpp metabolism, those involved in signal transduction, particularly those encoding two-component systems which are sensitive to osmotic pressure, and those encoding transcription factors which are responsive to a variety of stress factors (*e.g.*, RssB analogues and/or sigma factors). Many other such genes and their protein products are known in the art.

15

B. Resistance to Chemical Stress

Aside from environmental stresses, cells may also experience a number of chemical stresses. These may fall into two categories. The first are natural waste products of metabolism and other cellular processes which are secreted by the cell to the surrounding medium. The second are chemicals present in the extracellular medium which do not originate from the cell. Generally, when cells excrete toxic waste products from the concentrated intracellular cytoplasm into the relatively much more dilute extracellular medium, these products dissipate such that extracellular levels of the possibly toxic compound are quite low. However, in large-scale fermentative culture of the bacterium, this may not be the case: so many bacteria are grown in a relatively small environment and at such a high metabolic rate that waste products may accumulate in the medium to nearly toxic levels. Examples of such wastes are carbon dioxide, metal ions, and reactive oxygen species such as hydrogen peroxide. These compounds may interfere with the activity or structure of cell surface molecules, or may re-enter the cell, where they can seriously damage proteins and nucleic acids alike. Certain other chemicals hazardous to the normal functioning of cells may be naturally found in the extracellular medium. For example, metal ions such as mercury, cadmium, nickel or

30

copper are frequently found in water sources, and may form tight complexes with cellular enzymes which prevent the normal functioning of these proteins.

C. Resistance to Antibiotics

5 Bacteriocidal proteins or antibiotics, may also be found in the extracellular milieu, either through the intervention of the researcher, or as a natural product from another organism, utilized to gain a competitive advantage. Microorganisms have several art-known mechanisms to protect themselves against antimicrobial chemicals. Degradation, modification, and export of compounds toxic to the cell are common
10 methods by which microorganisms eliminate or detoxify antibiotics. Cytoplasmic 'efflux-pumps' are known in several prokaryotes and show similarities to the so-called 'multidrug resistance' proteins from higher eukaryotes (Neyfakh, A. A. , *et al.* (1991) *Proc. Natl. Acad. Sci. USA* 88: 4781-4785). Examples of such proteins include emrAB from *E. coli* (Lomovskaya, O. and K. Lewis (1992) *Proc. Natl. Acad. Sci. USA* 89:
15 8938-8942), lmrB from *B. subtilis* (Kumano, M. *et al.* (1997) *Microbiology* 143: 2775-2782), smr from *S. aureus* (Grinius, L.G. *et al.* (1992) *Plasmid* 27: 119-129) or cmr from *C. glutamicum* (Kaidoh, K. *et al.* (1997) *Micro. Drug Resist.* 3: 345-350). *C. glutamicum* itself is non-pathogenic, in contrast to several other members of the genus *Corynebacterium* , such as *C. diphtheriae* or *C. pseudotuberculosis*. Several pathogenic
20 *Corynebacteria* are known to have multiple resistances against a variety of antibiotics, such as *C. jeikeium* and *C. urealyticum* (Soriano, F. *et al.* (1995) *Antimicrob. Agents Chemother.* 39: 208-214).

Lincosamides are recognized as effective antibiotics against *Corynebacterium* species (Soriano, F. *et al.* (1995) *Antimicrob. Agents Chemother.* 39: 208-214). An
25 unexpected result of the present invention was the identification of a gene encoding a lincosamide-resistance protein (in particular, a lincomycin-resistance protein). The LMRB protein from *C. glutamicum* shows 40% homology to the product of the lmrB gene from *B. subtilis* (see Genbank accession no. AL009126), as calculated using version 1.7 of the program CLUSTALW (Thompson, J.D., Higgins, D.G., Gibson, T. J.
30 (1994) *Nucl. Acids Res.* 22: 4673-4680) using standard parameters (PAIRWISE ALIGNMENT PARAMETERS: slow/accurate alignments: Gap Open Penalty = 10.00, Gap Extension Penalty = 0.10, Protein weight matrix = BLOSUM 30, DNA weight

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- matrix = IUB, Fast/Approximate alignments: Gap penalty = 3, K-tuple (word) size = 1, No. of top diagonals = 5, Window size = 5, Toggle Slow/Fast pairwise alignments = slow. Multiple alignment parameters: Gap Opening Penalty = 10.00, Gap Extension Penalty = 0.05, Delay divergent sequences = 40%, DNA transitions weight = 0.50,
- 5 Protein weight matrix = BLOSUM series, DNA weight matrix = IUB, Use negative matrix = OFF).

- Environmental stress, chemical stress, and antibiotic or other antimicrobial stress may influence the behavior of the microorganisms during fermentor culture, and may have an impact on the production of the desired compound from these organisms.
- 10 For example, osmotic stress of a microorganism may cause inappropriate or inappropriately rapid uptake of one or more compounds which can ultimately lead to cellular damage or death due to osmotic shock. Similarly, chemicals present in the culture, either exogenously added (e.g., antimicrobial compounds intended to eliminate unwanted microbes) or generated by the bacteria themselves (e.g., waste compounds
- 15 such as heavy metals or oxygen radicals, or even antimicrobial compounds) may result in inhibition of fine chemical production or even death of the organism. The genes of the invention encode *C. glutamicum* proteins which act to prevent cell damage or death, by specifically counteracting the source or effect of the environmental or chemical stress.

20

III. Elements and Methods of the Invention

- The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as SRT nucleic acid and protein molecules, which increase the ability of *C. glutamicum* to survive in chemically or environmentally hazardous
- 25 settings. In one embodiment, the SRT molecules function to confer resistance to one or more environmental or chemical stresses to *C. glutamicum*. In a preferred embodiment, the activity of the SRT molecules of the present invention has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the SRT molecules of the invention are modulated in activity, such that the
- 30 yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum* is also modulated.

The language, "SRT protein" or "SRT polypeptide" includes proteins which participate in the resistance of *C. glutamicum* to one or more environmental or chemical stresses. Examples of SRT proteins include those encoded by the SRT genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "SRT gene" or "SRT nucleic acid sequence" include nucleic acid sequences encoding an SRT protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of SRT genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (e.g., kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (i.e., fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (e.g., the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound. The terms "resistance" and "tolerance" are art-known and include the ability of a cell to not be affected by exposure to a chemical or an environment which would otherwise be detrimental to the normal functioning of these organisms. The terms "stress" or "hazard" include factors which are detrimental to the normal functioning of

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cells such as *C. glutamicum*. Examples of stresses include "chemical stress", in which a cell is exposed to one or more chemicals which are detrimental to the cell, and "environmental stress" where a cell is exposed to an environmental condition outside of those to which it is adapted. Chemical stresses may be either natural metabolic waste products such as, but not limited to reactive oxygen species or carbon dioxide, or chemicals otherwise present in the environment, including, but not limited to heavy metal ions or bacteriocidal proteins such as antibiotics. Environmental stresses may be, but are not limited to temperatures outside of the normal range, suboptimal oxygen availability, osmotic pressures, or extremes of pH, for example.

10 In another embodiment, the SRT molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. Using recombinant genetic techniques, one or more of the SRT proteins of the invention may be manipulated such that its function is modulated. The alteration of activity of stress response, resistance or tolerance genes
15 such that the cell is increased in tolerance to one or more stresses may improve the ability of that cell to grow and multiply in the relatively stressful conditions of large-scale fermentor culture. For example, by overexpressing or engineering a heat-shock induced chaperone molecule such that it is optimized in activity, one may increase the ability of the bacterium to correctly fold proteins in the face of nonoptimal temperature
20 conditions. By having fewer misfolded (and possibly misregulated or nonfunctional) proteins, the cell is increased in its ability to function normally in such a culture, which should in turn provide increased viability. This overall increase in number of cells having greater viability and activity in the culture should also result in an increase in the yield, production, and/or efficiency of production of one or more desired fine chemicals,
25 due at least to the relatively greater number of cells producing these chemicals in the culture.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the
30 isolated *C. glutamicum* SRT DNAs and the predicted amino acid sequences of the *C. glutamicum* SRT proteins are shown the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively.,.

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Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode chemical and environmental stress, resistance, and tolerance proteins.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention (e.g., the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, e.g., the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence. Ranges and identity values intermediate to the above-recited values, (e.g., 75%-80% identical, 85-87% identical, 91-92% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included.

The SRT proteins or biologically active portions or fragments thereof of the invention can confer resistance or tolerance to one or more chemical or environmental stresses, or may have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode SRT polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of SRT-encoding nucleic acid (e.g., SRT DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides

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of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated
5 from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated SRT nucleic acid molecule can contain less than
10 about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (*e.g.*, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or
15 other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* SRT DNA can be
20 isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).
25 Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO of the
30 Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate

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extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an SRT nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing, correspond to the *Corynebacterium glutamicum* SRT DNAs of the invention. This DNA comprises sequences encoding SRT proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the nucleic acid sequences of the Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, or RXS number having the designation "RXA", "RXN", or "RXS" followed by 5 digits (*i.e.*, RXA01524, RXN00493, or RXS01027). Each of the nucleic acid sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the odd-numbered sequences of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may be also be distinguished by their differing RXA, RXN, or RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an

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even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence. For example, the coding region for RXA01524 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The sequences of the nucleic acid molecules of the invention are identified by the same

5 RXA, RXN, or RXS designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequence designated RXA01524 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA01524, the amino acid sequence designated RXN00034 is a

10 translation of the coding region of the nucleotide sequence of nucleic acid molecule RXN00034, and the amino acid sequence in designated RXS00568 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXS00568. The correspondence between the RXA, RXN, and RXS nucleotide and amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated

15 gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, or RXS designation. For example, SEQ ID NO:7, designated, as indicated on Table 1, as "F RXA00498", is an F-designated gene, as are SEQ ID NOs: 25, 33, and 37 (designated on Table 1 as "F RXA01345", "F RXA02543", and "F RXA02282", respectively).

20 In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the *dapD* gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version

25 relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID

30 NO: of the Sequence Listing, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is sufficiently complementary to one of the nucleotide sequences shown in the Sequence

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Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences of the invention,, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an SRT protein. The nucleotide sequences determined from the cloning of the SRT genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning SRT homologues in other cell types and organisms, as well as SRT homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing),, an anti-sense sequence of one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone SRT homologues.

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Probes based on the SRT nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-
5 factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an SRT protein, such as by measuring a level of an SRT-encoding nucleic acid in a sample of cells, *e.g.*, detecting SRT mRNA levels or determining whether a genomic SRT gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein
10 or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to confer resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses. As used herein, the language "sufficiently
15 homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the protein or portion thereof is capable of
20 participating in the resistance of *C. glutamicum* to one or more chemical or environmental stresses. Protein members of such metabolic pathways, as described herein, function to increase the resistance or tolerance of *C. glutamicum* to one or more environmental or chemical hazards or stresses. Examples of such activities are also described herein. Thus, "the function of an SRT protein" contributes to the overall
25 resistance of *C. glutamicum* to elements of its surroundings which may impede its normal growth or functioning, and/or contributes, either directly or indirectly, to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of SRT protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least
30 about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of

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the Sequence Listing). Ranges and identity values intermediate to the above-recited values, (e.g., 75%-80% identical, 85-87% identical, or 91-92% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower
5 limits are intended to be included.

Portions of proteins encoded by the SRT nucleic acid molecules of the invention are preferably biologically active portions of one of the SRT proteins. As used herein, the term "biologically active portion of an SRT protein" is intended to include a portion, e.g., a domain/motif, of an SRT protein that is capable of imparting resistance or
10 tolerance to one or more environmental or chemical stresses or hazards, or has an activity as set forth in Table 1. To determine whether an SRT protein or a biologically active portion thereof can increase the resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses or hazards, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as
15 detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an SRT protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the SRT protein or peptide (e.g., by
20 recombinant expression *in vitro*) and assessing the activity of the encoded portion of the SRT protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (e.g., a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic
25 code and thus encode the same SRT protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (e.g., an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C.*
30 *glutamicum* protein which is substantially homologous to an amino acid sequence of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

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It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00084 (SEQ ID NO:189), a nucleotide sequence which is greater than and/or at least 56% identical to the nucleotide sequence designated RXA00605 (SEQ ID NO:11), and a nucleotide sequence which is greater than and/or at least 50% identical to the nucleotide sequence designated RXA00886 (SEQ ID NO:39). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* SRT nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by one of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of SRT proteins may exist within a population (*e.g.*, the *C. glutamicum* population). Such genetic polymorphism in the SRT gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an SRT protein, preferably a *C. glutamicum* SRT protein. Such

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natural variations can typically result in 1-5% variance in the nucleotide sequence of the SRT gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in SRT that are the result of natural variation and that do not alter the functional activity of SRT proteins are intended to be within the scope of the invention.

5 Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* SRT DNA of the invention can be isolated based on their homology to the *C. glutamicum* SRT nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in
10 another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent
15 conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such
20 stringent conditions are known to those of ordinary skill in the art in the art and can be found in Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an
25 isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C.*
30 *glutamicum* SRT protein.

In addition to naturally-occurring variants of the SRT sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be

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introduced by mutation into a nucleotide sequence of the invention, thereby leading to changes in the amino acid sequence of the encoded SRT protein, without altering the functional ability of the SRT protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a

5 nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the SRT proteins (*e.g.*, an even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said SRT protein, whereas an "essential" amino acid residue is required for SRT protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only

10 semi-conserved in the domain having SRT activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SRT activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding SRT proteins that contain changes in amino acid residues that are not essential for SRT activity. Such SRT proteins differ in amino acid sequence from a sequence of

15 an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the SRT activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the invention and is capable of increasing the resistance or tolerance of *C. glutamicum* to

20 one or more environmental or chemical stresses, or has one or more of the activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95%

25 homologous to one of these sequences in, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be

30 introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one

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sequence (*e.g.*, one of the amino acid sequences of the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an SRT protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an SRT protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an SRT coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an SRT activity described herein to identify mutants that retain SRT activity. Following mutagenesis of one the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, the encoded protein can be expressed recombinantly and the activity of the protein can

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be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding SRT proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire SRT coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an SRT protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO.: 120 (RXA00600) comprises nucleotides 1 to 1098). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding SRT. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding SRT disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of SRT mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of SRT mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of SRT mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to

increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-
5 fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-
10 methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid
15 methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of
20 interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an SRT protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by
25 conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or
30 an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in

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which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

10 In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave SRT mRNA transcripts to thereby inhibit translation of SRT mRNA. 15 A ribozyme having specificity for an SRT-encoding nucleic acid can be designed based upon the nucleotide sequence of an SRT cDNA disclosed herein (*i.e.*, SEQ ID NO:119 (RXA00600)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an SRT-encoding mRNA. See, *e.g.*, Cech *et al.* 20 U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, SRT mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

25 Alternatively, SRT gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an SRT nucleotide sequence (*e.g.*, an SRT promoter and/or enhancers) to form triple helical structures that prevent transcription of an SRT gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-30 36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

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B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an SRT protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185,

Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-,
5 *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI^q*-, T7-, T5-, T3-, *gal*-, *trc*-, *ara*-, SP6-, *amy*, SPO2, λ -P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MF α , AC, P-60, CYC1, GAPDH, TEF, *rp28*, ADH, promoters from plants such as CaMV/35S, SSU, OCS, *lib4*, *usp*, STLS1, B33, *nos* or ubiquitin- or phaseolin-promoters. It is also possible to use
10 artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described
15 herein (e.g., SRT proteins, mutant forms of SRT proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of SRT proteins in prokaryotic or eukaryotic cells. For example, SRT genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992)
20 "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics
25 of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the
30 recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion
5 vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein
10 from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase
15 (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the SRT protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin.
20 Recombinant SRT protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-
25 III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the
30 pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7

gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the SRT protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York (ISBN 0 444 904018).

Alternatively, the SRT proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the SRT proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (e.g., the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New
5 plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

10 In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements.
15 For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed.*, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY,
20 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable
25 tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters
30 (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and

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European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

5 The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to SRT mRNA. Regulatory sequences operatively
10 linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid
15 or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

20 Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due
25 to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

 A host cell can be any prokaryotic or eukaryotic cell. For example, an SRT protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or
30 mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those of ordinary skill in the art. Microorganisms related

to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms

5 "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA)) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-

10 dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the

15 expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418,

20 hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an SRT protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

25 To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an SRT gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the SRT gene. Preferably, this SRT gene is a *Corynebacterium glutamicum* SRT gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source.

30 In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous SRT gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively,

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the vector can be designed such that, upon homologous recombination, the endogenous SRT gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous SRT protein). In the homologous recombination vector, the altered portion of the SRT gene is flanked at its 5' and 3' ends by additional nucleic acid of the SRT gene to allow for homologous recombination to occur between the exogenous SRT gene carried by the vector and an endogenous SRT gene in a microorganism. The additional flanking SRT nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced SRT gene has homologously recombined with the endogenous SRT gene are selected, using art-known techniques.

15 In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an SRT gene on a vector placing it under control of the lac operon permits expression of the SRT gene only in the presence of IPTG. Such regulatory systems are well known in the art.

20 In another embodiment, an endogenous SRT gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced SRT gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SRT protein. In still another
25 embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SRT gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SRT gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described SRT gene and protein modifications may be readily
30 produced using the methods of the invention, and are meant to be included in the present invention.

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A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an SRT protein. Accordingly, the invention further provides methods for producing SRT proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an SRT protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SRT protein) in a suitable medium until SRT protein is produced. In another embodiment, the method further comprises isolating SRT proteins from the medium or the host cell.

C. Isolated SRT Proteins

Another aspect of the invention pertains to isolated SRT proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of SRT protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of SRT protein having less than about 30% (by dry weight) of non-SRT protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-SRT protein, still more preferably less than about 10% of non-SRT protein, and most preferably less than about 5% non-SRT protein. When the SRT protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SRT protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of SRT protein having less than about 30% (by dry weight) of chemical precursors or non-SRT chemicals, more preferably less than

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about 20% chemical precursors or non-SRT chemicals, still more preferably less than about 10% chemical precursors or non-SRT chemicals, and most preferably less than about 5% chemical precursors or non-SRT chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the SRT protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* SRT protein in a microorganism such as *C. glutamicum*.

An isolated SRT protein or a portion thereof of the invention can contribute to the resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses or hazards, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to mediate the resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses or hazards. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an SRT protein of the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the SRT protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the SRT protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper

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and/or lower limits are intended to be included. The preferred SRT proteins of the present invention also preferably possess at least one of the SRT activities described herein. For example, a preferred SRT protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes
5 under stringent conditions, to a nucleotide sequence of the invention, and which can increase the resistance or tolerance of *C. glutamicum* to one or more environmental or chemical stresses, or which has one or more of the activities set forth in Table 1.

In other embodiments, the SRT protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the SRT protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%,
15 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which
20 has at least one of the SRT activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains
25 to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention.

Biologically active portions of an SRT protein include peptides comprising amino acid sequences derived from the amino acid sequence of an SRT protein, *e.g.*, an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the
30 amino acid sequence of a protein homologous to an SRT protein, which include fewer amino acids than a full length SRT protein or the full length protein which is homologous to an SRT protein, and exhibit at least one activity of an SRT protein.

Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an SRT protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an SRT protein include one or more selected domains/motifs or portions thereof having biological activity.

SRT proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the SRT protein is expressed in the host cell. The SRT protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an SRT protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native SRT protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-SRT antibody, which can be produced by standard techniques utilizing an SRT protein or fragment thereof of this invention.

The invention also provides SRT chimeric or fusion proteins. As used herein, an SRT "chimeric protein" or "fusion protein" comprises an SRT polypeptide operatively linked to a non-SRT polypeptide. An "SRT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to SRT, whereas a "non-SRT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the SRT protein, *e.g.*, a protein which is different from the SRT protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the SRT polypeptide and the non-SRT polypeptide are fused in-frame to each other. The non-SRT polypeptide can be fused to the N-terminus or C-terminus of the SRT polypeptide. For example, in one embodiment the fusion protein is a GST-SRT fusion protein in which the SRT sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant SRT proteins. In another embodiment, the fusion protein is an SRT protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression

and/or secretion of an SRT protein can be increased through use of a heterologous signal sequence.

Preferably, an SRT chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the
5 different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene
10 can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel
15 *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An SRT-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the SRT protein.

Homologues of the SRT protein can be generated by mutagenesis, *e.g.*, discrete
20 point mutation or truncation of the SRT protein. As used herein, the term "homologue" refers to a variant form of the SRT protein which acts as an agonist or antagonist of the activity of the SRT protein. An agonist of the SRT protein can retain substantially the same, or a subset, of the biological activities of the SRT protein. An antagonist of the
25 SRT protein can inhibit one or more of the activities of the naturally occurring form of the SRT protein, by, for example, competitively binding to a downstream or upstream member of the SRT system which includes the SRT protein. Thus, the *C. glutamicum* SRT protein and homologues thereof of the present invention may increase the tolerance or resistance of *C. glutamicum* to one or more chemical or environmental stresses.

In an alternative embodiment, homologues of the SRT protein can be identified
30 by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the SRT protein for SRT protein agonist or antagonist activity. In one embodiment, a variegated library of SRT variants is generated by combinatorial mutagenesis at the nucleic acid

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level and is encoded by a variegated gene library. A variegated library of SRT variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SRT sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of SRT sequences therein. There are a variety of methods which can be used to produce libraries of potential SRT homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential SRT sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the SRT protein coding can be used to generate a variegated population of SRT fragments for screening and subsequent selection of homologues of an SRT protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an SRT coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the SRT protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SRT homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of

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vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify SRT homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated SRT library, using methods well known in the art.

10 D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of SRT protein regions required for function; modulation of an SRT protein activity; modulation of the activity of an SRT pathway; and modulation of cellular production of a desired compound, such as a fine chemical.

The SRT nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.

Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the

body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in the Sequence Listing) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The SRT nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The resistance processes in which the molecules of the invention participate are utilized by a wide variety of cells; by comparing the sequences

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of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

The genes of the invention, *e.g.*, the gene encoding LMRB (SEQ ID NO:1) or other gene of the invention encoding a chemical or environmental resistance or tolerance protein (*e.g.*, resistance against one or more antibiotics), may be used as genetic markers for the genetic transformation of (*e.g.*, the transfer of additional genes into or disruption of preexisting genes of) organisms such as *C. glutamicum* or other bacterial species. Use of these nucleic acid molecules permits efficient selection of organisms which have incorporated a given transgene cassette (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon, or other nucleic acid element), based on a trait which permits the survival of the organism in an otherwise hostile or toxic environment (*e.g.*, in the presence of an antimicrobial compound). By employing one or more of the genes of the invention as genetic markers, the speed and ease with which organisms having desirable transformed traits (*e.g.*, modulated fine chemical production) are engineered and isolated are improved. While it is advantageous to use the genes of the invention for selection of transformed *C. glutamicum* and related bacteria, it is possible, as described herein, to use homologs (*e.g.*, homologs from other organisms), allelic variants or fragments of the gene retaining desired activity. Furthermore, 5' and 3' regulatory elements of the genes of the invention may be modified as described herein (*e.g.*, by nucleotide substitution, insertion, deletion, or replacement with a more desirable genetic element) to modulate the transcription of the gene. For example, an LMRB variant in which the nucleotide sequence in the region from -1 to -200 5' to the start codon has been altered to modulate (preferably increase) the transcription and/or translation of LMRB may be employed, as can constructs in which a gene of the invention (*e.g.*, the LMRB gene (SEQ ID NO:1)) is functionally coupled to one or more regulatory signals (*e.g.*, inducer or repressor binding sequences) which can be used for modulating gene expression.

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Similarly, more than one copy of a gene (functional or inactivated) of the invention may be employed.

An additional application of the genes of the invention (*e.g.*, the gene encoding LMRB (SEQ ID NO:1) or other drug- or antibiotic-resistance gene) is in the discovery of new antibiotics which are active against *Corynebacteria* and/or other bacteria. For example, a gene of the invention may be expressed (or overexpressed) in a suitable host to generate an organism with increased resistance to one or more drugs or antibiotics (in the case of LMRB, lincosamides in particular, especially lincomycin). This type of resistant host can subsequently be used to screen for chemicals with bacteriostatic and/or bacteriocidal activity, such as novel antibiotic compounds. It is possible, in particular, to use the genes of the invention (*e.g.*, the LMRB gene) to identify new antibiotics which are active against those microorganisms which are already resistant to standard antibiotic compounds.

The invention provides methods for screening molecules which modulate the activity of an SRT protein, either by interacting with the protein itself or a substrate or binding partner of the SRT protein, or by modulating the transcription or translation of SRT nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more SRT proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the SRT protein is assessed.

Manipulation of the SRT nucleic acid molecules of the invention may result in the production of SRT proteins having functional differences from the wild-type SRT proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity. The goal of such manipulations is to increase the viability and activity of the cell when the cell is exposed to the environmental and chemical stresses and hazards which frequently accompany large-scale fermentative culture. Thus, by increasing the activity or copy number of a heat-shock-regulated protease, one may increase the ability of the cell to destroy incorrectly folded proteins, which may otherwise interfere with normal cellular functioning (for example, by continuing to bind substrates or cofactors although the protein lacks the activity to act on these molecules appropriately). The same is true for the overexpression or optimization of activity of one or more chaperone molecules

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induced by heat or cold shock. These proteins aid in the correct folding of nascent polypeptide chains, and thus their increased activity or presence should increase the percentage of correctly folded proteins in the cell, which in turn should increase the overall metabolic efficiency and viability of the cells in culture. The overexpression or optimization of the transporter molecules activated by osmotic shock should result in an increased ability on the part of the cell to maintain intracellular homeostasis, thereby increasing the viability of these cells in culture. Similarly, the overproduction or increase in activity by mutagenesis of proteins involved in the development of cellular resistance to chemical stresses of various kinds (either by transport of the offending chemical out of the cell or by modification of the chemical to a less hazardous substance) should increase the fitness of the organism in the environment containing the hazardous substance (*i.e.*, large-scale fermentative culture), and thereby may permit relatively larger numbers of cells to survive in such a culture. The net effect of all of these mutagenesis strategies is to increase the quantity of fine-chemical-producing compounds in the culture, thereby increasing the yield, production, and/or efficiency of production of one or more desired fine chemicals from the culture.

This aforementioned list of mutagenesis strategies for SRT proteins to result in increased yields of a desired compound is not meant to be limiting; variations on these mutagenesis strategies will be readily apparent to one of ordinary skill in the art. By these mechanisms, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated SRT nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: Genes Included in the Application

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	RXA01524	GR00424	29041	30483	Lincomycine RESISTANCE PROTEIN
3	4	RXA00497	GR00124	52	348	10 KD CHAPERONIN
5	6	RXN00493	VV0086	14389	16002	60 KD CHAPERONIN
7	8	F RXA00498	GR00124	363	1601	60 KD CHAPERONIN
9	10	RXA01217	GR00353	802	203	GENERAL STRESS PROTEIN CTC
11	12	RXA00605	GR00159	7412	5865	CATALASE (EC 1.11.1.6)
13	14	RXA00404	GR00089	2909	594	CARBON STARVATION PROTEIN A
15	16	RXN03119	VV0098	86877	87008	SUPEROXIDE DISMUTASE [MN] (EC 1.15.1.1)
17	18	RXN03120	VV0098	87351	87476	SUPEROXIDE DISMUTASE [MN] (EC 1.15.1.1)
19	20	RXN00575	VV0323	14716	15252	PHOSPHOTHRICIN-RESISTANCE PROTEIN
21	22	F RXA00575	GR00156	2130	1648	PHOSPHOTHRICIN-RESISTANCE PROTEIN

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
23	24	RXN01345	VV0123	4883	3432	Moleculares chaperon (HSP70/DnaK family)
25	26	F RXA01345	GR00391	1172	6	Molecular chaperones (HSP70/DnaK family)
27	28	RXA02541	GR00726	13657	12473	DNAJ PROTEIN
29	30	RXA02542	GR00726	14518	13865	GRPE PROTEIN
31	32	RXN02543	VV0057	22031	20178	DNAK PROTEIN
33	34	F RXA02543	GR00726	16375	14522	DNAK PROTEIN
35	36	RXN02280	VV0152	1849	26	TRAP1
37	38	F RXA02282	GR00659	1145	1480	Molecular chaperone, HSP90 family
39	40	RXA00886	GR00242	12396	13541	DNAJ PROTEIN
41	42	RXS00568	VV0251	2928	1582	TRIGGER FACTOR
43	44	RXN03038	VV0017	42941	43666	PS1 PROTEIN VORLÄUFER
45	46	RXN03039	VV0018	2	631	PS1 PROTEIN VORLÄUFER
47	48	RXN03040	VV0018	761	1069	PS1 PROTEIN VORLÄUFER
49	50	RXN03051	VV0022	2832	3566	PS1 PROTEIN VORLÄUFER
51	52	RXN03054	VV0026	1906	3486	PS1 PROTEIN VORLÄUFER
53	54	RXN02949	VV0025	31243	31575	PREPROTEIN TRANSLOKASE SECE UNTEREINHEIT
55	56	RXN02462	VV0124	11932	13749	PREPROTEIN TRANSLOKASE SECA UNTEREINHEIT
57	58	RXN01559	VV0171	7795	5954	PROTEIN-EXPORT MEMBRANE PROTEIN SECD
59	60	RXN00046	VV0119	5363	6058	Signal Erkennung particle GTPase
61	62	RXN01863	VV0206	1172	24	/O/C Thioedoxin-ähnliche oxidoeductase
63	64	RXN00833	VV0180	8039	8533	THIOL PEROXIDASE (EC 1.11.1.-)

Chaperones

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function
65	66	RXN01676	VV0179	12059	11304	THIOL:DISULFIDE AUSTAUSCH PROTEIN DSBD
67	68	RXN00380	VV0223	836	216	THIOL:DISULFIDE AUSTAUSCH PROTEIN TLPA
69	70	RXN00937	VV0079	42335	42706	THIOREDOXIN
71	72	RXN02325	VV0047	5527	6393	THIOREDOXIN
73	74	RXN01837	VV0320	7103	7879	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8)
75	76	RXN01926	VV0284	1	741	PEPTID KETTE RELEASE FACTOR 3
77	78	RXN02002	VV0111	141	518	PEPTID KETTE RELEASE FACTOR 3
79	80	RXN02736	VV0074	13600	14556	PUTATIVES OXPPCYCLE PROTEIN OPCA
81	82	RXS03217				SMALL COLD-SHOCK PROTEIN
83	84	F RXA01917	GR00549	3465	3665	SMALL COLD-SHOCK PROTEIN

Proteins involved in stress responses

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function
85	86	RXA02184	GR00641	19628	19248	COLD SHOCK-LIKE PROTEIN CSPC
87	88	RXA00810	GR00218	792	992	SMALL COLD-SHOCK PROTEIN
89	90	RXA01674	GR00467	1878	2771	PROBABLE HYDROGEN PEROXIDE-INDUCIBLE GENES ACTIVATOR
91	92	RXA02431	GR00708	2	1192	damage-inducible protein P
93	94	RXA02446	GR00709	11640	11206	OSMOTICALLY INDUCIBLE PROTEIN C
95	96	RXA02861	GR10006	551	1633	probable metallothionein u0308aa - Mycobacterium leprae
97	98	RXA00981	GR00276	3388	4017	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
99	100	RXN00786	VV0321	1680	706	LYTB PROTEIN
101	102	RXS01027	VV0143	5761	6768	DIADENOSINE 5',5"-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
103	104	RXS01528	VV0050	17276	16749	DIADENOSINE 5',5"-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
105	106	RXS01716	VV0319	3259	2774	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
107	108	RXS01835	VV0143	10575	10045	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
109	110	RXS02497	VV0007	15609	16535	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
111	112	RXS02972	VV0319	2763	2353	EXOPOLYPHOSPHATASE (EC 3.6.1.11)

Resistance and tolerance

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function
113	114	RXA02159	GR00640	6231	6743	ARGININE HYDROXIMATE RESISTANCE PROTEIN
115	116	RXA02201	GR00646	5837	6199	ARSENATE REDUCTASE
117	118	RXA00399	GR00159	1843	1457	ARSENICAL-RESISTANCE PROTEIN ACR3
119	120	RXA00800	GR00159	2940	1843	ARSENICAL-RESISTANCE PROTEIN ACR3
121	122	RXA02200	GR00646	4651	5760	ARSENICAL-RESISTANCE PROTEIN ACR3
123	124	RXA02202	GR00646	6278	6916	ARSENICAL-RESISTANCE PROTEIN ACR3
125	126	RXA02205	GR00646	9871	8993	BACITRACIN RESISTANCE PROTEIN (PUTATIVE UNDECAPRENOL KINASE) (EC 2.7.1.66)
127	128	RXA00900	GR00245	4052	3201	BICYCLOMYCIN RESISTANCE PROTEIN

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function
129	130	RXN00901	VW0140	8581	8168	BICYCLOMYCIN RESISTANCE PROTEIN
131	132	F RXA00901	GR00245	4357	3980	BICYCLOMYCIN RESISTANCE PROTEIN
133	134	RXA00289	GR00046	3263	4438	CHLORAMPHENICOL RESISTANCE PROTEIN
135	136	RXN01984	VW0056	1515	1811	CHLORAMPHENICOL RESISTANCE PROTEIN
137	138	F RXA01984	GR00574	282	4	CHLORAMPHENICOL RESISTANCE PROTEIN
139	140	RXA00109	GR00015	1176	565	COPPER RESISTANCE PROTEIN C PRECURSOR
141	142	RXA00109	GR00015	1176	565	COPPER RESISTANCE PROTEIN C PRECURSOR
143	144	RXA00996	GR00283	1763	1023	DAUNORUBICIN RESISTANCE ATP-BINDING PROTEIN DRRA
145	146	RXN00829	VW0180	7950	5611	DAUNORUBICIN RESISTANCE PROTEIN
147	148	F RXA00829	GR00224	2	256	DAUNORUBICIN RESISTANCE PROTEIN
149	150	F RXA00834	GR00225	463	2025	DAUNORUBICIN RESISTANCE PROTEIN
151	152	RXA00995	GR00283	1023	283	DAUNORUBICIN RESISTANCE PROTEIN
153	154	RXN00803	VW0009	53858	52629	DAUNORUBICIN RESISTANCE TRANSMEMBRANE PROTEIN
155	156	F RXA00803	GR00214	4560	5162	METHYLENOMYCIN A RESISTANCE PROTEIN
157	158	RXA01407	GR00410	3918	3028	METHYLENOMYCIN A RESISTANCE PROTEIN
159	160	RXA01408	GR00410	4384	4184	METHYLENOMYCIN A RESISTANCE PROTEIN
161	162	RXN01922	VW0020	2031	3182	METHYLENOMYCIN A RESISTANCE PROTEIN
163	164	F RXA01922	GR00552	3	1109	METHYLENOMYCIN A RESISTANCE PROTEIN
165	166	RXA02060	GR00626	1	339	MYCINAMICIN-RESISTANCE PROTEIN MYRA
167	168	RXN01936	VW0127	40116	41387	MACROLIDE-EFFLUX PROTEIN
169	170	F RXA01936	GR00555	9796	8975	NICKEL RESISTANCE PROTEIN
171	172	F RXA01937	GR00555	10246	9821	NICKEL RESISTANCE PROTEIN
173	174	RXN01010	VW0209	3776	4894	QUINOLONE RESISTANCE NORA PROTEIN
175	176	F RXA01010	GR00288	774	4	QUINOLONE RESISTANCE NORA PROTEIN
177	178	RXN03142	VW0136	5754	4612	QUINOLONE RESISTANCE NORA PROTEIN
179	180	F RXA01150	GR00323	3807	2917	QUINOLONE RESISTANCE NORA PROTEIN
181	182	RXN02964	VW0102	7931	6714	QUINOLONE RESISTANCE NORA PROTEIN
183	184	F RXA02116	GR00636	911	6	QUINOLONE RESISTANCE NORA PROTEIN
185	186	RXA00858	GR00233	1680	2147	TELLURIUM RESISTANCE PROTEIN TERC
187	188	RXA02305	GR00663	2921	2070	DAUNOMYCIN C-14 HYDROXYLASE
189	190	RXA00084	GR00013	2367	1543	VIBRIOBACTIN UTILIZATION PROTEIN VIUB
191	192	RXA00843	GR00228	3236	3580	ARSENATE REDUCTASE
193	194	RXA01052	GR00296	3398	3706	MERCURIC REDUCTASE (EC 1.16.1.1)
195	196	RXA01053	GR00296	3772	4191	MERCURIC REDUCTASE (EC 1.16.1.1)
197	198	RXA01054	GR00296	4229	4717	MERCURIC REDUCTASE (EC 1.16.1.1)
199	200	RXN03123	VW0106	808	1245	HEAVY METAL TOLERANCE PROTEIN PRECURSOR
201	202	F RXA00993	GR00282	641	6	HEAVY METAL TOLERANCE PROTEIN PRECURSOR
203	204	RXA01051	GR00296	3298	2690	VANZ PROTEIN, teicoplanin resistance protein
205	206	RXN01873	VW0248	2054	819	Hypothetical Drug Resistance Protein
207	208	F RXA01873	GR00535	855	1946	Hypothetical Drug Resistance Protein
209	210	RXN00034	VW0020	16933	18381	MULTIDRUG RESISTANCE PROTEIN B
211	212	F RXA02273	GR00655	8058	9002	Hypothetical Drug Resistance Protein
213	214	RXN03075	VW0042	2491	3216	Hypothetical Drug Transporter
215	216	F RXA02907	GR10044	1395	2120	Hypothetical Drug Transporter
217	218	RXA00479	GR00119	16290	14101	Hypothetical Drug Transporter
219	220	RXN03124	VW0108	4	963	Hypothetical Drug Transporter
221	222	F RXA01180	GR00336	4	765	Hypothetical Drug Transporter

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
223	224	RXA02586	GR00741	10296	10027	Hypothetical Drug Transporter
225	226	RXA02587	GR00741	12343	10253	Hypothetical Drug Transporter
227	228	RXN03042	VV0018	2440	1835	Hypothetical Drug Transporter
229	230	F RXA02893	GR10035	1841	1236	Hypothetical Drug Transporter
231	232	RXA01616	GR00450	1684	203	MULTIDRUG EFFLUX PROTEIN QACB
233	234	RXA01666	GR00463	2307	3683	MULTIDRUG RESISTANCE PROTEIN
235	236	RXA00062	GR00009	13252	11855	MULTIDRUG RESISTANCE PROTEIN B
237	238	RXA00215	GR00032	13834	15294	MULTIDRUG RESISTANCE PROTEIN B
239	240	RXN03064	VV0038	4892	6223	MULTIDRUG RESISTANCE PROTEIN B
241	242	F RXA00565	GR00151	4892	5884	MULTIDRUG RESISTANCE PROTEIN B
243	244	F RXA02878	GR10016	1837	1481	MULTIDRUG RESISTANCE PROTEIN B
245	246	RXA00648	GR00169	2713	1304	MULTIDRUG RESISTANCE PROTEIN B
247	248	RXN01320	VV0082	13146	11500	MULTIDRUG RESISTANCE PROTEIN B
249	250	F RXA01314	GR00382	744	4	MULTIDRUG RESISTANCE PROTEIN B
251	252	F RXA01320	GR00383	1979	1200	MULTIDRUG RESISTANCE PROTEIN B
253	254	RXN02926	VV0082	11497	9866	MULTIDRUG RESISTANCE PROTEIN B
255	256	F RXA01319	GR00383	1197	4	MULTIDRUG RESISTANCE PROTEIN B
257	258	RXA01578	GR00439	1423	29	MULTIDRUG RESISTANCE PROTEIN B
259	260	RXA02087	GR00629	7076	5730	MULTIDRUG RESISTANCE PROTEIN B
261	262	RXA02088	GR00629	8294	7080	MULTIDRUG RESISTANCE PROTEIN B
263	264	RXA00764	GR00204	3284	2169	MULTIDRUG RESISTANCE PROTEIN B
265	266	RXN03125	VV0108	972	1142	BMRU PROTEIN Bacillus subtilis bmrU, multidrug efflux transporter
267	268	RXN01553	VV0135	25201	26520	Hypothetical Drug Transporter
269	270	RXN00535	VV0219	5155	5871	Hypothetical Drug Permease
271	272	RXN00453	VV0076	1173	3521	Hypothetical Drug Resistance Protein
273	274	RXN00932	VV0171	13120	13593	Hypothetical Drug Transporter
275	276	RXN03022	VV0002	65	511	MULTIDRUG RESISTANCE PROTEIN B
277	278	RXN03151	VV0163	489	4	MYCINAMICIN-RESISTANCE PROTEIN MYRA
279	280	RXN02832	VV0358	547	5	LYSOSTAPHIN IMMUNITY FACTOR
281	282	RXN00165	VV0232	3275	1860	MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL
283	284	RXN01190	VV0169	8992	10338	MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL
285	286	RXN01102	VV0059	6128	4884	QUINOLONE RESISTANCE NORA PROTEIN
287	288	RXN00788	VV0321	3424	3648	CHLORAMPHENICOL RESISTANCE PROTEIN
289	290	RXN02119	VV0102	11242	9602	A201A-RESISTANCE ATP-BINDING PROTEIN
291	292	RXN01605	VV0137	7124	5610	DAUNORUBICIN RESISTANCE TRANSMEMBRANE PROTEIN
293	294	RXN01091	VV0326	567	4	MAZG PROTEIN
295	296	RXS02979	VV0149	2150	2383	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
297	298	RXS02987	VV0234	527	294	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
299	300	RXS03095	VV0057	4056	4424	CADMIUM EFFLUX SYSTEM ACCESSORY PROTEIN HOMOLOG

TABLE 2 - Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moockel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

AF038651	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquininate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element ISJ1831	Vertes et al. "Isolation and characterization of ISJ1831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

E01377	Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937	Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040	Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desethiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041	Desethiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desethiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307	Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376	Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377	Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484	Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108	Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112	Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

		Mutated aspartokinase alpha subunit	
E06827			Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	ilvA	Threonine dehydratase	Moockel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	ilvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H.-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Letten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y.-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthraniolate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)

Table 2 (continued)

M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	accD; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rosol, I. et al. "The <i>Corynebacterium glutamicum</i> accD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIIIM; cgIIIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The <i>Corynebacterium glutamicum</i> cglIIM gene encoding a 5-cytosine in an McrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxido-reductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

Table 2 (continued)

	bioB	Biotin synthase	
U31281			Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)

Table 2 (continued)

	trpL, trpE	Putative leader peptide; anthranilate synthase component 1	
X55994			Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEBS Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)
X66078	cspI	PsI protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PS I, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PS I is similar to the <i>Mycobacterium</i> antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)

Table 2 (continued)

	leuA	Isopropylmalate synthase	
X70959			Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mitrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pla-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)

Table 2 (continued)

	16S rDNA	16S ribosomal RNA	
X82061			Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting 'Arthrobacter aureus C70,'" <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

Table 2 (continued)

X90360	Promoter fragment F22		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361	Promoter fragment F34		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362	Promoter fragment F37		Patek, M. et al. "Promoters from <i>C. glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90363	Promoter fragment F45		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364	Promoter fragment F64		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365	Promoter fragment F75		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366	Promoter fragment PF101		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367	Promoter fragment PF104		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368	Promoter fragment PF109		Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	Ammonium transport system	amt	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	Glycine betaine transport system	betP	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649		orf4	Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	Lysine exporter protein; Lysine export regulator protein	lysE; lysG	Vrjlic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)

Table 2 (continued)

Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Y18059		Attachment site Corynephage 304L	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z29563	thrC	Threonine synthase	
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)

* A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21054							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19350							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19351							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19352							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19353							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19354							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19355							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19356							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21055							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21077							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21553							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21580							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	39101							
<i>Brevibacterium</i>	<i>butanicum</i>	21196							
<i>Brevibacterium</i>	<i>divaricatum</i>	21792	P928						
<i>Brevibacterium</i>	<i>flavum</i>	21474							
<i>Brevibacterium</i>	<i>flavum</i>	21129							
<i>Brevibacterium</i>	<i>flavum</i>	21518							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>flavum</i>			B11472					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>	21128							
<i>Brevibacterium</i>	<i>flavum</i>	21427							
<i>Brevibacterium</i>	<i>flavum</i>	21475							
<i>Brevibacterium</i>	<i>flavum</i>	21517							
<i>Brevibacterium</i>	<i>flavum</i>	21528							
<i>Brevibacterium</i>	<i>flavum</i>	21529							
<i>Brevibacterium</i>	<i>flavum</i>			B11477					
<i>Brevibacterium</i>	<i>flavum</i>			B11478					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>healii</i>	15527							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21004							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21089							
<i>Brevibacterium</i>	<i>ketosoreductum</i>	21914							
<i>Brevibacterium</i>	<i>lactofermentum</i>				70				
<i>Brevibacterium</i>	<i>lactofermentum</i>				74				
<i>Brevibacterium</i>	<i>lactofermentum</i>				77				
<i>Brevibacterium</i>	<i>lactofermentum</i>	21798							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21799							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21800							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21801							
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11470					
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11471					

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CEGT	NCIMB	CBS	NCIC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

TABLE 4: ALIGNMENT RESULTS

<u>ID #</u>	<u>length</u> (NT)	<u>Genbank Hit</u>	<u>Length</u>	<u>Accession</u>	<u>Name of Genbank Hit</u>	<u>Source of Genbank Hit</u>	<u>% homology</u> (GAP)	<u>Date of</u> <u>Deposit</u>
rx00062	1521	GB_HTG2:AC007366	185001	AC007366	Homo sapiens clone NH0501G22, *** SEQUENCING IN PROGRESS *** , 3 unordered pieces.	Homo sapiens	39,080	5-Jun-99
rx00084	948	GB_PR3:HSU80741	912	U80741	Homo sapiens CAGH44 mRNA, partial cds.	Homo sapiens	39,264	18-DEC-1997
		GB_PL1:BNDNATRNA	1732	X89901	B.nigra DNA for tRNA like gene.	Brassica nigra	36,725	6-Feb-97
		GB_PR3:HSU80741	912	U80741	Homo sapiens CAGH44 mRNA, partial cds.	Homo sapiens	38,957	18-DEC-1997
rx00109	735	GB_GSS9:AQ163721	388	AQ163721	HS_2245_A1_F07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2245 Col=13 Row=K, genomic survey sequence.	Homo sapiens	45,066	16-OCT-1998
		GB_HTG4:AC007054	171979	AC007054	Drosophila melanogaster chromosome 2 clone BACR45O18 (D527) RPCI-98	Drosophila melanogaster	36,589	13-OCT-1999
					45.O.18 map 41E-41E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 13 unordered pieces.			
		GB_HTG4:AC007054	171979	AC007054	Drosophila melanogaster chromosome 2 clone BACR45O18 (D527) RPCI-98	Drosophila melanogaster	36,589	13-OCT-1999
					45.O.18 map 41E-41E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 13 unordered pieces.			
rx00215	1449	GB_BA1:SC9C7	31360	AL035161	Streptomyces coelicolor cosmid 9C7.	Streptomyces coelicolor	44,444	12-Jan-99
		GB_BA1:SCE94	38532	AL049628	Streptomyces coelicolor cosmid E94.	Streptomyces coelicolor	36,313	12-Apr-99
		GB_BA2:AF110185	20302	AF110185	Burkholderia pseudomallei strain 1026b DbhB (dbhB), general secretory pathway protein D (gspD), general secretory pathway protein E (gspE), general secretory pathway protein F (gspF), GspC (gspC), general secretory pathway protein G (gspG), general secretory pathway protein H (gspH), general secretory pathway protein I (gspI), general secretory pathway protein J (gspJ), general secretory pathway protein K (gspK), general secretory pathway protein L (gspL), general secretory pathway protein M (gspM), and general secretory pathway protein N (gspN) genes, complete cds; and unknown genes.	Burkholderia pseudomallei	44,159	2-Aug-99
rx00289	1299	GB_EST6:N80167	384	N80167	za65g02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:297458 3', mRNA sequence.	Homo sapiens	40,420	29-MAR-1996
		GB_STS:G37084	384	G37084	SHGC-56832 Human Homo sapiens STS genomic, sequence tagged site.	Homo sapiens	40,420	30-MAR-1998
		GB_STS:G37084	384	G37084	SHGC-56832 Human Homo sapiens STS genomic, sequence tagged site.	Homo sapiens	40,420	30-MAR-1998
rx00404	2439	GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	60,271	17-Jun-98
		GB_BA1:ECU82598	136742	U82598	Escherichia coli genomic sequence of minutes 9 to 12.	Escherichia coli	54,256	15-Jan-97
		GB_BA2:AE000165	12003	AE000165	Escherichia coli K-12 MG1655 section 55 of 400 of the complete genome.	Escherichia coli	54,256	12-Nov-98
rx00479	2313	GB_BA1:SCF43A	35437	AL096837	Streptomyces coelicolor cosmid F43A.	Streptomyces coelicolor	36,245	13-Jul-99
					A3(2)			
		GB_GSS2:CNS015U4	1036	AL105910	Drosophila melanogaster genome survey sequence SP6 end of BAC BACN14G08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.	Drosophila melanogaster	37,573	26-Jul-99

Table 4 (continued)

GB_PR3:HSA494O16	50502	AL117328	Human DNA sequence from clone 494O16 on chromosome 22, complete sequence.	Homo sapiens	36,475	23-Nov-99
GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome, segment 145/162.	Mycobacterium tuberculosis	40,250	17-Jun-98
GB_BA2:AF079544	817	AF079544	Mycobacterium avium GroESL operon, partial sequence.	Mycobacterium avium	64,439	16-Aug-98
GB_BA1:MTGROEOP	2987	X60350	M.tuberculosis groE gene for KCS and 10-kDa products.	Mycobacterium tuberculosis	62,857	23-Apr-92
GB_GSS10:AQ199703	439	AQ199703	RPC111-46O13. TJ RPC1-11 Homo sapiens genomic clone RPC1-11-46O13, genomic survey sequence.	Homo sapiens	42,657	20-Apr-99
GB_PR2:AC002127	144165	AC002127	Human BAC clone RG305H12 from 7q21, complete sequence.	Homo sapiens	37,052	27-MAY-1997
GB_STS:G51234	439	G51234	SHGC-80708 Human Homo sapiens STS genomic, sequence tagged site.	Homo sapiens	42,657	25-Jun-99
GB_BA1:MTCY441	35187	Z80225	Mycobacterium tuberculosis H37Rv complete genome, segment 118/162.	Mycobacterium tuberculosis	56,183	18-Jun-98
GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	37,217	10-DEC-1996
GB_BA1:BSUB0014	213420	Z99117	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.	Bacillus subtilis	36,553	26-Nov-97
GB_BA2:AF069070	2776	AF069070	Endosymbiont of Onchocerca volvulus catalase gene, complete cds.	Endosymbiont of Onchocerca volvulus	55,396	25-Nov-98
GB_BA1:OVCAT	1845	X82176	Onchocerca volvulus endobacterial mRNA for catalase.	Onchocerca volvulus	55,396	26-Nov-98
GB_BA1:SC2G5	38404	AL035478	Streptomyces coelicolor cosmid 2G5.	Streptomyces coelicolor	39,530	11-Jun-99
GB_HTG1:HS74O16	169401	AL110119	Homo sapiens chromosome 21 clone RPCIP704O1674 map 21q21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	36,327	27-Aug-99
GB_HTG1:HS74O16	169401	AL110119	Homo sapiens chromosome 21 clone RPCIP704O1674 map 21q21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	36,327	27-Aug-99
GB_HTG1:HS74O16	169401	AL110119	Homo sapiens chromosome 21 clone RPCIP704O1674 map 21q21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	35,119	27-Aug-99
GB_EST36:A1898007	609	A1898007	EST267450 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED31K22, mRNA sequence.	Lycopersicon esculentum	34,323	27-Jul-99
GB_BA2:PAU93274	8008	U93274	Pseudomonas aeruginosa YafE (yafE), LeuB (leuB), Asd (asd), FimV (fimV), and HisT (hisT) genes, complete cds; TrpF (trpF) gene, partial cds; and unknown	Pseudomonas aeruginosa	35,895	23-Jun-98
GB_BA2:PAU93274	8008	U93274	Pseudomonas aeruginosa YafE (yafE), LeuB (leuB), Asd (asd), FimV (fimV), and HisT (hisT) genes, complete cds; TrpF (trpF) gene, partial cds; and unknown	Pseudomonas aeruginosa	41,417	23-Jun-98
GB_IN2:CELH34C03	27748	AF100662	Caenorhabditis elegans cosmid H34C03.	Caenorhabditis elegans	34,152	28-OCT-1998
GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING IN PROGRESS *** 33 unordered pieces.	Homo sapiens	37,472	24-Jun-99
GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING IN PROGRESS *** 33 unordered pieces.	Homo sapiens	37,472	24-Jun-99

Table 4 (continued)

rx00810 324	GB_BA1:MTY15C10	33050	Z95436	Myobacterium tuberculosis H37Rv complete genome; segment 154/162.	Myobacterium tuberculosis	34,615	17-Jun-98
rx00829 2463	GB_BA1:MLCB2548	38916	AL023093	Myobacterium leprae cosmid B2548.	Myobacterium leprae	34,615	27-Aug-99
	GB_BA1:ECOUW76	225419	U00039	E. coli chromosomal region from 76.0 to 81.5 minutes.	Escherichia coli	52,997	7-Nov-96
	GB_BA1:SC5C7	41906	AL031515	Streptomyces coelicolor cosmid 5C7.	Streptomyces coelicolor	65,269	7-Sep-98
	GB_BA1:SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor	37,490	24-MAY-1999
rx00843 468	GB_BA1:STMDRRRC	3374	L76359	Streptomyces peucetius daunorubicin resistance protein (dfrC) gene, complete	Streptomyces peucetius	55,279	24-DEC-1996
	GB_BA1:MTCY9C4	15916	Z77250	Myobacterium tuberculosis H37Rv complete genome; segment 113/162.	Myobacterium tuberculosis	40,000	17-Jun-98
	GB_BA1:MTCY9C4	15916	Z77250	Myobacterium tuberculosis H37Rv complete genome; segment 113/162.	Myobacterium tuberculosis	37,773	17-Jun-98
rx00858 568	GB_BA1:SCC54	30753	AL035591	Streptomyces coelicolor cosmid C54.	Streptomyces coelicolor	39,602	11-Jun-99
	GB_EST18:N96610	547	N96610	21285 Lambda-PRL1 Arabidopsis thaliana cDNA clone F10G3T7, mRNA	Arabidopsis thaliana	37,801	5-Jan-98
rx00886 1269	GB_EST18:T45493	436	T45493	8756 Lambda-PRL2 Arabidopsis thaliana cDNA clone 133C14T7, mRNA	Arabidopsis thaliana	34,194	4-Aug-98
	GB_BA1:SYCSLLH	132106	D64006	Synechocystis sp. PCC6803 complete genome, 2527, 3138604-3270709.	Synechocystis sp.	37,459	13-Feb-99
	GB_BA1:SCDNAJ	5611	X77458	S. coelicolor dnaK, grpE and dnaJ genes.	Streptomyces coelicolor	49,744	21-Nov-96
	GB_BA1:STMDNAK	4648	L46700	Streptomyces coelicolor (strain A3(2)) dnaK operon encoding molecular chaperones (dnaK, dnaJ), grpE and hspR genes, complete cds's.	Streptomyces coelicolor	49,583	22-Nov-96
	GB_BA2:ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	Escherichia coli	38,314	U18997
rx00900 975	GB_BA2:ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	Escherichia coli	37,759	U18997
	GB_BA2:AE000393	10516	AE000393	Escherichia coli K-12 MG1655 section 283 of 400 of the complete genome.	Escherichia coli	38,314	12-Nov-98
	GB_HTG3:AC010757	175571	AC010757	Homo sapiens chromosome 18 clone 128_C_18 map 18, *** SEQUENCING IN PROGRESS ***; 20 unordered pieces.	Homo sapiens	34,857	22-Sep-99
	GB_HTG3:AC010757	175571	AC010757	Homo sapiens chromosome 18 clone 128_C_18 map 18, *** SEQUENCING IN PROGRESS ***; 20 unordered pieces.	Homo sapiens	34,857	22-Sep-99
rx00981 753	GB_HTG3:AC011283	87295	AC011283	Homo sapiens clone MS2016A09, *** SEQUENCING IN PROGRESS ***; 1 unordered pieces.	Homo sapiens	35,448	07-OCT-1999
	GB_OV:GGA245664	512	AJ245664	Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene).	Gallus gallus	37,538	28-Sep-99
	GB_PL2:AC007887	159434	AC007887	Genomic sequence for Arabidopsis thaliana BAC F1504 from chromosome 1, complete sequence.	Arabidopsis thaliana	37,600	04-OCT-1999
	GB_GSS1:CNS00RNW542	AL087338	AL087338	Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	41,264	28-Jun-99
rx00995 864	GB_EST29:AI553951	450	AI553951	te54d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090497 3' similar to gb:X02067 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN);, mRNA sequence.	Homo sapiens	42,627	13-Apr-99
	GB_PR3:AC003029	139166	AC003029	Homo sapiens Chromosome 12q24 PAC RPC13-462E2 (Roswell Park Cancer Institute Human PAC library) complete sequence.	Homo sapiens	38,915	17-Sep-98
rx00996 864	GB_BA1:EAY14603	4479	Y14603	Erwinia amylovora srIA, srIE, srIB, srID, srIM and srIR genes.	Erwinia amylovora	37,694	6-Jan-98
	GB_BA2:AE001001	10730	AE001001	Archaeoglobus fulgidus section 106 of 172 of the complete genome.	Archaeoglobus fulgidus	41,078	15-DEC-1997
	GB_EST30:AV018764	242	AV018764	AV018764 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1190006M16, mRNA sequence.	Mus musculus	39,669	28-Aug-99

Table 4 (continued)

GB_GSS3:B24189	377	B24189	F19E16TF IGF Arabidopsis thaliana genomic clone F19E16, genomic survey sequence.	Arabidopsis thaliana	44,385	10-OCT-1997
GB_OV:AF007068	356	AF007068	Coturnix coturnix arylalkylamine N-acetyltransferase mRNA, partial cds.	Coturnix coturnix	46,629	12-Jul-97
GB_EST10:AA166324	514	AA166324	ms50c09.r1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus cDNA clone IMAGE:614992 5' similar to SW:NEST_RAT P21263 NESTIN.1; mRNA sequence.	Mus musculus	38,677	19-DEC-1996
GB_EST7:W89968	46	W89968	mf64g11.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:419108 5' similar to SW:NEST_RAT P21263 NESTIN. [1]; mRNA sequence.	Mus musculus	58,696	12-Sep-96
GB_GSS12:AQ381423	579	AQ381423	RPC111-135F10.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-135F10, genomic survey sequence.	Homo sapiens	37,651	21-MAY-1999
GB_HTG6:AC010901	206121	AC010901	Homo sapiens clone RP11-544J22, WORKING DRAFT SEQUENCE, 1 unordered pieces.	Homo sapiens	36,011	04-DEC-1999
GB_GSS5:AQ746932	837	AQ746932	HS_5538_A1_A11_T7A RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=1114 Col=21 Row=A, genomic survey sequence.	Homo sapiens	38,640	19-Jul-99
GB_IN1:CELC13D9	43487	AF016420	Caenorhabditis elegans cosmid C13D9.	Caenorhabditis elegans	39,344	2-Aug-97
GB_IN1:CELC13D9	43487	AF016420	Caenorhabditis elegans cosmid C13D9.	Caenorhabditis elegans	38,780	2-Aug-97
GB_OV:CHKMAFG1	1316	D28601	Chicken novel maf-related gene mafG encoding bZip nuclear protein MafG, promoter region and exon 1.	Gallus gallus	39,205	7-Feb-99
GB_HTG6:AC010765	146468	AC010765	Homo sapiens clone RP11-115N6, *** SEQUENCING IN PROGRESS ***; 26 unordered pieces.	Homo sapiens	32,961	07-DEC-1999
GB_HTG6:AC010765	146468	AC010765	Homo sapiens clone RP11-115N6, *** SEQUENCING IN PROGRESS ***; 26 unordered pieces.	Homo sapiens	38,476	07-DEC-1999
GB_PL1:PHNPNGLP	962	D45425	Pharbitis nil mRNA for Pharbitis nil Germin-like protein precursor, complete cds.	Ipomoea nil	42,925	10-Feb-99
GB_HTG2:HSJ402N21	170302	AL049553	Homo sapiens chromosome 6 clone RP3-402N21 map p21.1-21.31, ***SEQUENCING IN PROGRESS***, in unordered pieces.	Homo sapiens	36,825	03-DEC-1999
GB_HTG2:HSJ402N21	170302	AL049553	Homo sapiens chromosome 6 clone RP3-402N21 map p21.1-21.31, ***SEQUENCING IN PROGRESS***, in unordered pieces.	Homo sapiens	36,825	03-DEC-1999
GB_IN2:CELF18A12	29784	AF016688	Caenorhabditis elegans cosmid F18A12.	Caenorhabditis elegans	35,794	08-OCT-1999
GB_IN2:CELF18A12	29784	AF016688	Caenorhabditis elegans cosmid F18A12.	Caenorhabditis elegans	40,625	08-OCT-1999
GB_RO:MUSMCFTR	6304	M60493	Mouse cystic fibrosis transmembrane conductance regulator (CFTR) mRNA, complete cds.	Mus musculus	37,793	10-Jun-94
GB_BA2:AF031037	1472	AF031037	Neisseria meningitidis chloramphenicol acetyltransferase gene, complete cds.	Neisseria meningitidis	35,014	21-Apr-98
GB_HTG1:PFMAL13PA80518	AL109815	AL109815	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS***, in unordered pieces.	Plasmodium falciparum	17,697	19-Aug-99
GB_HTG1:PFMAL13PA80518	AL109815	AL109815	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS***, in unordered pieces.	Plasmodium falciparum	17,697	19-Aug-99
GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	Homo sapiens	38,195	14-Aug-98
GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	Homo sapiens	36,611	14-Aug-98
GB_HTG3:AC011500_1300851	AC011500	AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS***, 246 unordered pieces.	Homo sapiens	36,446	AC011500
GB_HTG3:AC010831	70233	AC010831	Homo sapiens clone 6_L_24, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,764	23-Sep-99

Table 4 (continued)

GB_HTG3:AC010831	70233	AC010831	Homo sapiens clone 6_L_24, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,764	23-Sep-99
GB_PR3:AC004058	38400	AC004058	Homo sapiens chromosome 4 clone B241P19 map 4q25, complete sequence.	Homo sapiens	40,778	30-Sep-98
GB_PR4:AF152365	246546	AF152365	Homo sapiens constitutive fragile region FRA3B sequence.	Homo sapiens	41,234	1-Aug-99
GB_HTG3:AC007890	121256	AC007890	Drosophila melanogaster chromosome 3 clone BACR02G21 (D722) RPCI-98	Drosophila melanogaster	39,432	3-Sep-99
			02.G.21 map 90E-91A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 89 unordered pieces.			
GB_HTG3:AC007890	121256	AC007890	Drosophila melanogaster chromosome 3 clone BACR02G21 (D722) RPCI-98	Drosophila melanogaster	39,432	3-Sep-99
			02.G.21 map 90E-91A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 89 unordered pieces.			
GB_BA1:BSUB0015	218410	Z99118	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.	Bacillus subtilis	38,201	26-Nov-97
GB_HTG2:AC008260	107439	AC008260	Drosophila melanogaster chromosome 2 clone BACR13J10 (D924) RPCI-98	Drosophila melanogaster	38,302	2-Aug-99
			13.J.10 map 47B-47C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 82 unordered pieces.			
GB_HTG2:AC008260	107439	AC008260	Drosophila melanogaster chromosome 2 clone BACR13J10 (D924) RPCI-98	Drosophila melanogaster	38,302	2-Aug-99
			13.J.10 map 47B-47C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 82 unordered pieces.			
GB_PR4:AF111170	148083	AF111170	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene.	Homo sapiens	37,873	14-Jul-99
GB_PR4:AF111170	148083	AF111170	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene.	Homo sapiens	40,220	14-Jul-99
GB_BA1:AEV13732	6740	Y13732	Alcaligenes eutrophus genes for ureases, ureD1, ureD2, ureA, ureB, and ORF1, ORF2.	Ralstonia eutropha	42,960	23-Sep-97
GB_BA2:AF088857	2908	AF088857	Vogesella indigofera indigoidine biosynthesis regulatory locus, complete	Vogesella indigofera	37,626	10-Sep-99
GB_IN1:CEM04D8	21552	Z32682	Caenorhabditis elegans cosmid M04D8, complete sequence.	Caenorhabditis elegans	37,237	23-Nov-98
GB_EST25:AI281910	276	AI281910	qt82d04.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:1961767 3', mRNA sequence.	Homo sapiens	38,406	21-DEC-1998
GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	99,933	9-Apr-97
GB_HTG3:AC009213	114735	AC009213	Drosophila melanogaster chromosome 3 clone BACR09F18 (D812) RPCI-98	Drosophila melanogaster	36,111	23-Aug-99
			09.F.18 map 98D-98D strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 109 unordered pieces.			
GB_HTG3:AC009213	114735	AC009213	Drosophila melanogaster chromosome 3 clone BACR09F18 (D812) RPCI-98	Drosophila melanogaster	36,111	23-Aug-99
			09.F.18 map 98D-98D strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 109 unordered pieces.			
GB_PL1:AB017159	1859	AB017159	Daucus carota mRNA for citrate synthase, complete cds.	Daucus carota	39,537	01-MAY-1999
GB_PR1:HUMGNOS48	23142	D26607	Homo sapiens endothelial nitric oxide synthase gene, complete cds.	Homo sapiens	36,419	13-Jul-99
GB_HTG3:AC011234	154754	AC011234	Homo sapiens clone NH0166D23, *** SEQUENCING IN PROGRESS***, 7 unordered pieces.	Homo sapiens	36,317	04-OCT-1999
GB_HTG3:AC009450	124337	AC009450	Homo sapiens chromosome 9 clone 30_C_23 map 9, *** SEQUENCING IN PROGRESS***, 20 unordered pieces.	Homo sapiens	35,303	22-Aug-99
GB_HTG3:AC009450	124337	AC009450	Homo sapiens chromosome 9 clone 30_C_23 map 9, *** SEQUENCING IN PROGRESS***, 20 unordered pieces.	Homo sapiens	35,303	22-Aug-99
GB_HTG3:AC009919	134724	AC009919	Homo sapiens clone 115_I_23, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,409	8-Sep-99
GB_BA1:ECONUC	1676	M84026	E.coli protein p7 (neu C) gene, complete cds.	Escherichia coli	35,189	26-Apr-93

Table 4 (continued)

GB_HTG2:AC007853	116280	AC007853	Drosophila melanogaster chromosome 3 clone BACR03L02 (D766) RPCI-98 03.L.2 map 96B-96C strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 80 unordered pieces.	Drosophila melanogaster	34,365	2-Aug-99	
GB_HTG2:AC007853	116280	AC007853	Drosophila melanogaster chromosome 3 clone BACR03L02 (D766) RPCI-98 03.L.2 map 96B-96C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 80 unordered pieces.	Drosophila melanogaster	34,365	2-Aug-99	
GB_HTG4:AC010037	166249	AC010037	Drosophila melanogaster chromosome 3LJ66B6 clone RPCI98-6E4, *** SEQUENCING IN PROGRESS *** , 52 unordered pieces.	Drosophila melanogaster	38,534	16-OCT-1999	
GB_HTG4:AC010037	166249	AC010037	Drosophila melanogaster chromosome 3LJ66B6 clone RPCI98-6E4, *** SEQUENCING IN PROGRESS *** , 52 unordered pieces.	Drosophila melanogaster	38,534	16-OCT-1999	
GB_PR4:AC005552	167228	AC005552	Homo sapiens chromosome 17, clone hRPK.212_E_8, complete sequence.	Homo sapiens	36,249	26-Nov-98	
GB_PR1:HS169C8F	245	Z57239	H.sapiens CpG island DNA genomic Mse1 fragment, clone 169c8, forward read cpg169c8.f11a.	Homo sapiens	45,679	18-OCT-1995	
GB_BA1:SERATTBXIS	3255	L11597	Saccharopolyspora erythraea excisionase (xis) gene, integrase (int) gene, complete cds's and attB site.	Saccharopolyspora erythraea	36,232	6-Jul-94	
GB_EST7:W97557	267	W97557	mf98a09.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:422296 5', mRNA sequence.	Mus musculus	42,969	16-Jul-96	
rx02087 1470	GB_PR3:AC005544	169045	AC005544	Homo sapiens chromosome 17, clone hRPK.349_A_8, complete sequence.	Homo sapiens	35,724	25-Sep-98
	GB_PL1:ATF20B18	104738	AL049483	Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18 (ESSA project).	Arabidopsis thaliana	35,890	24-MAR-1999
rx02088 1338	GB_PL2:ATT25K17	89904	AL049171	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project).	Arabidopsis thaliana	38,128	27-Aug-99
	GB_HTG3:AC008697	167932	AC008697	Homo sapiens chromosome 5 clone CIT978SKB_70D3, *** SEQUENCING IN PROGRESS *** , 54 unordered pieces.	Homo sapiens	36,662	3-Aug-99
	GB_HTG3:AC008697	167932	AC008697	Homo sapiens chromosome 5 clone CIT978SKB_70D3, *** SEQUENCING IN PROGRESS *** , 54 unordered pieces.	Homo sapiens	36,662	3-Aug-99
	GB_HTG3:AC008703	213971	AC008703	Homo sapiens chromosome 5 clone CIT978SKB_76P12, *** SEQUENCING IN PROGRESS *** , 54 unordered pieces.	Homo sapiens	34,768	3-Aug-99
rx02159 636	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,843	1-Jul-98
	GB_BA2:AF031518	2045	AF031518	Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.	Corynebacterium glutamicum	88,679	5-Jan-99
	GB_BA2:AF041436	516	AF041436	Corynebacterium glutamicum arginine repressor (argR) gene, complete cds.	Corynebacterium glutamicum	100,000	5-Jan-99
rx02184 504	GB_BA1:BSZ92953	8164	Z92953	B.subtilis yws[A,B,C] genes and rbs[A,C,D,K,R] genes.	Bacillus subtilis	38,951	24-Jun-98
	GB_EST36:A1878071	593	A1878071	fc57a12.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to TR:Q13151 Q13151 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A0 ;, mRNA sequence.	Danio rerio	36,774	21-Jul-99

Table 4 (continued)

GB_EST37:A1958166	641	A1958166	fc91f01.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to TR:Q13151 Q13151 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A0 ; mRNA sequence.	Danio rerio	36,774	20-Aug-99
GB_PR3:HSA494O16	50502	AL117328	Human DNA sequence from clone 494O16 on chromosome 22, complete sequence.	Homo sapiens	38,648	23-Nov-99
GB_HTG2:AC008161	158440	AC008161	Mus musculus clone 182_H_5, *** SEQUENCING IN PROGRESS ***; 29 unordered pieces.	Mus musculus	35,938	28-Jul-99
GB_HTG2:AC008161	158440	AC008161	Mus musculus clone 182_H_5, *** SEQUENCING IN PROGRESS ***; 29 unordered pieces.	Mus musculus	35,938	28-Jul-99
GB_EST4:H16949	465	H16949	ym34a11.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:50010 5'; Homo sapiens mRNA sequence.	Homo sapiens	38,267	29-Jun-95
GB_EST4:H16949	465	H16949	ym34a11.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:50010 5'; Homo sapiens mRNA sequence.	Homo sapiens	36,552	29-Jun-95
GB_IN1:CELC41A3	37149	U41541	Caenorhabditis elegans cosmid C41A3.	Caenorhabditis elegans	41,678	08-DEC-1995
GB_EST33:AV080151	236	AV080151	AV080151 Mus musculus stomach C57BL/6J adult Mus musculus cDNA clone 2210413B04, mRNA sequence.	Mus musculus	43,348	25-Jun-99
GB_GSS5:AQ766877	545	AQ766877	HS_2017_B2_B08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2017 Col=16 Row=D, genomic survey sequence.	Homo sapiens	35,568	28-Jul-99
GB_HTG2:AC005959	127587	AC005959	Homo sapiens, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Homo sapiens	40,310	11-Nov-98
GB_HTG2:AC005959	127587	AC005959	Homo sapiens, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Homo sapiens	40,310	11-Nov-98
GB_IN1:BRPTUBBA	4571	M36380	B.pahangi beta-tubulin gene, complete cds.	Brugia pahangi	37,703	26-Apr-93
GB_RO:MUSPAFR	1140	D50872	Mouse gene for platelet activating factor receptor, complete cds.	Mus musculus	38,420	10-Feb-99
GB_PR3:HUMARL1A	1008	L28997	Homo sapiens ARL1 mRNA, complete cds.	Homo sapiens	42,188	13-Jan-95
GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	42,000	27-Aug-99
GB_EST4:H35255	407	H35255	EST111890 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone RPNCO03, mRNA sequence.	Rattus sp.	39,098	2-Apr-98
GB_HTG1:HS791K14	155318	AL035685	Homo sapiens chromosome 20 clone RP4-791K14, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	39,456	23-Nov-99
GB_HTG1:HS791K14	155318	AL035685	Homo sapiens chromosome 20 clone RP4-791K14, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	39,456	23-Nov-99
GB_BA2:AF036166	895	AF036166	Xanthomonas campestris organic hydroperoxide resistance protein (ohr) gene, complete cds.	Xanthomonas campestris	49,369	19-MAY-1998
GB_EST5:N25122	620	N25122	yx19d10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262195 5', mRNA sequence.	Homo sapiens	35,417	28-DEC-1995
GB_EST5:N25122	620	N25122	yx19d10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262195 5', mRNA sequence.	Homo sapiens	37,172	28-DEC-1995
GB_BA2:DP093358	1267	U93358	Deinococcus proteolyticus 40 kDa heat shock chaperone protein (dnaJ) gene, complete cds.	Deinococcus proteolyticus	42,115	17-Jan-98
GB_EST30:A1658096	343	A1658096	fc14c09.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:DNJ2_HUMAN P31689 DNAJ PROTEIN HOMOLOG 2.; mRNA sequence.	Danio rerio	52,059	06-MAY-1999
GB_EST37:A1959242	545	A1959242	fd25h11.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:DNJ2_HUMAN P31689 DNAJ PROTEIN HOMOLOG 2.; mRNA sequence.	Danio rerio	45,438	20-Aug-99

Table 4 (continued)

rx02542 777	EM_PAT:E10832	1856	E10832	DNA encoding Dnak protein which is one of heat shock protein from	Corynebacterium glutamicum	99,000	08-OCT-1997 (Rel. 52, Created) 30-Apr-99
rx02543 1977	GB_EST24:Z82017	396	Z82017	SSZ82017 Porcine small intestine cDNA library Sus scrofa cDNA clone c12c06 5' similar to eukaryotic initiation factor 4 gamma, mRNA sequence.	Sus scrofa	37,067	14-OCT-1993
	GB_OM:CATERYTHRO681		L10606	Cat erythropoietin mRNA, 3' end.	Felis catus	39,409	08-OCT-1997
	EM_PAT:E10832	1856	E10832	DNA encoding Dnak protein which is one of heat shock protein from	Corynebacterium glutamicum	97,306	(Rel. 52, Created) 23-Apr-92
rx02586 393	GB_BA1:MPHSP70	2179	X59437	M paratuberculosis gene for 70 kD heat shock protein.	Mycobacterium avium	73,404	17-Jun-98
	GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	subsp. paratuberculosis	72,028	30-Jan-99
	GB_IN2:AC006472	156362	AC006472	Drosophila melanogaster, chromosome 2R, region 45E1-46A2, BAC clone BACR48G21, complete sequence.	Drosophila melanogaster	37,958	16-OCT-1999
rx02587 2214	GB_HTG4:AC010020	106541	AC010020	Drosophila melanogaster chromosome 3L/66D10 clone RPC198-2613, *** SEQUENCING IN PROGRESS ***	Drosophila melanogaster	37,333	16-OCT-1999
	GB_HTG4:AC010020	106541	AC010020	Drosophila melanogaster chromosome 3L/66D10 clone RPC198-2613, *** SEQUENCING IN PROGRESS ***	Drosophila melanogaster	37,333	16-OCT-1999
	GB_BA1:MLCL622	42498	Z95398	Mycobacterium leprae cosmid L622.	Mycobacterium leprae	39,848	24-Jun-97
rx03217 331	GB_RO:AF074879	3316	AF074879	Rattus norvegicus testis-specific protein TSPY gene, complete cds.	Rattus norvegicus	35,830	6-Jul-99
	GB_RO:RNJ001380	2641	AJ001380	Rattus norvegicus Tspy partial genomic sequence, exons 1-6.	Rattus norvegicus	37,702	29-Jun-98
	GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	37,888	27-Aug-99
rx03217 331	GB_HTG2:HSJ662M14	174772	AL079336	Homo sapiens chromosome 20 clone RP4-662M14, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,420	4-Feb-00
	GB_HTG2:HSJ662M14	174772	AL079336	Homo sapiens chromosome 20 clone RP4-662M14, *** SEQUENCING IN PROGRESS ***	Homo sapiens	35,962	4-Feb-00

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

5 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
10 2.46 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \times \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \times 4\text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \times 6\text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \times 6\text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \times 2\text{H}_2\text{O}$, 500 mg/l complexing agent
15 (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca. 18 h at 37°C. The DNA was purified by
25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

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Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (see e.g., Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

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Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see e.g., Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

25

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

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the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such

5 strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous

10 plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in

15 Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903

20 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597,

25 Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vector into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by

30 protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.*

(1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

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(1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or
5 ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt,
10 molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuic acid, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic
15 acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A
20 Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if
25 necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to
30 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

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is also possible to maintain a constant culture pH through the addition of NaOH or NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes.

For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2.5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

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Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be

found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's *Encyclopedia of Industrial Chemistry* (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,

Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 5 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, 10 F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to 15 determine the overall yield, production, and/or efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. 20 Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

25 Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and 30 the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

EXAMPLE 11: Cloning of a *Corynebacterium glutamicum* Gene Involved in Lincomycin Resistance Using a Reporter Gene Approach

30

A. Identification of the Gene Encoding the LMRB Protein

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Plasmid pSL130 was constructed by ligation of the *aceB* promoter region (paceB) of *C. glutamicum* (Kim, H.J. *et al.* (1997) *J. Microbiol. Biotechnol.* 7: 287-292) into the polylinker of the lac operon fusion vector pRS415, which lacks a promoter (Simon, R.W. *et al.* (1987) *Gene* 53: 85-96). Plasmid pSL145 was constructed by
5 ligating the resulting paceB-lac region into the *E. coli* cloning vector pACYC184. *E. coli* DH5 α F' was transformed with pSL145 and the resulting strain was used as a host for screening of a genomic *C. glutamicum* library (in pSL109).

Transformants were screened by growth on agar medium containing 5-bromo-4-chloro-3-indolyl-beta-D-galactopyranoside (X-Gal). A white colony, containing DNA
10 influencing lacZ expression, was selected for further analysis. This clone was found to contain a 4 kB fragment from the gene library. Subclones were constructed in pSL109 and a subclone which retained the white phenotype on X-Gal plates was identified. This subclone was found to contain a 2.6 kB BamHI-XhoI fragment (plasmid pSL149-5). The fragment was sequenced and identified as a membrane protein-encoding gene
15 (LMRB gene).

The 1442 nucleotides of the coding sequence of the LMRB gene encode a polypeptide of 481 amino acid residues with a high percentage of hydrophobic amino acids. A Genbank search determined that the LMRB protein is 40% identical to the protein product of the *lmrB* gene from *Bacillus subtilis* (Genbank Accession AL009126,
20 TREMBL Accession P94422), as determined using a CLUSTAL W analysis (using standard parameters).

The LMRN protein contains a sequence pattern: 158-A-P-A-L-G-P-T-L-S-G-167 (SEQ ID NO:301), which resembles the known multi-drug-resistance-protein consensus motif G-X-X-X-G-P-X-X-G-G (SEQ ID NO:302) (Paulsen, I.T., and Skurray, R.A.
25 (1993) *Gene* 124: 1-11). Therefore, the LMRB protein was classified as a drug resistance protein.

B. In vivo Analysis of lmrB Function

The *lmrB* gene was overexpressed in *C. glutamicum* ASO19E12 (Kim, H.J. *et al.* (1997) *J. Microbiol. Biotechnol.* 7: 287-292) using the plasmid pSL149-5, described
30 above.

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Disruption of the LMRB gene was accomplished by use of the vector pSL18-lmrB. This vector was constructed as follows: an internal fragment of the LMRB gene was amplified by PCR under standard conditions using primers 5'-

CTCCAGGATTGCTCCGAAGG-3' (SEQ ID NO:303) and 5'-

- 5 CACAGTGGTTGACCACTGGC-3' (SEQ ID NO:304). The resulting PCR product was treated with T7 DNA polymerase and T7 polynucleotide kinase, and was cloned into the SmaI site of plasmid pSL18 (Kim, Y.H. and H.-S. Lee (1996) *J. Microbiol. Biotechnol.* 6: 315-320). The disruption of the LMRB gene in *C. glutamicum* ASO19E12 was performed by conjugation, as previously described (Schwarzer and
10 Puhler (1991) *Bio/Technology* 9:84-87).

C. glutamicum cells transformed with pSL149-5 displayed similar resistances as untransformed cells against erythromycin, penicillin G, tetracycline, chloramphenicol, spectinomycin, nalidixic acid, gentamycin, streptomycin, ethidium bromide, carbonyl cyanide m-chlorophenylhydrazone (CCCP), and sodium dodecyl sulfate. Significant
15 differences were observed, however, in the resistance of transformed and untransformed cells to lincomycin.

LMRB-overexpressing *C. glutamicum* cells were found to be able to grow in the presence of 20 µg/ml lincomycin. In contrast, cells which do not overexpress LMRB (or cells carrying a LMRB disruption) were not able to grow on agar media containing 5
20 µg/ml lincomycin. This effect was clearly visible in liquid culture. LMRB overexpression led to a 9-fold increased resistance (compared to wild-type) against lincomycin and LMRB disruption resulted in a decreased resistance (28% of wild-type) to this antibiotic.

25 **Example 12: Analysis of the Gene Sequences of the Invention**

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA*
30 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100,

wordlength = 12 to obtain nucleotide sequences homologous to SRT nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to SRT protein molecules of the invention. To obtain gapped alignments
5 for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

10 Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap
15 length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be
20 accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a
25 length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention
30 were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the

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top 500 hits were retained for further analysis. A subsequent FASTA search (e.g., a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP
5 program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of
10 the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment
15 homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 13: Construction and Operation of DNA Microarrays

20 The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.*
25 (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label
30 may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic

acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers
5 which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270:
10 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and
15 undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

20 The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis.
25 Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for
30 example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C.*

glutamicum or other *Corynebacteria*. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons
5 of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

**Example 14: Analysis of the Dynamics of Cellular Protein Populations
(Proteomics)**

10 The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (e.g., in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (e.g.,
15 during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic
20 techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the
25 consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation,
30 such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and

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include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

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Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the

5 following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a stress, resistance, or tolerance gene, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said stress, resistance, or tolerance gene is selected from the group consisting of nucleic acid molecules involved in a stress response, tolerance, or resistance to temperature stresses, pH stresses, oxygen stresses, osmotic stresses, toxic chemicals, oxygen radicals, antibiotics, or to lincomycin.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or

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a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine

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and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

- 5 17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.
18. An isolated stress, resistance, or tolerance polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
- 10 19. The protein of claim 18, wherein said stress, resistance, or tolerance polypeptide is selected from the group consisting of proteins involved in a stress response, tolerance, or resistance to temperature stresses, pH stresses, oxygen stresses, osmotic stresses, toxic chemicals, oxygen radicals, antibiotics, or to lincomycin.
- 15 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 20 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded
- 25 by any of the F-designated genes set forth in Table 1.
22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.
- 30 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID

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NOs of the Sequence Listing,, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*, *Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*, *Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*, *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.

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30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more SEQ ID NOs 1 through 304 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.
36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the nucleic acid molecule is disrupted.
37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the

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Sequence Listing , wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing .

- 5 38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

SEQUENCE LISTING

<110> BASF Aktiengesellschaft
 <120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
 RESISTANCE AND TOLERANCE PROTEINS
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 Met Asp Ser Gln Ile
 1 5
 aat act cag acc tct ccg gca gct gcg aag ctg cct agg gag gtc gtt 163
 Asn Thr Gln Thr Ser Pro Ala Ala Ala Lys Leu Pro Arg Glu Val Val
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 gtt gtt ctt tcg atc ctc gtg gtt tcc gcg atg atc atg att ctt aat 211
 Val Val Leu Ser Ile Leu Val Val Ser Ala Met Ile Met Ile Leu Asn
 25 30 35
 gaa acc att ctg tcg gtt gcg ttg cct tcc atc atg gaa gat ttc tcc 259
 Glu Thr Ile Leu Ser Val Ala Leu Pro Ser Ile Met Glu Asp Phe Ser
 40 45 50
 gtg cct gaa act act gca cag tgg ttg acc act ggc ttt atg ttg acg 307
 Val Pro Glu Thr Thr Ala Gln Trp Leu Thr Thr Gly Phe Met Leu Thr
 55 60 65
 atg gca gtg gtg att cca act act ggt tat ctg ctt gat cgt ttt tcc 355
 Met Ala Val Val Ile Pro Thr Thr Gly Tyr Leu Leu Asp Arg Phe Ser
 70 75 80 85
 act aag acg atc ttt gtt act gcg ttg ttg ttc ttt acg gtt ggt acg 403
 Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe Phe Thr Val Gly Thr
 90 95 100
 ttg act gcg gcg ttg gct cca acg ttt gcg gtg ctg ctt ggt gct cgt 451
 Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val Leu Leu Gly Ala Arg
 105 110 115
 atc gtt cag gcg gtt ggt act gcg ctg gtg atg cct ttg ctg atg acg 499
 Ile Val Gln Ala Val Gly Thr Ala Leu Val Met Pro Leu Leu Met Thr

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att att tcc atc gtg att tct gtt gcg ccg gcg ctt ggt cct acg ttg Ile Ile Ser Ile Val Ile Ser Val Ala Pro Ala Leu Gly Pro Thr Leu 150 155 160 165			595
tct ggt gtc att ctt aac tct ttg acc tgg cac tgg ttg ttt tgg atg Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His Trp Leu Phe Trp Met 170 175 180			643
atg ctt ccg atc gtt gtt atc gct ttg gta att ggt ttc ttc ttg atc Met Leu Pro Ile Val Val Ile Ala Leu Val Ile Gly Phe Phe Leu Ile 185 190 195			691
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ctc ggc aag caa gac aaa gca ctg atg gat ctc cga gcc ttc aag gtg Leu Gly Lys Gln Asp Lys Ala Leu Met Asp Leu Arg Ala Phe Lys Val 265 270 275			931
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gga gtt act gct ttg gtg acc ggt ttg gtt gtt atg ccc ggc ggc ctc Gly Val Thr Ala Leu Val Thr Gly Leu Val Val Met Pro Gly Gly Leu 310 315 320 325			1075
ctc cag ggt ctg atc agc cca ttc atc gga cgt ttc tac gac aag gtc Leu Gln Gly Leu Ile Ser Pro Phe Ile Gly Arg Phe Tyr Asp Lys Val 330 335 340			1123
ggt cca cgt ccg ctg ctg att ccc gga gca att gcg ctg gct atc gcg Gly Pro Arg Pro Leu Leu Ile Pro Gly Ala Ile Ala Leu Ala Ile Ala 345 350 355			1171

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 Ala Ser Ser Met Thr Phe Leu Asn Glu Asn Ser Pro Val Trp Met Val
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gtg gtc atg cac gtt gtg ttc agc atc ggc atg tgt ttg atg atg acc 1267
 Val Val Met His Val Val Phe Ser Ile Gly Met Cys Leu Met Met Thr
 375 380 385

cct ctc atg acc acc gct ctc ggc gcc ctt ccg aag cac ctc tat ggt 1315
 Pro Leu Met Thr Thr Ala Leu Gly Ala Leu Pro Lys His Leu Tyr Gly
 390 395 400 405

cac ggc tcc gca att ttg aac acg ttc caa cag ctc gca ggc gca gcc 1363
 His Gly Ser Ala Ile Leu Asn Thr Phe Gln Gln Leu Ala Gly Ala Ala
 410 415 420

gga aca gcg atc atg att gca gca ctt tcc ttc ggc act tcc att gca 1411
 Gly Thr Ala Ile Met Ile Ala Ala Leu Ser Phe Gly Thr Ser Ile Ala
 425 430 435

gcg tct tcg gga tct gcg cat gct gaa gct gtt gcc gct ggt acc aag 1459
 Ala Ser Ser Gly Ser Ala His Ala Glu Ala Val Ala Ala Gly Thr Lys
 440 445 450

gtt gcg ttc atc gca ggc gca atc atc gcg gtg atc gct ttg gtt gtt 1507
 Val Ala Phe Ile Ala Gly Ala Ile Ile Ala Val Ile Ala Leu Val Val
 455 460 465

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 Ser Leu Phe Val Thr Arg Val Glu Glu Glu Ala His
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 35 40 45

Met Glu Asp Phe Ser Val Pro Glu Thr Thr Ala Gln Trp Leu Thr Thr
 50 55 60

Gly Phe Met Leu Thr Met Ala Val Val Ile Pro Thr Thr Gly Tyr Leu
 65 70 75 80

Leu Asp Arg Phe Ser Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe
 85 90 95

Phe Thr Val Gly Thr Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val
 100 105 110

Leu Leu Gly Ala Arg Ile Val Gln Ala Val Gly Thr Ala Leu Val Met
 115 120 125

Pro Leu Leu Met Thr Val Thr Leu Thr Val Val Pro Ala Glu Arg Arg
 130 135 140

Gly Ser Met Met Gly Ile Ile Ser Ile Val Ile Ser Val Ala Pro Ala
 145 150 155 160

Leu Gly Pro Thr Leu Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His
 165 170 175

Trp Leu Phe Trp Met Met Leu Pro Ile Val Val Ile Ala Leu Val Ile
 180 185 190

Gly Phe Phe Leu Ile Lys Asn Ile Gly Glu Thr Lys Ile Thr Pro Leu
 195 200 205

Asp Val Leu Ser Val Ile Leu Ser Val Phe Ala Phe Gly Gly Leu Val
 210 215 220

Tyr Gly Phe Ser Ser Phe Gly Ala Ile Leu Glu Gly Glu Gly Thr Val
 225 230 235 240

Gly Ile Phe Ala Ile Val Val Gly Ala Ile Ala Leu Leu Ile Phe Ala
 245 250 255

Leu Arg Gln His Gln Leu Gly Lys Gln Asp Lys Ala Leu Met Asp Leu
 260 265 270

Arg Ala Phe Lys Val Arg Asn Phe Ser Phe Ser Leu Thr Thr Ile Leu
 275 280 285

Leu Ala Phe Gly Ala Met Leu Gly Thr Val Met Val Leu Pro Ile Tyr
 290 295 300

Leu Gln Thr Ser Leu Gly Val Thr Ala Leu Val Thr Gly Leu Val Val
 305 310 315 320

Met Pro Gly Gly Leu Leu Gln Gly Leu Ile Ser Pro Phe Ile Gly Arg
 325 330 335

Phe Tyr Asp Lys Val Gly Pro Arg Pro Leu Leu Ile Pro Gly Ala Ile
 340 345 350

Ala Leu Ala Ile Ala Ala Ser Ser Met Thr Phe Leu Asn Glu Asn Ser
 355 360 365

Pro Val Trp Met Val Val Val Met His Val Val Phe Ser Ile Gly Met
 370 375 380

Cys Leu Met Met Thr Pro Leu Met Thr Thr Ala Leu Gly Ala L u Pro
385 390 395 400

Lys His Leu Tyr Gly His Gly Ser Ala Ile Leu Asn Thr Phe Gln Gln
405 410 415

Leu Ala Gly Ala Ala Gly Thr Ala Ile Met Ile Ala Ala Leu Ser Phe
420 425 430

Gly Thr Ser Ile Ala Ala Ser Ser Gly Ser Ala His Ala Glu Ala Val
435 440 445

Ala Ala Gly Thr Lys Val Ala Phe Ile Ala Gly Ala Ile Ile Ala Val
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His

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<223> RXA00497

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Asn Val Asn Ile Lys Pro Leu Glu Asp Lys Ile Leu Val Gln Ile Asn
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gaa gca gag acc acc acc gct tcc ggc ctg gtc att cca gat tcc gct 153
Glu Ala Glu Thr Thr Thr Ala Ser Gly Leu Val Ile Pro Asp Ser Ala
20 25 30

aag gaa aag cca caa gag gca acc gtt atc gca gtt ggc cca ggc cgc 201
Lys Glu Lys Pro Gln Glu Ala Thr Val Ile Ala Val Gly Pro Gly Arg
35 40 45 50

ttc gat gac aag ggt aac cgc atc cca ctg gac atc aag gaa gat gac 249
Phe Asp Asp Lys Gly Asn Arg Ile Pro Leu Asp Ile Lys Glu Asp Asp
55 60 65

gtt gtg atc ttc tcc cgt tac ggc ggc acc gag atc aag ttc ggt ggc 297
Val Val Ile Phe Ser Arg Tyr Gly Gly Thr Glu Ile Lys Phe Gly Gly
70 75 80

gtg gag tac ttg ctt ctc tcc gct cgt gac atc ctc gca atc gtc gag 345
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 Lys

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 35 40 45
 Gly Arg Phe Asp Asp Lys Gly Asn Arg Ile Pro Leu Asp Ile Lys Glu
 50 55 60
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 Val Glu Lys

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 Met Ala Lys Leu Ile
 1 5
 gct ttt gac cag gac gcc cgc gaa ggc att ctc cgg ggc gtt gac gct 163
 Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu Arg Gly Val Asp Ala
 10 15 20

ctg gca aac gct gtc aag gta acc ctc ggc cca cgc ggc cgt aac gtg	211
Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro Arg Gly Arg Asn Val	
25 30 35	
ggt ctt gat aag gca ttc ggc gga cct ctg gtc acc aac gac ggt gtc	259
Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val Thr Asn Asp Gly Val	
40 45 50	
acc att gcc cgc gac atc gac ctt gag gat cct ttt gag aac ctc ggt	307
Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro Phe Glu Asn Leu Gly	
55 60 65	
gcg cag ctg gtg aag tcc gtt gct gtt aag acc aac gac atc gct ggt	355
Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr Asn Asp Ile Ala Gly	
70 75 80 85	
gac ggc acc acg act gca act ctg ctt gct cag gca ctc att gct gaa	403
Asp Gly Thr Thr Ala Thr Leu Leu Ala Gln Ala Leu Ile Ala Glu	
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ggc ctg cgc aac gtt gct gct ggc gca aac cca atg gag ctc aac aag	451
Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro Met Glu Leu Asn Lys	
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Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu Glu Leu Lys Ala Arg	
120 125 130	
gca acc gag gtg tct gac acc aag gaa atc gca aac gtc gct acc gtt	547
Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala Asn Val Ala Thr Val	
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tca tcc cgc gat gaa gtt gtc ggc gag atc gtt gct gca gcg atg gaa	595
Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val Ala Ala Ala Met Glu	
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Lys Val Gly Lys Asp Gly Val Val Thr Val Glu Glu Ser Gln Ser Ile	
170 175 180	
gag act gct ctc gag gtc acc gaa ggt att tct ttc gac aag ggc tac	691
Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser Phe Asp Lys Gly Tyr	
185 190 195	
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Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr Gln Gln Ala Val Leu	
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gac aac cct gca gtg ctg ctt gtt cgc aac aag att tct tcc ctc cca	787
Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys Ile Ser Ser Leu Pro	
215 220 225	
gac ttc ctc cca ttg ctg gag aag gtt gtg gag tcc aac cgt cct ttg	835
Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu Ser Asn Arg Pro Leu	
230 235 240 245	

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cgc aag ctg cgt gtc gaa gat gcc atc aac gct gct cgc gca gca gca Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala Ala Arg Ala Ala Ala 390 395 400 405	1315
caa gaa ggc gtt atc gct ggt ggc ggt tcc gct ttg gtt cag atc gct Gln Glu Gly Val Ile Ala Gly Gly Gly Ser Ala Leu Val Gln Ile Ala 410 415 420	1363
gag act ctg aag gct tac gcc gaa gag ttc gaa ggc gac cag aag gtc Glu Thr Leu Lys Ala Tyr Ala Glu Glu Phe Glu Gly Asp Gln Lys Val 425 430 435	1411
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gcc tcc aac gca ggt ctt gac ggc tct gtt gtt gtt gca cgc act gct Ala Ser Asn Ala Gly Leu Asp Gly Ser Val Val Val Ala Arg Thr Ala 455 460 465	1507
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Ala Leu Pro Asn Gly Glu Gly Phe Asn Ala Ala Thr Leu Glu Tyr Gly
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 490 495 500

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 505 510 515

gct tct gtt gtt gag aag cct gca gaa gaa gca gcc gat gca cat gca 1699
 Ala Ser Val Val Glu Lys Pro Ala Glu Glu Ala Ala Asp Ala His Ala
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 Gly His His His His
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 35 40 45

Thr Asn Asp Gly Val Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro
 50 55 60

Phe Glu Asn Leu Gly Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr
 65 70 75 80

Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln
 85 90 95

Ala Leu Ile Ala Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
 100 105 110

Met Glu Leu Asn Lys Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu
 115 120 125

Glu Leu Lys Ala Arg Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala
 130 135 140

Asn Val Ala Thr Val Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val
 145 150 155 160

Ala Ala Ala Met Glu Lys Val Gly Lys Asp Gly Val Val Thr Val Glu

165										170										175																											
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225										230										235																											
Ser	Asn	Arg	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	Pro	Ser	Asn	Arg	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	Pro	Ser	Asn	Arg	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	Pro
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275										280										285																											
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325										330										335																											
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340										345										350																											
Asn	Thr	Asp	Ser	Thr	Trp	Asp	Arg	Glu	Lys	Ala	Glu	Glu	Arg	Leu	Ala	As																															

465	470	475	480
Thr Leu Glu Tyr Gly Asn Leu Ile Asn Asp Gly Val Ile Asp Pro Val			
485		490	495
Lys Val Thr His Ser Ala Val Val Asn Ala Thr Ser Val Ala Arg Met			
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Val Leu Thr Thr Glu Ala Ser Val Val Glu Lys Pro Ala Glu Glu Ala			
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Ala Asp Ala His Ala Gly His His His His			
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 Met Ala Lys Leu Ile 5
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 Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu Arg Gly Val Asp Ala 20
 10 15
 ctg gca aac gct gtc aag gta acc ctc ggc cca cgc ggc cgt aac gtg 211
 Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro Arg Gly Arg Asn Val 35
 25 30
 gtt ctt gat aag gca ttc ggc gga cct ctg gtc acc aac gac ggt gtc 259
 Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val Thr Asn Asp Gly Val 50
 40 45
 acc att gcc cgc gac atc gac ctt gag gat cct ttt gag aac ctc ggt 307
 Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro Phe Glu Asn Leu Gly 65
 55 60
 gcg cag ctg gtg aag tcc gtt gct gtt aag acc aac gac atc gct ggt 355
 Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr Asn Asp Ile Ala Gly 85
 70 75 80
 gac ggc acc acg act gca act ctg ctt gct cag gca ctc att gct gaa 403
 Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln Ala Leu Ile Ala Glu 100
 90 95
 ggc ctg cgc aac gtt gct gct ggc gca aac cca atg gag ctc aac aag 451

Gly	Leu	Arg	Asn	Val	Ala	Ala	Gly	Ala	Asn	Pro	Met	Glu	L	u	Asn	Lys			
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ggt	att	tct	gca	gct	gca	gaa	aag	acc	ttg	gaa	gag	ttg	aag	gca	cgc		499		
Gly	Il	Ser	Ala	Ala	Ala	Glu	Lys	Thr	Leu	Glu	Glu	Leu	Lys	Ala	Arg				
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gca	acc	gag	gtg	tct	gac	acc	aag	gaa	atc	gca	aac	gtc	gct	acc	gtt		547		
Ala	Thr	Glu	Val	Ser	Asp	Thr	Lys	Glu	Ile	Ala	Asn	Val	Ala	Thr	Val				
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tca	tcc	cgc	gat	gaa	gtt	gtc	ggc	gag	atc	gtt	gct	gca	gcg	atg	gaa		595		
Ser	Ser	Arg	Asp	Glu	Val	Val	Gly	Glu	Ile	Val	Ala	Ala	Ala	Met	Glu				
			150			155			160					165					
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Lys	Val	Gly	Lys	Asp	Gly	Val	Val	Thr	Val	Glu	Glu	Ser	Gln	Ser	Ile				
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gag	act	gct	ctc	gag	gtc	acc	gaa	ggt	att	tct	ttc	gac	aag	ggc	tac		691		
Glu	Thr	Ala	Leu	Glu	Val	Thr	Glu	Gly	Ile	Ser	Phe	Asp	Lys	Gly	Tyr				
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ctt	tcc	cct	tat	ttc	atc	aac	gac	aac	gac	act	cag	cag	gct	gtc	ctg		739		
Leu	Ser	Pro	Tyr	Phe	Ile	Asn	Asp	Asn	Asp	Thr	Gln	Gln	Ala	Val	Leu				
			200				205					210							
gac	aac	cct	gca	gtg	ctg	ctt	gtt	cgc	aac	aag	att	tct	tcc	ctc	cca		787		
Asp	Asn	Pro	Ala	Val	Leu	Leu	Val	Arg	Asn	Lys	Ile	Ser	Ser	Leu	Pro				
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gac	ttc	ctc	cca	ttg	ctg	gag	aag	gtt	gtg	gag	tcc	aac	cgt	cct	ttg		835		
Asp	Phe	Leu	Pro	Leu	Leu	Glu	Lys	Val	Val	Glu	Ser	Asn	Arg	Pro	Leu				
			230			235			240					245					
ctg	atc	atc	gca	gaa	gac	gtc	gag	ggc	gag	cct	ttg	cag	acc	ctg	gtt		883		
Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	Pro	Leu	Gln	Thr	Leu	Val				
			250					255						260					
gtg	aac	tcc	atc	cgc	aag	acc	atc	aag	gtc	gtt	gca	gtg	aag	tcc	cct		931		
Val	Asn	Ser	Ile	Arg	Lys	Thr	Ile	Lys	Val	Val	Ala	Val	Lys	Ser	Pro				
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tac	ttc	ggt	gac	cga	cgc	aag	gcg	ttc	atg	gat	gac	ctg	gct	att	gtc		979		
Tyr	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Phe	Met	Asp	Asp	Leu	Ala	Ile	Val				
			280				285					290							
acc	aag	gca	act	gtc	gtg	gat	cca	gaa	gtg	ggc	atc	aac	ctc	aac	gaa		1027		
Thr	Lys	Ala	Thr	Val	Val	Asp	Pro	Glu	Val	Gly	Ile	Asn	Leu	Asn	Glu				
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gct	ggc	gaa	gaa	gtt	ttc	ggt	acc	gca	cgc	cgc	atc	acc	gtt	tcc	aag		1075		
Ala	Gly	Glu	Glu	Val	Phe	Gly	Thr	Ala	Arg	Arg	Ile	Thr	Val	Ser	Lys				
			310			315			320					325					
gac	gaa	acc	atc	atc	gtt	gat	ggt	gca	ggt	tcc	gca	gaa	gac	gtt	gaa		1123		
Asp	Glu	Thr	Ile	Ile	Val	Asp	Gly	Ala	Gly	Ser	Ala	Glu	Asp	Val	Glu				

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gca cgt cgc ggc cag atc cgt cgc gaa atc gcc aac acc gat tcc acc			1171
Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala Asn Thr Asp Ser Thr			
345	350	355	
tggt gat cgc gaa aag gca gaa gag cgt ttg gct aag ctc tcc ggt ggt			1219
Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala Lys Leu Ser Gly Gly			
360	365	370	
att gct gtc atc cgc gtt ggt gca gca act gaa acc gaa gtc aac gac			1267
Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu Thr Glu Val Asn Asp			
375	380	385	
cgc aag ctg cgt gtc gaa gat gcc atc aac gct gct cgc gca gca gca			1315
Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala Ala Arg Ala Ala Ala			
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caa gaa ggc gtt atc gct ggt ggc			1339
Gln Glu Gly Val Ile Ala Gly Gly			
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Arg Gly Val Asp Ala Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro			
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Arg Gly Arg Asn Val Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val			
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Thr Asn Asp Gly Val Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro			
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Phe Glu Asn Leu Gly Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr			
65	70	75	80
Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln			
85	90	95	
Ala Leu Ile Ala Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro			
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Met Glu Leu Asn Lys Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu			
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Glu Leu Lys Ala Arg Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala			
130	135	140	
Asn Val Ala Thr Val Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val			

145		150		155		160									
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Glu	Ser	Gln	Ser	Ile	Glu	Thr	Ala	Leu	Glu	Val	Thr	Glu	Gly	Ile	Ser
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Ph	Asp	Lys	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Ile	Asn	Asp	Asn	Asp	Thr
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Gln	Gln	Ala	Val	Leu	Asp	Asn	Pro	Ala	Val	Leu	Leu	Val	Arg	Asn	Lys
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Ile	Ser	Ser	Leu	Pro	Asp	Phe	Leu	Pro	Leu	Leu	Glu	Lys	Val	Val	Glu
225					230					235					240
Ser	Asn	Arg	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	Pro
				245					250					255	
Leu	Gln	Thr	Leu	Val	Val	Asn	Ser	Ile	Arg	Lys	Thr	Ile	Lys	Val	Val
			260					265					270		
Ala	Val	Lys	Ser	Pro	Tyr	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Phe	Met	Asp
		275					280					285			
Asp	Leu	Ala	Ile	Val	Thr	Lys	Ala	Thr	Val	Val	Asp	Pro	Glu	Val	Gly
	290					295					300				
Ile	Asn	Leu	Asn	Glu	Ala	Gly	Glu	Glu	Val	Phe	Gly	Thr	Ala	Arg	Arg
305					310					315					320
Ile	Thr	Val	Ser	Lys	Asp	Glu	Thr	Ile	Ile	Val	Asp	Gly	Ala	Gly	Ser
				325					330					335	
Ala	Glu	Asp	Val	Glu	Ala	Arg	Arg	Gly	Gln	Ile	Arg	Arg	Glu	Ile	Ala
			340					345					350		
Asn	Thr	Asp	Ser	Thr	Trp	Asp	Arg	Glu	Lys	Ala	Glu	Glu	Arg	Leu	Ala
		355					360					365			
Lys	Leu	Ser	Gly	Gly	Ile	Ala	Val	Ile	Arg	Val	Gly	Ala	Ala	Thr	Glu
	370					375					380				
Thr	Glu	Val	Asn	Asp	Arg	Lys	Leu	Arg	Val	Glu	Asp	Ala	Ile	Asn	Ala
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Ala	Arg	Ala	Ala	Ala	Gln	Glu	Gly	Val	Ile	Ala	Gly	Gly			
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                                         Met Ala Lys Tyr Gln
                                         1                               5

acc att gag gct gct gtc cgc tct gag ttc ggc aag ggc tct gca cgt 163
Thr Ile Glu Ala Ala Val Arg Ser Glu Phe Gly Lys Gly Ser Ala Arg
                        10                               15                               20

cgt gca cgc gtt gct ggc cag atc cct gct gtt gtt tac ggc gca gat 211
Arg Ala Arg Val Ala Gly Gln Ile Pro Ala Val Val Tyr Gly Ala Asp
                        25                               30                               35

gtt gag tcc aac ctg cac gtc acc atc gac cac cgc acc ttc gct gcg 259
Val Glu Ser Asn Leu His Val Thr Ile Asp His Arg Thr Phe Ala Ala
                        40                               45                               50

ctg gtt cgc cag gaa ggc gta aac gct gtt ctt gag ctc gac atc gag 307
Leu Val Arg Gln Glu Gly Val Asn Ala Val Leu Glu Leu Asp Ile Glu
                        55                               60                               65

ggc cag aag cag ctc acc atg atc aag cac atc gac cag aac gtg ctg 355
Gly Gln Lys Gln Leu Thr Met Ile Lys His Ile Asp Gln Asn Val Leu
                        70                               75                               80                               85

acc ttc cac atc gac cac ttg gac ctg ctt gcc att aag cgc ggc gaa 403
Thr Phe His Ile Asp His Leu Asp Leu Leu Ala Ile Lys Arg Gly Glu
                        90                               95                               100

aag gtt gag gtt gac gtt cca gtt atc gtc gag ggc gag cca gct cca 451
Lys Val Glu Val Asp Val Pro Val Ile Val Glu Gly Glu Pro Ala Pro
                        105                               110                               115

ggc acc atg tgg gtt cag gat gct gac acc atc aag gtt gag gct gac 499
Gly Thr Met Trp Val Gln Asp Ala Asp Thr Ile Lys Val Glu Ala Asp
                        120                               125                               130

gtt ctg tcc atc cct gaa gag ttc acc gtt tcc atc gaa ggc ctt gag 547
Val Leu Ser Ile Pro Glu Glu Phe Thr Val Ser Ile Glu Gly Leu Glu
                        135                               140                               145

ctc ggc gca cag atc acc gca gct gac atc aag ctc gag ggc gac acc 595
Leu Gly Ala Gln Ile Thr Ala Ala Asp Ile Lys Leu Glu Gly Asp Thr
                        150                               155                               160                               165

acc ctg gtt gag gat cct gag acc ctc atc gtc aac atc gtt ctc cca 643
Thr Leu Val Glu Asp Pro Glu Thr Leu Ile Val Asn Ile Val Leu Pro
                        170                               175                               180

gct gtc gag gaa gaa gac acc gaa gag gac gaa gca gct gaa gaa gca 691
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190

195

723

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 20 25 30

Val Tyr Gly Ala Asp Val Glu Ser Asn Leu His Val Thr Ile Asp His
 35 40 45

Arg Thr Phe Ala Ala Leu Val Arg Gln Glu Gly Val Asn Ala Val Leu
 50 55 60

Glu Leu Asp Ile Glu Gly Gln Lys Gln Leu Thr Met Ile Lys His Ile
 65 70 75 80

Asp Gln Asn Val Leu Thr Phe His Ile Asp His Leu Asp Leu Leu Ala
 85 90 95

Ile Lys Arg Gly Glu Lys Val Glu Val Asp Val Pro Val Ile Val Glu
 100 105 110

Gly Glu Pro Ala Pro Gly Thr Met Trp Val Gln Asp Ala Asp Thr Ile
 115 120 125

Lys Val Glu Ala Asp Val Leu Ser Ile Pro Glu Glu Phe Thr Val Ser
 130 135 140

Ile Glu Gly Leu Glu Leu Gly Ala Gln Ile Thr Ala Ala Asp Ile Lys
 145 150 155 160

Leu Glu Gly Asp Thr Thr Leu Val Glu Asp Pro Glu Thr Leu Ile Val
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Asn Ile Val Leu Pro Ala Val Glu Glu Glu Asp Thr Glu Glu Asp Glu
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<223> RXA00605

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Asp Gln Ile Val Asp Arg Gly Met Arg Pro Lys Leu Ser Gly Asn Thr
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acc cgc cac aac gga gca cca gtt cca tct gag aac atc tcc gca acc      149
Thr Arg His Asn Gly Ala Pro Val Pro Ser Glu Asn Ile Ser Ala Thr
      25                      30                      35

gca ggc cca cag ggt cca aac gtt ctc aat gag att cac ctc att gaa      197
Ala Gly Pro Gln Gly Pro Asn Val Leu Asn Asp Ile His Leu Ile Glu
      40                      45                      50                      55

aag ctc gca cac ttt aac cgc gag aac gtt cca gag cgt atc cct cac      245
Lys Leu Ala His Phe Asn Arg Glu Asn Val Pro Glu Arg Ile Pro His
                        60                      65                      70

gca aag ggc cac ggc gct ttc ggt gag ctg cac atc acc gag gac gta      293
Ala Lys Gly His Gly Ala Phe Gly Glu Leu His Ile Thr Glu Asp Val
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tcc gaa tac acc aag gca gac ctg ttc cag cct ggt aag gtc acc ccg      341
Ser Glu Tyr Thr Lys Ala Asp Leu Phe Gln Pro Gly Lys Val Thr Pro
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ctg gct gtt cgc ttc tct act gtt gct ggt gag cag ggc tcc cca gat      389
Leu Ala Val Arg Phe Ser Thr Val Ala Gly Glu Gln Gly Ser Pro Asp
      105                      110                      115

acc tgg cgc gac gtc cac ggc ttc gct ctt cgc ttc tac acc gaa gag      437
Thr Trp Arg Asp Val His Gly Phe Ala Leu Arg Phe Tyr Thr Glu Glu
      120                      125                      130                      135

ggc aac tac gac atc gtg ggt aac aac acc cca acc ttc ttc ctt cgt      485
Gly Asn Tyr Asp Ile Val Gly Asn Asn Thr Pro Thr Phe Phe Leu Arg
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gac ggc atg aag ttc ccg gac ttc atc cac tca cag aag cgt ctc aac      533
Asp Gly Met Lys Phe Pro Asp Phe Ile His Ser Gln Lys Arg Leu Asn
                        155                      160                      165

aag aac ggt ctg cgc gat gca gac atg cag tgg gat ttc tgg acc cgc      581
Lys Asn Gly Leu Arg Asp Ala Asp Met Gln Trp Asp Phe Trp Thr Arg
      170                      175                      180

gca cct gaa tct gca cac cag gtg acc tac ctg atg ggt gac cgc ggt      629
Ala Pro Glu Ser Ala His Gln Val Thr Tyr Leu Met Gly Asp Arg Gly

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cag tgg atc aac gct gaa ggt aag cca gtt tgg gtt aag tac cac ttc Gln Trp Ile Asn Ala Glu Gly Lys Pro Val Trp Val Lys Tyr His Phe 220 225 230			725
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gtt gca ggc gag aac gct gac tac cag cgc gaa gac ctc tac aac gct Val Ala Gly Glu Asn Ala Asp Tyr Gln Arg Glu Asp Leu Tyr Asn Ala 250 255 260			821
att gaa aac ggc gac ttc cca atc tgg gac gtc aag gtt cag atc atg Ile Glu Asn Gly Asp Phe Pro Ile Trp Asp Val Lys Val Gln Ile Met 265 270 275			869
cct ttc gag gat gca gag aac tac cgc tgg aac cca ttc gac ctg acc Pro Phe Glu Asp Ala Glu Asn Tyr Arg Trp Asn Pro Phe Asp Leu Thr 280 285 290 295			917
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cgc atg ctc cag gca cgt atc ttc gca tac gct gac cag cag cgt tac Arg Met Leu Gln Ala Arg Ile Phe Ala Tyr Ala Asp Gln Gln Arg Tyr 345 350 355			1109
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gag gtc aac acc tac agc cgc gaa ggt tcc atg cag tac atc ttc gac Glu Val Asn Thr Tyr Ser Arg Glu Gly Ser Met Gln Tyr Ile Phe Asp 380 385 390			1205
gct gag ggc gag cct tcc tac agc cct aac cgc tac gac aag ggc gca Ala Glu Gly Glu Pro Ser Tyr Ser Pro Asn Arg Tyr Asp Lys Gly Ala 395 400 405			1253
ggc tac ctg gat aac ggt acg gat tcc tcc tcc aac cac acc tcc tac Gly Tyr Leu Asp Asn Gly Thr Asp Ser Ser Ser Asn His Thr Ser Tyr 410 415 420			1301

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 Gly Gln Ala Asp Asp Ile Tyr Val Asn Pro Asp Pro His Gly Thr Asp
 425 430 435
 ctg gtt cgt gct gct tac gtc aag cac cag gat gat gac gac ttc atc 1397
 Leu Val Arg Ala Ala Tyr Val Lys His Gln Asp Asp Asp Phe Ile
 440 445 450 455
 cag cca ggc atc cta tac cgc gag gtc ctg gat gag ggc gag aag gag 1445
 Gln Pro Gly Ile Leu Tyr Arg Glu Val Leu Asp Glu Gly Glu Lys Glu
 460 465 470
 cga ttg gca gac aac atc tcc aac gca atg cag ggc atc tct gag gca 1493
 Arg Leu Ala Asp Asn Ile Ser Asn Ala Met Gln Gly Ile Ser Glu Ala
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 acc gag cca cgc gtc tac gac tac tgg aac aac gtt gat gag aac ctc 1541
 Thr Glu Pro Arg Val Tyr Asp Tyr Trp Asn Asn Val Asp Glu Asn Leu
 490 495 500
 ggc gct cgc gtc aag gag ctt tac ctc cag aag aag gct taagtccttc 1590
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<213> Corynebacterium glutamicum

<400> 12

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 Ser Glu Asn Ile Ser Ala Thr Ala Gly Pro Gln Gly Pro Asn Val Leu
 35 40 45
 Asn Asp Ile His Leu Ile Glu Lys Leu Ala His Phe Asn Arg Glu Asn
 50 55 60
 Val Pro Glu Arg Ile Pro His Ala Lys Gly His Gly Ala Phe Gly Glu
 65 70 75 80
 Leu His Ile Thr Glu Asp Val Ser Glu Tyr Thr Lys Ala Asp Leu Phe
 85 90 95
 Gln Pro Gly Lys Val Thr Pro Leu Ala Val Arg Phe Ser Thr Val Ala
 100 105 110
 Gly Glu Gln Gly Ser Pro Asp Thr Trp Arg Asp Val His Gly Phe Ala
 115 120 125

Leu Arg Phe Tyr Thr Glu Glu Gly Asn Tyr Asp Ile Val Gly Asn Asn
 130 135 140
 Thr Pro Thr Phe Phe Leu Arg Asp Gly Met Lys Phe Pro Asp Phe Ile
 145 150 155 160
 His Ser Gln Lys Arg Leu Asn Lys Asn Gly Leu Arg Asp Ala Asp Met
 165 170 175
 Gln Trp Asp Phe Trp Thr Arg Ala Pro Glu Ser Ala His Gln Val Thr
 180 185 190
 Tyr Leu Met Gly Asp Arg Gly Thr Pro Lys Thr Ser Arg His Gln Asp
 195 200 205
 Gly Phe Gly Ser His Thr Phe Gln Trp Ile Asn Ala Glu Gly Lys Pro
 210 215 220
 Val Trp Val Lys Tyr His Phe Lys Thr Arg Gln Gly Trp Asp Cys Phe
 225 230 235 240
 Thr Asp Ala Glu Ala Ala Lys Val Ala Gly Glu Asn Ala Asp Tyr Gln
 245 250 255
 Arg Glu Asp Leu Tyr Asn Ala Ile Glu Asn Gly Asp Phe Pro Ile Trp
 260 265 270
 Asp Val Lys Val Gln Ile Met Pro Phe Glu Asp Ala Glu Asn Tyr Arg
 275 280 285
 Trp Asn Pro Phe Asp Leu Thr Lys Thr Trp Ser Gln Lys Asp Tyr Pro
 290 295 300
 Leu Ile Pro Val Gly Tyr Phe Ile Leu Asn Arg Asn Pro Arg Asn Phe
 305 310 315 320
 Phe Ala Gln Ile Glu Gln Leu Ala Leu Asp Pro Gly Asn Ile Val Pro
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 Gly Val Gly Leu Ser Pro Asp Arg Met Leu Gln Ala Arg Ile Phe Ala
 340 345 350
 Tyr Ala Asp Gln Gln Arg Tyr Arg Ile Gly Ala Asn Tyr Arg Asp Leu
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 Pro Val Asn Arg Pro Ile Asn Glu Val Asn Thr Tyr Ser Arg Glu Gly
 370 375 380
 Ser Met Gln Tyr Ile Phe Asp Ala Glu Gly Glu Pro Ser Tyr Ser Pro
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 Asn Arg Tyr Asp Lys Gly Ala Gly Tyr Leu Asp Asn Gly Thr Asp Ser
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 Ser Ser Asn His Thr Ser Tyr Gly Gln Ala Asp Asp Ile Tyr Val Asn
 420 425 430

Pro Asp Pro His Gly Thr Asp Leu Val Arg Ala Ala Tyr Val Lys His
 435 440 445

Gln Asp Asp Asp Asp Phe Ile Gln Pro Gly Ile Leu Tyr Arg Glu Val
 450 455 460

Leu Asp Glu Gly Glu Lys Glu Arg Leu Ala Asp Asn Ile Ser Asn Ala
 465 470 475 480

Met Gln Gly Ile Ser Glu Ala Thr Glu Pro Arg Val Tyr Asp Tyr Trp
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Asn Asn Val Asp Glu Asn Leu Gly Ala Arg Val Lys Glu Leu Tyr Leu
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Gln Lys Lys Ala
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 Val Ala Leu Lys Arg
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ccc gaa gag aaa aca gta aag atc gtg acc ata aaa cag act gac aac 163
 Pro Glu Glu Lys Thr Val Lys Ile Val Thr Ile Lys Gln Thr Asp Asn
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atc aat gac gat gat ttg gtg tac agc aac gct act gac ctt cca gta 211
 Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala Thr Asp Leu Pro Val
 25 30 35

ggc gtg aag aag tcc cct aaa atg tca ccg acc gcc cgc gtt ggt ctc 259
 Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr Ala Arg Val Gly Leu
 40 45 50

ctt gtc ttt ggg gtt atc gcg gcg gtg ggt tgg gga gca atc gct ttc 307
 Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp Gly Ala Ile Ala Phe
 55 60 65

tcc cgt ggc gaa aca atc aac tct gtg tgg ctg gtt ttg gcg gca gtt 355
 Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu Val Leu Ala Ala Val
 70 75 80 85

ggt tcc tat atc att gcg ttt tct ttc tat gcc cga ctg att gaa tac	403
Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala Arg Leu Ile Glu Tyr	
90 95 100	
aaa gtt gtt aag ccg aaa gat cag cga gca acc ccg gcg gaa tac gtt	451
Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr Pro Ala Glu Tyr Val	
105 110 115	
aat gac ggc aag gac tat gtc cca acg gat cgt cgt gtg ctt ttt ggc	499
Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg Arg Val Leu Phe Gly	
120 125 130	
cac cac ttt gca gct att gca ggt gcc ggt cca ttg gtt gga cct gtc	547
His His Phe Ala Ala Ile Ala Gly Ala Gly Pro Leu Val Gly Pro Val	
135 140 145	
atg gcc gcg cag atg ggc tac ctg cca ggc acc ttg tgg att atc ctc	595
Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr Leu Trp Ile Ile Leu	
150 155 160 165	
ggt gtg att ttc gcc ggt gca gtg cag gac tac cta gtg ctg tgg gtg	643
Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr Leu Val Leu Trp Val	
170 175 180	
tct act cgt agg cgt gga cgc tca ctt ggc cag atg gtt cgt gat gaa	691
Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln Met Val Arg Asp Glu	
185 190 195	
atg ggc acg gtc ggt gga gct gcc ggt atc ttg gcg acc atc tcc atc	739
Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu Ala Thr Ile Ser Ile	
200 205 210	
atg atc atc att atc gcg gtg ctc gca ttg atc gtg gtt aat gca ctg	787
Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile Val Val Asn Ala Leu	
215 220 225	
gct gat tca cca tgg ggc gtt ttc tcc atc acc atg acc atc cca att	835
Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr Met Thr Ile Pro Ile	
230 235 240 245	
gca ctg ttc atg ggt gtg tac ttg cgt tac ctg cgc cca ggt cgt gtt	883
Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu Arg Pro Gly Arg Val	
250 255 260	
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Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu Leu Leu Ala Ile Val	
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Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly Val Glu Trp Phe Thr	
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tgg tct aag acc act ttg gcg ttg gcc ttg atc ggt tac gga atc atg	1027
Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile Gly Tyr Gly Ile Met	
295 300 305	
gct gcg att ttg ccg gtg tgg ctg ctg ctt gca ccg cgc gat tac ctg	1075

Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala Pro Arg Asp Tyr Leu 310 315 320 325	
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cgt gtg gct cgc ttt atg atg acc gat acc ttg ggc aat gtt cca ggt Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu Gly Asn Val Pro Gly 540 545 550	1747

535	540	545	
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Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val Gly Asn Trp Ile Ser			
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Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile Leu Leu Met Gly Val			
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Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe Pro Leu Phe Gly Ile			
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Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala Leu Val Leu Val Val			
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Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp Ile Pro Ala Val Pro			
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Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala Ser Trp Gln Lys Ile			
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Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala Gln Asn Ala Asn Phe			
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cgc gat gca aag tct caa ggc ctt acc gaa ttt ggt gcc gct aaa tct			2131
Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe Gly Ala Ala Lys Ser			
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cct gag gca atc gat gcg gtt atc cga aac acc atg att cag ggc atc			2179
Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr Met Ile Gln Gly Ile			
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Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val Val Val Gly Ala Ala			
	695	700	705
att gcg gtg tgc atc aag tcc atc agg gct cgt gca gcc gga aca cct			2275
Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg Ala Ala Gly Thr Pro			
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Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser Glu Phe Phe Ala Pro			
	730	735	740
act gga ttc ctt gca tct tcc agg gat aag gaa gtc cag gcc atg tgg			2371
Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu Val Gln Ala Met Trp			
	745	750	755
gac gag cgc tac cca ggc ggt gcg ccc gtg tct tct gga ggg cac			2416
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2439

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<211> 772

<212> PRT

<213> Corynebacterium glutamicum

<400> 14

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Thr	Asp	Leu	Pro	Val	Gly	Val	Lys	Lys	Ser	Pro	Lys	Met	Ser	Pro	Thr
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Ala	Arg	Val	Gly	Leu	Leu	Val	Phe	Gly	Val	Ile	Ala	Ala	Val	Gly	Trp
	50					55					60				
Gly	Ala	Ile	Ala	Phe	Ser	Arg	Gly	Glu	Thr	Ile	Asn	Ser	Val	Trp	Leu
65					70					75					80
Val	Leu	Ala	Ala	Val	Gly	Ser	Tyr	Ile	Ile	Ala	Phe	Ser	Phe	Tyr	Ala
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Arg	Leu	Ile	Glu	Tyr	Lys	Val	Val	Lys	Pro	Lys	Asp	Gln	Arg	Ala	Thr
			100					105					110		
Pro	Ala	Glu	Tyr	Val	Asn	Asp	Gly	Lys	Asp	Tyr	Val	Pro	Thr	Asp	Arg
		115					120					125			
Arg	Val	Leu	Phe	Gly	His	His	Phe	Ala	Ala	Ile	Ala	Gly	Ala	Gly	Pro
	130					135					140				
Leu	Val	Gly	Pro	Val	Met	Ala	Ala	Gln	Met	Gly	Tyr	Leu	Pro	Gly	Thr
145					150					155					160
Leu	Trp	Ile	Ile	Leu	Gly	Val	Ile	Phe	Ala	Gly	Ala	Val	Gln	Asp	Tyr
				165				170						175	
Leu	Val	Leu	Trp	Val	Ser	Thr	Arg	Arg	Arg	Gly	Arg	Ser	Leu	Gly	Gln
			180					185					190		
Met	Val	Arg	Asp	Glu	Met	Gly	Thr	Val	Gly	Gly	Ala	Ala	Gly	Ile	Leu
		195					200					205			
Ala	Thr	Ile	Ser	Ile	Met	Ile	Ile	Ile	Ile	Ala	Val	Leu	Ala	Leu	Ile
	210					215					220				
Val	Val	Asn	Ala	Leu	Ala	Asp	Ser	Pro	Trp	Gly	Val	Phe	Ser	Ile	Thr
225				230						235					240
Met	Thr	Ile	Pro	Ile	Ala	Leu	Phe	Met	Gly	Val	Tyr	Leu	Arg	Tyr	Leu
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 275 280 285
 Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile
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 Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala
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 Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu
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 Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser
 355 360 365
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 370 375 380
 Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys
 385 390 395 400
 Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser
 405 410 415
 Phe Val Ala Met Met Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His
 420 425 430
 Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro
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 Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp
 450 455 460
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 465 470 475 480
 Thr Val Ile Ser Arg Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met
 485 490 495
 Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe
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 Trp Tyr His Phe Ala Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr
 515 520 525
 Val Asp Ala Gly Thr Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu
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 Gly Asn Val Pro Gly Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val
 545 550 555 560

Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile
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 Pro Leu Phe Gly Ile Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala
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 610 615 620
 Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala
 625 630 635 640
 Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala
 645 650 655
 Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe
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 Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr
 675 680 685
 Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val
 690 695 700
 Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg
 705 710 715 720
 Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser
 725 730 735
 Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu
 740 745 750
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 Ser Gly Gly His
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                                         Met  Leu  Asp  Met  Trp
                                         1      5

gag  cac  gct  ttc  tac  ctg  cag  tac  atg  aac  gtt  aag  gca  gat  tac  gtc      163
Glu  His  Ala  Phe  Tyr  Leu  Gln  Tyr  Met  Asn  Val  Lys  Ala  Asp  Tyr  Val
                        10                        15                        20

aag  gct  gtt  tgg  aac  gtc  ttc  aac  tgg  gac  gac  gca  aga  gca  cgc  ttc      211
Lys  Ala  Val  Trp  Asn  Val  Phe  Asn  Trp  Asp  Asp  Ala  Arg  Ala  Arg  Phe
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 <223> RXN00575

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 Met Val Glu Arg Asp
 1 5
 ttc act atc cga cca atc cgc gag ggt gat ttc cct cag gtg agg gac 163
 Phe Thr Ile Arg Pro Ile Arg Glu Gly Asp Phe Pro Gln Val Arg Asp
 10 15 20
 atc tac gaa ttg ggc ctg gag acg gga cat gcg act tat gag act tct 211
 Ile Tyr Glu Leu Gly Leu Glu Thr Gly His Ala Thr Tyr Glu Thr Ser
 25 30 35
 ggt ccc acg tgg gac cag ttc tcc caa tct aaa atc atg gat acc gtc 259
 Gly Pro Thr Trp Asp Gln Phe Ser Gln Ser Lys Ile Met Asp Thr Val
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 Met Val Ala Val Glu Asn Asn Asp Pro Asp Phe Ile Leu Gly Trp Val
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 Ser Ala Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly Val Val Glu

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Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly Ile Gly Gly				
	90	95	100	
gct ttg ctc gac gcc ctt atc acc tac tgc gaa agc aac ggc atc tgg				451
Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn Gly Ile Trp				
	105	110	115	
tcg atc cac tcc tgg atc ttc ccg gaa aac ctc ggt tct gcg aaa ctg				499
Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser Ala Lys Leu				
	120	125	130	
cat gaa tcg aag ggc ttc gtg aag gtg ggc acc atg cac caa atg gca				547
His Glu Ser Lys Gly Phe Val Lys Val Gly Thr Met His Gln Met Ala				
	135	140	145	
agg atg ccc tac ggc gag atg gaa gga caa tgg cgc gat tgt gat ctg				595
Arg Met Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp Cys Asp Leu				
	150	155	160	165
tgg gag tgc ctc tta tcc gtt cca gag caa gct caa agt tcc				637
Trp Glu Cys Leu Leu Ser Val Pro Glu Gln Ala Gln Ser Ser				
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<212> PRT

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Thr Tyr Glu Thr Ser Gly Pro Thr Trp Asp Gln Phe Ser Gln Ser Lys
35 40 45

Ile Met Asp Thr Val Met Val Ala Val Glu Asn Asn Asp Pro Asp Phe
50 55 60

Ile Leu Gly Trp Val Ser Ala Ala Pro Ile Ser Ser Arg Gln Val Phe
65 70 75 80

His Gly Val Val Glu Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly
85 90 95

Arg Gly Ile Gly Gly Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu
100 105 110

Ser Asn Gly Ile Trp Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu

115

120

125

Gly Ser Ala Lys Leu His Glu Ser Lys Gly Phe Val Lys Val Gly Thr
 130 135 140

Met His Gln Met Ala Arg Met Pro Tyr Gly Glu Met Glu Gly Gln Trp
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Gln Ser Ser

<210> 21

<211> 606

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(583)

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 Val Arg Asp Ile Tyr
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gaa ttg ggc ctg gag acg gga cat gcg act tat gag act tct ggt ccc 163
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acg tgg gac cag ttc tcc caa tct aaa atc atg gat acc gtc atg gtg 211
 Thr Trp Asp Gln Phe Ser Gln Ser Lys Ile Met Asp Thr Val Met Val
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gcg gta gaa aac aac gac ccg gac ttc atc ctc gga tgg gtg tct gct 259
 Ala Val Glu Asn Asn Asp Pro Asp Phe Ile Leu Gly Trp Val Ser Ala
 40 45 50

gct cca att tca agc cga cag gtt ttc cat gga gtg gtg gaa gat tcc 307
 Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly Val Val Glu Asp Ser
 55 60 65

atc tat atc cac ccc cag ggc caa ggc cga gga atc ggc ggc gct ttg 355
 Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly Ile Gly Gly Ala Leu
 70 75 80 85

ctc gac gcc ctt atc acc tac tgc gaa agc aac ggc atc tgg tgc atc 403
 Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn Gly Ile Trp Ser Ile
 90 95 100

cac tcc tgg atc ttc ccg gaa aac ctc ggt tct gcg aaa ctg cat gaa 451

His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser Ala Lys Leu His Glu
 105 110 115

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 Ser Lys Gly Phe Val Lys Val Gly Thr Met His Gln Met Ala Arg Met
 120 125 130

ccc tac ggc gag atg gaa gga caa tgg cgc gat tgt gat ctg tgg gag 547
 Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp Cys Asp Leu Trp Glu
 135 140 145

tgc ctc tta tcc gtt cca gag caa gct caa agt tcc taaagcaatt 593
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<210> 22

<211> 161

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<213> Corynebacterium glutamicum

<400> 22

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Asp Thr Val Met Val Ala Val Glu Asn Asn Asp Pro Asp Phe Ile Leu
 35 40 45

Gly Trp Val Ser Ala Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly
 50 55 60

Val Val Glu Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly
 65 70 75 80

Ile Gly Gly Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn
 85 90 95

Gly Ile Trp Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser
 100 105 110

Ala Lys Leu His Glu Ser Lys Gly Phe Val Lys Val Gly Thr Met His
 115 120 125

Gln Met Ala Arg Met Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp
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Ser

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXN01345

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                                         Met Arg Phe Gly Leu
                                         1           5

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Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Ala Val Asp Arg Gly Asn
                    10                15                20

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Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly Asp Thr His Asp Phe
                    25                30                35

att cca tct gtg gtg gcc ctc aag gca gat agg att gtc gcg ggt tgg 259
Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg Ile Val Ala Gly Trp
                    40                45                50

gat gct att gag gtt ggg cag gac cac cct tcc ttc gta cgt tct ttc 307
Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser Phe Val Arg Ser Phe
                    55                60                65

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Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu Ala Thr Pro Val Tyr
                    70                75                80                85

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Leu Gly Asp His Val His Pro Leu Gly Ala Val Leu Glu Ala Phe Ala
                    90                95                100

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Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln Thr Gln Leu Gly Asp
                    105                110                115

acc tcc ccg atc gaa gta gtc att ggt gtg ccc gcc aac tcc cac agc 499
Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro Ala Asn Ser His Ser
                    120                125                130

gcc cag cga ctg ctc acc atg tcc gcc ttc agc gcc aca ggc atc acc 547
Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser Ala Thr Gly Ile Thr
                    135                140                145

gtt gtc ggt ttg gtc aat gag ccc agc gcc gca gct ttc gag tac acc 595
Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala Ala Phe Glu Tyr Thr
                    150                155                160                165
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agc ccc gga gat att tcc ctg ctc agt gaa atc aag att cct ttt gat 1411
 Ser Pro Gly Asp Ile Ser Leu Leu Ser Glu Ile Lys Ile Pro Phe Asp
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agc tcc atc acc gat gtg gat gct acc gag att tca cgt ttc gat ggc 1459
 Ser Ser Ile Thr Asp Val Asp Ala Thr Glu Ile Ser Arg Phe Asp Gly
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 Pro Glu Val Glu Glu Thr Ile Thr Val Asn Asp Asn Gly Val Ala Ser
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att tcc atc aag ata ctc ggc ggc gtt acc gtc gag cac aca att 1552
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 <213> Corynebacterium glutamicum

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 35 40 45

Ile Val Ala Gly Trp Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser
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Phe Val Arg Ser Phe Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu
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Ala Thr Pro Val Tyr Leu Gly Asp His Val His Pro Leu Gly Ala Val
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Leu Glu Ala Phe Ala Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln
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Thr Gln Leu Gly Asp Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro
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 130 135 140
 Ala Thr Gly Ile Thr Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala
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 Ala Phe Glu Tyr Thr His Arg His Ala Arg Thr Leu Asn Ser Lys Arg
 165 170 175
 Gln Ala Ile Val Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser
 180 185 190
 Leu Ile Arg Ile Asp Gly Thr His His Glu Val Val Ser Ser Ile Gly
 195 200 205
 Ile Ser Arg Leu Gly Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys
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 Ala Leu Lys Ala Ala Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala
 225 230 235 240
 Lys Asn Thr Leu Leu Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val
 245 250 255
 Pro Gln Ser Arg Arg Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr
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 Val Pro Val Asn Lys Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys
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 Ser Leu Ser Ile Met Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp
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 Ser Asp Ile Ala Gly Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro
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 Leu Val Ser Arg Leu Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg
 325 330 335
 Ser Pro Phe Pro Ser Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala
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 Asp Pro Ser Ser Gly Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile
 355 360 365
 Gly Val Phe Arg Glu His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro
 370 375 380
 Leu Ile Ala Pro Asp Thr Asp Ser Ala Thr Val Ala Lys Arg Cys Tyr
 385 390 395 400
 Lys Ala Val His Asn Ile Gly Trp Phe Arg Phe Val Glu Tyr Ser Thr
 405 410 415
 Val Ser Glu Asp Gly Ser Pro Gly Asp Ile Ser Leu Leu Ser Glu Ile
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Lys Ile Pro Phe Asp Ser Ser Ile Thr Asp Val Asp Ala Thr Glu Ile
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Ser Arg Phe Asp Gly Pro Glu Val Glu Glu Thr Ile Thr Val Asn Asp
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Glu His Thr Ile

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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1267)

<223> FRXA01345

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Met Arg Phe Gly Leu
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gac ttg gga act acc cgc aca atc gcg gcc gcc gtg gac cgc gga aac 163
Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Ala Val Asp Arg Gly Asn
10 15 20

tat ccc atc gtc act gtg gaa gat tct tta ggc gac acc cac gat ttc 211
Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly Asp Thr His Asp Phe
25 30 35

att cca tct gtg gtg gcc ctc aag gca gat agg att gtc gcg ggt tgg 259
Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg Ile Val Ala Gly Trp
40 45 50

gat gct att gag gtt ggg cag gac cac cct tcc ttc gta cgt tct ttc 307
Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser Phe Val Arg Ser Phe
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aaa cgc cta ctc tct gaa ccc aat gtc acg gaa gcc acc ccg gtc tac 355
Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu Ala Thr Pro Val Tyr
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Leu Gly Asp His Val His Pro Leu Gly Ala Val Leu Glu Ala Phe Ala
90 95 100

gaa aac gtg gtc act gcg ctg cgt gca ttt cag acg caa ttg gga gat 451
Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln Thr Gln Leu Gly Asp
105 110 115

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Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro Ala Asn Ser His Ser	
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gcc cag cga ctg ctc acc atg tcc gcc ttc agc gcc aca ggc atc acc	547
Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser Ala Thr Gly Ile Thr	
135 140 145	
gtt gtc ggt ttg gtc aat gag ccc agc gcc gca gct ttc gag tac acc	595
Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala Ala Phe Glu Tyr Thr	
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His Arg His Ala Arg Thr Leu Asn Ser Lys Arg Gln Ala Ile Val Val	
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Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser Leu Ile Arg Ile Asp	
185 190 195	
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Gly Thr His His Glu Val Val Ser Ser Ile Gly Ile Ser Arg Leu Gly	
200 205 210	
ggc gat gat ttc gat gaa atc ctc ctc caa tgc gcg ctc aag gcc gca	787
Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys Ala Leu Lys Ala Ala	
215 220 225	
ggc aga cag cac gat gcg ttt ggc aag cgt gct aaa aac acg ctt ctc	835
Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala Lys Asn Thr Leu Leu	
230 235 240 245	
gac gaa tcc cgc aac gcg aag gaa gct ctt gtt ccg caa tcc cgt cgc	883
Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val Pro Gln Ser Arg Arg	
250 255 260	
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Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr Val Pro Val Asn Lys	
265 270 275	
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Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys Ser Leu Ser Ile Met	
280 285 290	
gaa ccc ctc atc ggc gtc gat gat ctt aaa gat tcc gac atc gca ggc	1027
Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp Ser Asp Ile Ala Gly	
295 300 305	
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Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro Leu Val Ser Arg Leu	
310 315 320 325	
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Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg Ser Pro Phe Pro Ser	
330 335 340	

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 Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala Asp Pro Ser Ser Gly
 345 350 355

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 Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile Gly Val Phe Arg Glu
 360 365 370

cac gat tct ggt cgt gcc gtg agc ttt gac ccg ctg atc gcc ccg gac 1267
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<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

Ile Val Ala Gly Trp Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser
 50 55 60

Phe Val Arg Ser Phe Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu
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Ala Thr Pro Val Tyr Leu Gly Asp His Val His Pro Leu Gly Ala Val
 85 90 95

Leu Glu Ala Phe Ala Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln
 100 105 110

Thr Gln Leu Gly Asp Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro
 115 120 125

Ala Asn Ser His Ser Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser
 130 135 140

Ala Thr Gly Ile Thr Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala
 145 150 155 160

Ala Phe Glu Tyr Thr His Arg His Ala Arg Thr Leu Asn Ser Lys Arg
 165 170 175

Gln Ala Ile Val Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser
 180 185 190

Leu Ile Arg Ile Asp Gly Thr His His Glu Val Val Ser Ser Ile Gly
 195 200 205

Ile Ser Arg Leu Gly Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys
 210 215 220
 Ala Leu Lys Ala Ala Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala
 225 230 235 240
 Lys Asn Thr Leu Leu Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val
 245 250 255
 Pro Gln Ser Arg Arg Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr
 260 265 270
 Val Pro Val Asn Lys Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys
 275 280 285
 Ser Leu Ser Ile Met Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp
 290 295 300
 Ser Asp Ile Ala Gly Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro
 305 310 315 320
 Leu Val Ser Arg Leu Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg
 325 330 335
 Ser Pro Phe Pro Ser Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala
 340 345 350
 Asp Pro Ser Ser Gly Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile
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 Gly Val Phe Arg Glu His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro
 370 375 380
 Leu Ile Ala Pro Asp
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 <213> Corynebacterium glutamicum

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 <223> RXA02541

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 Val Asn Asn Ser Glu
 1 5
 tgg gca aat aag aac tat tac gca gac ctg ggg gtc tcc tcg tcc gct 163
 Trp Ala Asn Lys Asn Tyr Tyr Ala Asp Leu Gly Val Ser Ser Ser Ala

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tca	gaa	gat	gag	atc	aaa	aag	gct	tac	cg	cgc	aag	ctc	gcc	agg	gaa	aat													211
Ser	Glu	Asp	Glu	Ile	Lys	Lys	Ala	Tyr	Arg	Lys	Leu	Ala	Arg	Glu	Asn														
			25					30					35																
cac	cca	gat	aaa	aat	cca	ggt	gac	aag	gcc	gct	gaa	gat	cga	ttc	aaa														259
His	Pro	Asp	Lys	Asn	Pro	Gly	Asp	Lys	Ala	Ala	Glu	Asp	Arg	Phe	Lys														
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aaa	gcg	gcc	gag	gca	tat	gac	gta	ctt	ggt	gat	gac	aag	aaa	cga	aaa														307
Lys	Ala	Ala	Glu	Ala	Tyr	Asp	Val	Leu	Gly	Asp	Asp	Lys	Lys	Arg	Lys														
	55					60					65																		
gaa	tac	gac	gag	ctc	aaa	gca	ctt	cta	gct	tct	ggt	gga	atc	cgc	gga														355
Glu	Tyr	Asp	Glu	Leu	Lys	Ala	Leu	Leu	Ala	Ser	Gly	Gly	Ile	Arg	Gly														
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gga	ttc	gga	agc	gga	ggt	gcg	gga	ttc	ccc	ggc	ggg	ttt	cgc	acg	tcg														403
Gly	Phe	Gly	Ser	Gly	Gly	Ala	Gly	Phe	Pro	Gly	Gly	Phe	Arg	Thr	Ser														
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acg	gga	gga	ttc	gac	acc	tca	gac	ctc	ttc	gga	gga	gga	caa	ggt	gga														451
Thr	Gly	Gly	Phe	Asp	Thr	Ser	Asp	Leu	Phe	Gly	Gly	Gly	Gln	Gly	Gly														
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ggg	ttt	tct	acg	gac	ggc	ggt	ttg	ggc	gat	atc	ttc	ggt	ggc	ctt	ttc														499
Gly	Phe	Ser	Thr	Asp	Gly	Gly	Leu	Gly	Asp	Ile	Phe	Gly	Gly	Leu	Phe														
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aac	cgc	ggc	gct	ggt	tct	cac	cag	tca	gct	agg	ccg	acg	cgg	ggg	gcg														547
Asn	Arg	Gly	Ala	Gly	Ser	His	Gln	Ser	Ala	Arg	Pro	Thr	Arg	Gly	Ala														
	135					140					145																		
gat	gta	caa	acc	gaa	ata	act	ctc	tcg	ttt	ggt	gag	gca	gcg	aaa	ggc														595
Asp	Val	Gln	Thr	Glu	Ile	Thr	Leu	Ser	Phe	Val	Glu	Ala	Ala	Lys	Gly														
	150				155				160					165															
acg	acc	atc	cca	gtg	gaa	ctc	acc	ggc	gat	gcg	ccc	tgc	aac	acc	tgc														643
Thr	Thr	Ile	Pro	Val	Glu	Leu	Thr	Gly	Asp	Ala	Pro	Cys	Asn	Thr	Cys														
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cac	gga	tcg	ggc	tcc	aaa	tca	ggc	cac	ccc	gca	aaa	tgt	gga	acc	tgt														691
His	Gly	Ser	Gly	Ser	Lys	Ser	Gly	His	Pro	Ala	Lys	Cys	Gly	Thr	Cys														
			185					190				195																	
gat	gga	acc	gga	ttc	acc	tct	gag	aac	aag	ggt	gct	ttc	gga	ttc	tcc														739
Asp	Gly	Thr	Gly	Phe	Thr	Ser	Glu	Asn	Lys	Gly	Ala	Phe	Gly	Phe	Ser														
		200					205					210																	
gct	cca	tgt	gca	acc	tgt	ggt	ggc	act	ggt	gaa	ata	atc	act	gat	cct														787
Ala	Pro	Cys	Ala	Thr	Cys	Gly	Gly	Thr	Gly	Glu	Ile	Ile	Thr	Asp	Pro														
	215					220					225																		
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Cys	Asp	Asn	Cys	His	Gly	Arg	Gly	Thr	Val	Arg	Lys	Ser	Arg	Ser	Ile														
	230				235				240						245														

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 Thr Val Arg Ile Pro Thr Gly Val Glu Asp Gly Gln Lys Val Arg Leu
 250 255 260

gca ggc caa ggc gaa gca gga cca aat ggc aaa cca gcg ggc gat ctc 931
 Ala Gly Gln Gly Glu Ala Gly Pro Asn Gly Lys Pro Ala Gly Asp Leu
 265 270 275

ttt gtg aaa gtc cac gtg aaa aag gac gat gtg ttc aca cgc gac ggc 979
 Phe Val Lys Val His Val Lys Lys Asp Asp Val Phe Thr Arg Asp Gly
 280 285 290

agc aac att ttg atc acc att ccc gtg agc ttc agc gag ctg gct ttg 1027
 Ser Asn Ile Leu Ile Thr Ile Pro Val Ser Phe Ser Glu Leu Ala Leu
 295 300 305

ggt ggc gct att tct gtg cca acg ctc aac aag cct gta aaa ctc aag 1075
 Gly Gly Ala Ile Ser Val Pro Thr Leu Asn Lys Pro Val Lys Leu Lys
 310 315 320 325

cta cct gcg gga acg cca gat ggt cgt act ttg cgt gta cgc ggt cgc 1123
 Leu Pro Ala Gly Thr Pro Asp Gly Arg Thr Leu Arg Val Arg Gly Arg
 330 335 340

ggt atc gaa gca cgt gat tcc act ggt gat ctg ctg gtt aca gtc cag 1171
 Gly Ile Glu Ala Arg Asp Ser Thr Gly Asp Leu Leu Val Thr Val Gln
 345 350 355

gtt tct gtc ccg aag aat ctg gat gac aac gct gcg gaa gct ctc cgc 1219
 Val Ser Val Pro Lys Asn Leu Asp Asp Asn Ala Ala Glu Ala Leu Arg
 360 365 370

gca tat gct gaa gca gaa act aat tca ggt ttt gat ccc cgc gct aac 1267
 Ala Tyr Ala Glu Ala Glu Thr Asn Ser Gly Phe Asp Pro Arg Ala Asn
 375 380 385

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<210> 28

<211> 395

<212> PRT

<213> Corynebacterium glutamicum

<400> 28

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Leu Ala Arg Glu Asn His Pro Asp Lys Asn Pro Gly Asp Lys Ala Ala
 35 40 45

Glu Asp Arg Phe Lys Lys Ala Ala Glu Ala Tyr Asp Val Leu Gly Asp
 50 55 60
 Asp Lys Lys Arg Lys Glu Tyr Asp Glu Leu Lys Ala Leu Leu Ala Ser
 65 70 75 80
 Gly Gly Ile Arg Gly Gly Phe Gly Ser Gly Gly Ala Gly Phe Pro Gly
 85 90 95
 Gly Phe Arg Thr Ser Thr Gly Gly Phe Asp Thr Ser Asp Leu Phe Gly
 100 105 110
 Gly Gly Gln Gly Gly Gly Phe Ser Thr Asp Gly Gly Leu Gly Asp Ile
 115 120 125
 Phe Gly Gly Leu Phe Asn Arg Gly Ala Gly Ser His Gln Ser Ala Arg
 130 135 140
 Pro Thr Arg Gly Ala Asp Val Gln Thr Glu Ile Thr Leu Ser Phe Val
 145 150 155 160
 Glu Ala Ala Lys Gly Thr Thr Ile Pro Val Glu Leu Thr Gly Asp Ala
 165 170 175
 Pro Cys Asn Thr Cys His Gly Ser Gly Ser Lys Ser Gly His Pro Ala
 180 185 190
 Lys Cys Gly Thr Cys Asp Gly Thr Gly Phe Thr Ser Glu Asn Lys Gly
 195 200 205
 Ala Phe Gly Phe Ser Ala Pro Cys Ala Thr Cys Gly Gly Thr Gly Glu
 210 215 220
 Ile Ile Thr Asp Pro Cys Asp Asn Cys His Gly Arg Gly Thr Val Arg
 225 230 235 240
 Lys Ser Arg Ser Ile Thr Val Arg Ile Pro Thr Gly Val Glu Asp Gly
 245 250 255
 Gln Lys Val Arg Leu Ala Gly Gln Gly Glu Ala Gly Pro Asn Gly Lys
 260 265 270
 Pro Ala Gly Asp Leu Phe Val Lys Val His Val Lys Lys Asp Asp Val
 275 280 285
 Phe Thr Arg Asp Gly Ser Asn Ile Leu Ile Thr Ile Pro Val Ser Phe
 290 295 300
 Ser Glu Leu Ala Leu Gly Gly Ala Ile Ser Val Pro Thr Leu Asn Lys
 305 310 315 320
 Pro Val Lys Leu Lys Leu Pro Ala Gly Thr Pro Asp Gly Arg Thr Leu
 325 330 335
 Arg Val Arg Gly Arg Gly Ile Glu Ala Arg Asp Ser Thr Gly Asp Leu
 340 345 350

Leu Val Thr Val Gln Val Ser Val Pro Lys Asn Leu Asp Asp Asn Ala
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<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(754)

<223> RXA02542

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Met Thr Thr Pro Asn
1 5
gga atg ccc gac aat cct ggg gat cct gaa aat acc gat cca gag gca 163
Gly Met Pro Asp Asn Pro Gly Asp Pro Glu Asn Thr Asp Pro Glu Ala
10 15 20
acc tct gct gat cgt gct gag cag gca gct gaa gaa gca gct gcc cgc 211
Thr Ser Ala Asp Arg Ala Glu Gln Ala Ala Glu Glu Ala Ala Ala Arg
25 30 35
caa gcg gag gaa tct cca ttt gga cag gcc tca gag gaa gaa att tct 259
Gln Ala Glu Glu Ser Pro Phe Gly Gln Ala Ser Glu Glu Glu Ile Ser
40 45 50
cca gag ctc gaa gca gag atc aat gat ctt cta tca gat gtt gat cca 307
Pro Glu Leu Glu Ala Glu Ile Asn Asp Leu Leu Ser Asp Val Asp Pro
55 60 65
gat ttg gat ggc gat ggt gaa gtg tcc gct gta gaa aca cag ctt gcc 355
Asp Leu Asp Gly Asp Gly Glu Val Ser Ala Val Glu Thr Gln Leu Ala
70 75 80 85
gaa cgc act gag gat ctg cag cga gtc acc gct gag tac gcc aac tac 403
Glu Arg Thr Glu Asp Leu Gln Arg Val Thr Ala Glu Tyr Ala Asn Tyr
90 95 100
cgt cga cgt acc gag cgt gaa cgc cag ggc atc atc gac acc gca cgc 451
Arg Arg Arg Thr Glu Arg Glu Arg Gln Gly Ile Ile Asp Thr Ala Arg
105 110 115
gca ggt gtt gtt acc caa ctt ctg ccg ttg ctc gac gat ctt gac ctg 499
Ala Gly Val Val Thr Gln Leu Leu Pro Leu Leu Asp Asp Leu Asp Leu
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120	125	130	
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135	140	145	
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Asp Lys Leu Ile Asn Ile Leu Gly Gly Leu Lys Val Glu Ser Phe Gly			
150	155	160	165
gag atc ggc gaa gca ttc gat cca gag atc cac gaa gca gta cag gat			643
Glu Ile Gly Glu Ala Phe Asp Pro Glu Ile His Glu Ala Val Gln Asp			
170	175	180	
ctc tca cag ggt gat gtc aag gtt ctg gga acg gta ctc cgc aag gga			691
Leu Ser Gln Gly Asp Val Lys Val Leu Gly Thr Val Leu Arg Lys Gly			
185	190	195	
tac cgc ctc ggc gac cgc gtc atc cgc acc gca atg gtc ctc att ggg			739
Tyr Arg Leu Gly Asp Arg Val Ile Arg Thr Ala Met Val Leu Ile Gly			
200	205	210	
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Asp Pro Glu Glu Ser			
215			

<210> 30

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

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20	25	30	
Glu Ala Ala Ala Arg Gln Ala Glu Glu Ser Pro Phe Gly Gln Ala Ser			
35	40	45	
Glu Glu Glu Ile Ser Pro Glu Leu Glu Ala Glu Ile Asn Asp Leu Leu			
50	55	60	
Ser Asp Val Asp Pro Asp Leu Asp Gly Asp Gly Glu Val Ser Ala Val			
65	70	75	80
Glu Thr Gln Leu Ala Glu Arg Thr Glu Asp Leu Gln Arg Val Thr Ala			
85	90	95	
Glu Tyr Ala Asn Tyr Arg Arg Arg Thr Glu Arg Glu Arg Gln Gly Ile			
100	105	110	
Ile Asp Thr Ala Arg Ala Gly Val Val Thr Gln Leu Leu Pro Leu Leu			
115	120	125	

Asp Asp Leu Asp Leu Ala Glu Gln His Gly Asp Leu Asn Glu Gly Pro
 130 135 140
 Leu Lys Ser Leu Ser Asp Lys Leu Ile Asn Ile Leu Gly Gly L u Lys
 145 150 155 160
 Val Glu Ser Phe Gly Glu Ile Gly Glu Ala Phe Asp Pro Glu Ile His
 165 170 175
 Glu Ala Val Gln Asp Leu Ser Gln Gly Asp Val Lys Val Leu Gly Thr
 180 185 190
 Val Leu Arg Lys Gly Tyr Arg Leu Gly Asp Arg Val Ile Arg Thr Ala
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 Met Val Leu Ile Gly Asp Pro Glu Glu Ser
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<220>
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 <222> (101)..(1954)
 <223> RXN02543

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 Met Gly Arg Ala Val
 1 5
 gga att gac ctt gga acc acc aac tct gtg gtt tcc gta ctt gaa ggc 163
 Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val Ser Val Leu Glu Gly
 10 15 20
 ggc gag cca gta gtt atc gca aac gca gaa ggc tca cgc acc acc cct 211
 Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly Ser Arg Thr Thr Pro
 25 30 35
 tcc gtc gtt gca ttc gca aag aac ggt gaa gtt cta gtc ggc cag tcc 259
 Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val Leu Val Gly Gln Ser
 40 45 50
 gct aag aac cag gcg gtc acc aac gtt gac cgc acc att cgc tcc gtc 307
 Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg Thr Ile Arg Ser Val
 55 60 65
 aag cgc cac atc ggc acc gac tgg tcc gtt gct atc gat gac aag aac 355
 Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala Ile Asp Asp Lys Asn
 70 75 80 85
 tac acc tca cag gaa atc tcg gct cgt acc ctg atg aag ctg aag cgc 403

Tyr	Thr	Ser	Gln	Glu	Ile	Ser	Ala	Arg	Thr	Leu	Met	Lys	Leu	Lys	Arg	
				90					95					100		
gac	gct	gaa	gca	tac	ctg	ggc	gag	gac	gtc	act	gat	gct	gtt	att	acc	451
Asp	Ala	Glu	Ala	Tyr	Leu	Gly	Glu	Asp	Val	Thr	Asp	Ala	Val	Ile	Thr	
			105					110					115			
ggt	cct	gca	tac	ttc	gag	gac	tca	cag	cgc	cag	gca	acc	aag	gaa	gct	499
Val	Pro	Ala	Tyr	Phe	Glu	Asp	Ser	Gln	Arg	Gln	Ala	Thr	Lys	Glu	Ala	
			120				125					130				
ggt	cag	atc	gca	ggc	ctt	aac	ggt	ctg	cgt	att	ggt	aac	gag	cca	acc	547
Gly	Gln	Ile	Ala	Gly	Leu	Asn	Val	Leu	Arg	Ile	Val	Asn	Glu	Pro	Thr	
			135			140					145					
gcg	gct	gca	ctt	gca	tac	ggc	ctt	gag	aag	ggc	gag	cag	gag	cag	acc	595
Ala	Ala	Ala	Leu	Ala	Tyr	Gly	Leu	Glu	Lys	Gly	Glu	Gln	Glu	Gln	Thr	
150					155					160					165	
att	ctg	gta	ttc	gac	ctc	ggt	ggc	ggc	acc	ttc	gac	gtc	tcc	ctc	cta	643
Ile	Leu	Val	Phe	Asp	Leu	Gly	Gly	Gly	Thr	Phe	Asp	Val	Ser	Leu	Leu	
				170					175					180		
gag	atc	ggc	gac	ggt	gtt	gtt	gag	gtt	cgc	gca	acc	tcc	ggc	gat	aac	691
Glu	Ile	Gly	Asp	Gly	Val	Val	Glu	Val	Arg	Ala	Thr	Ser	Gly	Asp	Asn	
			185					190					195			
gag	ctc	ggt	ggc	gac	gac	tgg	gat	cag	cgt	atc	gtt	gac	tgg	ctg	gta	739
Glu	Leu	Gly	Gly	Asp	Asp	Trp	Asp	Gln	Arg	Ile	Val	Asp	Trp	Leu	Val	
		200					205					210				
gag	aag	ttc	cag	tcc	tcc	aac	ggc	att	gac	ctg	acc	aag	gac	aag	atg	787
Glu	Lys	Phe	Gln	Ser	Ser	Asn	Gly	Ile	Asp	Leu	Thr	Lys	Asp	Lys	Met	
	215					220					225					
gcc	ctg	cag	cgt	ctg	cgt	gag	gca	gct	gag	aag	gca	aag	atc	gag	ctg	835
Ala	Leu	Gln	Arg	Leu	Arg	Glu	Ala	Ala	Glu	Lys	Ala	Lys	Ile	Glu	Leu	
230					235					240					245	
tcc	tct	tcc	cag	agt	gca	aac	atc	aac	ctt	cct	tac	atc	acc	gtt	gat	883
Ser	Ser	Ser	Gln	Ser	Ala	Asn	Ile	Asn	Leu	Pro	Tyr	Ile	Thr	Val	Asp	
				250					255					260		
gca	gac	aag	aac	cca	ctg	ttc	ttg	gat	gag	acc	ctt	tcc	cgt	gcc	gag	931
Ala	Asp	Lys	Asn	Pro	Leu	Phe	Leu	Asp	Glu	Thr	Leu	Ser	Arg	Ala	Glu	
			265					270					275			
ttc	cag	cgc	atc	acc	cag	gac	ctc	ctg	gcc	cgc	acc	aag	act	cct	ttc	979
Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	Leu	Ala	Arg	Thr	Lys	Thr	Pro	Phe	
			280				285					290				
aac	cag	gtt	gtt	aag	gac	gct	ggc	gtg	tcc	gtc	tcg	gag	atc	gac	cac	1027
Asn	Gln	Val	Val	Lys	Asp	Ala	Gly	Val	Ser	Val	Ser	Glu	Ile	Asp	His	
		295				300					305					
gtt	gtt	ctc	gtc	ggt	ggt	tcc	acc	cgt	atg	cct	gct	gtt	acc	gaa	ctg	1075
Val	Val	Leu	Val	Gly	Gly	Ser	Thr	Arg	Met	Pro	Ala	Val	Thr	Glu	Leu	

310	315	320	325	
gtc aag gaa ctg acc ggt gga cgt gag cca aac aag ggt gtt aac cca				1123
Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn Lys Gly Val Asn Pro				
330		335	340	
gat gag gtt gtt gca gtt ggt gca gca ctt cag gcc ggt gtt ctc cgc				1171
Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln Ala Gly Val Leu Arg				
345		350	355	
ggc gag gtc aag gat gtt ctt ctt ctt gac gtc acc cca ctg tcc ctc				1219
Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val Thr Pro Leu Ser Leu				
360		365	370	
ggc att gag acc aag ggt ggc gtg atg acc aag ctc atc gag cgc aac				1267
Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys Leu Ile Glu Arg Asn				
375		380	385	
acc acc atc cct acc aag cgt tcc gag acc ttc acc acc gca gag gac				1315
Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe Thr Thr Ala Glu Asp				
390		395	400	405
aac cag cct tct gtt cag atc cag gtc ttc cag ggc gag cgt gaa atc				1363
Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln Gly Glu Arg Glu Ile				
410		415	420	
gca acc gcc aac aag ctg ctc gga tcc ttc gag ctc ggc ggc atc gca				1411
Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu Leu Gly Gly Ile Ala				
425		430	435	
cct gca cca cgt ggc gtc cca cag atc gag gtc act ttc gac atc gac				1459
Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Ile Asp				
440		445	450	
gcc aac ggc atc gtc cac gtc acc gca aag gac aag ggt act ggc aag				1507
Ala Asn Gly Ile Val His Val Thr Ala Lys Asp Lys Gly Thr Gly Lys				
455		460	465	
gaa aac acc atc acc att cag gac ggc tcc ggt ctc tcc cag gat gaa				1555
Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly Leu Ser Gln Asp Glu				
470		475	480	485
att gat cgc atg atc aag gat gct gaa gct cac gct gat gag gac aag				1603
Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His Ala Asp Glu Asp Lys				
490		495	500	
aag cgc cgc gag gag cag gaa gtc cgc aac aac gct gag tcc ctg gtt				1651
Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn Ala Glu Ser Leu Val				
505		510	515	
tac cag acc cgc aag ttc gtt gaa gag aac tcc gag aag gtc tcc gaa				1699
Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser Glu Lys Val Ser Glu				
520		525	530	
gac ctc aag gca aag gtc gaa gag gca gcc aag ggc gtt gaa gaa gca				1747
Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys Gly Val Glu Glu Ala				
535		540	545	

ctc aag ggc gag gac ctc gag gca atc aag gct gca gtt gag aag ctg 1795
 Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala Ala Val Glu Lys Leu
 550 555 560 565

aac acc gag tcc cag gaa atg ggt aag gct atc tac gag gct gac gct 1843
 Asn Thr Glu Ser Gln Glu Met Gly Lys Ala Ile Tyr Glu Ala Asp Ala
 570 575 580

gct gct ggt gca acc cag gct gac gca ggt gca gaa ggc gct gca gat 1891
 Ala Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala Glu Gly Ala Ala Asp
 585 590 595

gac aat gtt gtt gac gct gaa gtt gtc gaa gac gac gca gct gac aat 1939
 Asp Asn Val Val Asp Ala Glu Val Val Glu Asp Asp Ala Ala Asp Asn
 600 605 610

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 Gly Glu Asp Lys Lys
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<210> 32

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 32

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 20 25 30

Ser Arg Thr Thr Pro Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val
 35 40 45

Leu Val Gly Gln Ser Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
 50 55 60

Thr Ile Arg Ser Val Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala
 65 70 75 80

Ile Asp Asp Lys Asn Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu
 85 90 95

Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr
 100 105 110

Asp Ala Val Ile Thr Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln
 115 120 125

Ala Thr Lys Glu Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
 130 135 140

Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly
 145 150 155 160

Glu Gln Glu Gln Thr Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
 165 170 175
 Asp Val Ser Leu Leu Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala
 180 185 190
 Thr Ser Gly Asp Asn Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile
 195 200 205
 Val Asp Trp Leu Val Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu
 210 215 220
 Thr Lys Asp Lys Met Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys
 225 230 235 240
 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro
 245 250 255
 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr
 260 265 270
 Leu Ser Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Ala Arg
 275 280 285
 Thr Lys Thr Pro Phe Asn Gln Val Val Lys Asp Ala Gly Val Ser Val
 290 295 300
 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
 305 310 315 320
 Ala Val Thr Glu Leu Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn
 325 330 335
 Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
 340 345 350
 Ala Gly Val Leu Arg Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
 355 360 365
 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys
 370 375 380
 Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
 385 390 395 400
 Thr Thr Ala Glu Asp Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln
 405 410 415
 Gly Glu Arg Glu Ile Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu
 420 425 430
 Leu Gly Gly Ile Ala Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val
 435 440 445
 Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp
 450 455 460

Lys Gly Thr Gly Lys Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly
 465 470 475 480
 Leu Ser Gln Asp Glu Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His
 485 490 495
 Ala Asp Glu Asp Lys Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn
 500 505 510
 Ala Glu Ser Leu Val Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser
 515 520 525
 Glu Lys Val Ser Glu Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys
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 Gly Val Glu Glu Ala Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala
 545 550 555 560
 Ala Val Glu Lys Leu Asn Thr Glu Ser Gln Glu Met Gly Lys Ala Ile
 565 570 575
 Tyr Glu Ala Asp Ala Ala Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala
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 <223> FRXA02543

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 Met Gly Arg Ala Val
 1 5
 gga att gac ctt gga acc acc aac tct gtg gtt tcc gta ctt gaa ggc 163
 Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val Ser Val Leu Glu Gly
 10 15 20
 ggc gag cca gta gtt atc gca aac gca gaa ggc tca cgc acc acc cct 211
 Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly Ser Arg Thr Thr Pro
 25 30 35

tcc gtc gtt gca ttc gca aag aac ggt gaa gtt cta gtc ggc cag tcc	259
Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val Leu Val Gly Gln Ser	
40 45 50	
gct aag aac cag gcg gtc acc aac gtt gac cgc acc att cgc tcc gtc	307
Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg Thr Ile Arg Ser Val	
55 60 65	
aag cgc cac atc ggc acc gac tgg tcc gtt gct atc gat gac aag aac	355
Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala Ile Asp Asp Lys Asn	
70 75 80 85	
tac acc tca cag gaa atc tcg gct cgt acc ctg atg aag ctg aag cgc	403
Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu Met Lys Leu Lys Arg	
90 95 100	
gac gct gaa gca tac ctg ggc gag gac gtc act gat gct gtt att acc	451
Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr Asp Ala Val Ile Thr	
105 110 115	
gtt cct gca tac ttc gag gac tca cag cgc cag gca acc aag gaa gct	499
Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln Ala Thr Lys Glu Ala	
120 125 130	
ggt cag atc gca ggc ctt aac gtt ctg cgt att gtt aac gag cca acc	547
Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile Val Asn Glu Pro Thr	
135 140 145	
gcg gct gca ctt gca tac ggc ctt gag aag ggc gag cag gag cag acc	595
Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly Glu Gln Glu Gln Thr	
150 155 160 165	
att ctg gta ttc gac ctc ggt ggc ggc acc ttc gac gtc tcc ctc cta	643
Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu	
170 175 180	
gag atc ggc gac ggt gtt gtt gag gtt cgc gca acc tcc ggc gat aac	691
Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala Thr Ser Gly Asp Asn	
185 190 195	
gag ctc ggt ggc gac gac tgg gat cag cgt atc gtt gac tgg ctg gta	739
Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile Val Asp Trp Leu Val	
200 205 210	
gag aag ttc cag tcc tcc aac ggc att gac ctg acc aag gac aag atg	787
Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu Thr Lys Asp Lys Met	
215 220 225	
gcc ctg cag cgt ctg cgt gag gca gct gag aag gca aag atc gag ctg	835
Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu	
230 235 240 245	
tcc tct tcc cag agt gca aac atc aac ctt cct tac atc acc gtt gat	883
Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro Tyr Ile Thr Val Asp	
250 255 260	
gca gac aag aac cca ctg ttc ttg gat gag acc ctt tcc cgt gcc gag	931

Ala	Asp	Lys	Asn	Pro	Leu	Phe	Leu	Asp	Glu	Thr	Leu	Ser	Arg	Ala	Glu		
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ttc	cag	cgc	atc	acc	cag	gac	ctc	ctg	gcc	cgc	acc	aag	act	cct	ttc	979	
Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	Leu	Ala	Arg	Thr	Lys	Thr	Pro	Phe		
		280					285					290					
aac	cag	gtt	gtt	aag	gac	gct	ggc	gtg	tcc	gtc	tcg	gag	atc	gac	cac	1027	
Asn	Gln	Val	Val	Lys	Asp	Ala	Gly	Val	Ser	Val	Ser	Glu	Ile	Asp	His		
		295				300					305						
gtt	gtt	ctc	gtc	ggc	ggc	tcc	acc	cgt	atg	cct	gct	gtt	acc	gaa	ctg	1075	
Val	Val	Leu	Val	Gly	Gly	Ser	Thr	Arg	Met	Pro	Ala	Val	Thr	Glu	Leu		
310					315					320					325		
gtc	aag	gaa	ctg	acc	ggc	gga	cgt	gag	cca	aac	aag	ggc	gtt	aac	cca	1123	
Val	Lys	Glu	Leu	Thr	Gly	Gly	Arg	Glu	Pro	Asn	Lys	Gly	Val	Asn	Pro		
				330					335					340			
gat	gag	gtt	gtt	gca	gtt	ggc	gca	gca	ctt	cag	gcc	ggc	gtt	ctc	cgc	1171	
Asp	Glu	Val	Val	Ala	Val	Gly	Ala	Ala	Leu	Gln	Ala	Gly	Val	Leu	Arg		
			345					350					355				
ggc	gag	gtc	aag	gat	gtt	ctt	ctt	ctt	gac	gtc	acc	cca	ctg	tcc	ctc	1219	
Gly	Glu	Val	Lys	Asp	Val	Leu	Leu	Leu	Asp	Val	Thr	Pro	Leu	Ser	Leu		
		360					365					370					
ggc	att	gag	acc	aag	ggc	ggc	gtg	atg	acc	aag	ctc	atc	gag	cgc	aac	1267	
Gly	Ile	Glu	Thr	Lys	Gly	Gly	Val	Met	Thr	Lys	Leu	Ile	Glu	Arg	Asn		
	375					380					385						
acc	acc	atc	cct	acc	aag	cgt	tcc	gag	acc	ttc	acc	acc	gca	gag	gac	1315	
Thr	Thr	Ile	Pro	Thr	Lys	Arg	Ser	Glu	Thr	Phe	Thr	Thr	Ala	Glu	Asp		
390					395					400					405		
aac	cag	cct	tct	gtt	cag	atc	cag	gtc	ttc	cag	ggc	gag	cgt	gaa	atc	1363	
Asn	Gln	Pro	Ser	Val	Gln	Ile	Gln	Val	Phe	Gln	Gly	Glu	Arg	Glu	Ile		
				410					415					420			
gca	acc	gcc	aac	aag	ctg	ctc	gga	tcc	ttc	gag	ctc	ggc	ggc	atc	gca	1411	
Ala	Thr	Ala	Asn	Lys	Leu	Leu	Gly	Ser	Phe	Glu	Leu	Gly	Gly	Ile	Ala		
			425					430					435				
cct	gca	cca	cgt	ggc	gtc	cca	cag	atc	gag	gtc	act	ttc	gac	atc	gac	1459	
Pro	Ala	Pro	Arg	Gly	Val	Pro	Gln	Ile	Glu	Val	Thr	Phe	Asp	Ile	Asp		
		440					445					450					
gcc	aac	ggc	atc	gtc	cac	gtc	acc	gca	aag	gac	aag	ggc	act	ggc	aag	1507	
Ala	Asn	Gly	Ile	Val	His	Val	Thr	Ala	Lys	Asp	Lys	Gly	Thr	Gly	Lys		
	455					460					465						
gaa	aac	acc	atc	acc	att	cag	gac	ggc	tcc	ggc	ctc	tcc	cag	gat	gaa	1555	
Glu	Asn	Thr	Ile	Thr	Ile	Gln	Asp	Gly	Ser	Gly	Leu	Ser	Gln	Asp	Glu		
470					475					480					485		
att	gat	cgc	atg	atc	aag	gat	gct	gaa	gct	cac	gct	gat	gag	gac	aag	1603	
Ile	Asp	Arg	Met	Ile	Lys	Asp	Ala	Glu	Ala	His	Ala	Asp	Glu	Asp	Lys		

490	495	500	
aag cgc cgc gag gag cag gaa gtc cgc aac aac gct gag tcc ctg gtt			1651
Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn Ala Glu Ser Leu Val			
505	510	515	
tac cag acc cgc aag ttc gtt gaa gag aac tcc gag aag gtc tcc gaa			1699
Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser Glu Lys Val Ser Glu			
520	525	530	
gac ctc aag gca aag gtc gaa gag gca gcc aag ggc gtt gaa gaa gca			1747
Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys Gly Val Glu Glu Ala			
535	540	545	
ctc aag ggc gag gac ctc gag gca atc aag gct gca gtt gag aag ctg			1795
Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala Ala Val Glu Lys Leu			
550	555	560	565
aac acc gag tcc cag gaa atg ggt aag gnt atc tnc gag gct gac gct			1843
Asn Thr Glu Ser Gln Glu Met Gly Lys Xaa Ile Xaa Glu Ala Asp Ala			
570	575	580	
nct gct ggt gca acc cag gct gac gca ggt gca gaa ggc gct gca gat			1891
Xaa Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala Glu Gly Ala Ala Asp			
585	590	595	
gac aat gtt gtt gac gct gaa gtt gtc gaa gac gac gca gct gac aat			1939
Asp Asn Val Val Asp Ala Glu Val Val Glu Asp Asp Ala Ala Asp Asn			
600	605	610	
ggt gag gac aag aag taaatgacta cccctaacgg aat			1977
Gly Glu Asp Lys Lys			
615			
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Ser Arg Thr Thr Pro Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val			
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Leu Val Gly Gln Ser Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg			
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Thr Ile Arg Ser Val Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala			
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Ile Asp Asp Lys Asn Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu			

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Asp	Ala	Val	Ile	Thr	Val	Pro	Ala	Tyr	Phe	Glu	Asp	Ser	Gln	Arg	Gln				
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Val	Asn	Glu	Pro	Thr	Ala	Ala	Ala	Leu	Ala	Tyr	Gly	Leu	Glu	Lys	Gly				
145					150					155					160				
Glu	Gln	Glu	Gln	Thr	Ile	Leu	Val	Phe	Asp	Leu	Gly	Gly	Gly	Thr	Phe				
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Asp	Val	Ser	Leu	Leu	Glu	Ile	Gly	Asp	Gly	Val	Val	Glu	Val	Arg	Ala				
			180					185					190						
Thr	Ser	Gly	Asp	Asn	Glu	Leu	Gly	Gly	Asp	Asp	Trp	Asp	Gln	Arg	Ile				
		195					200					205							
Val	Asp	Trp	Leu	Val	Glu	Lys	Phe	Gln	Ser	Ser	Asn	Gly	Ile	Asp	Leu				
	210					215					220								
Thr	Lys	Asp	Lys	Met	Ala	Leu	Gln	Arg	Leu	Arg	Glu	Ala	Ala	Glu	Lys				
225					230					235					240				
Ala	Lys	Ile	Glu	Leu	Ser	Ser	Ser	Gln	Ser	Ala	Asn	Ile	Asn	Leu	Pro				
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Tyr	Ile	Thr	Val	Asp	Ala	Asp	Lys	Asn	Pro	Leu	Phe	Leu	Asp	Glu	Thr				
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Leu	Ser	Arg	Ala	Glu	Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	Leu	Ala	Arg				
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Thr	Lys	Thr	Pro	Phe	Asn	Gln	Val	Val	Lys	Asp	Ala	Gly	Val	Ser	Val				
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Ser	Glu	Ile	Asp	His	Val	Val	Leu	Val	Gly	Gly	Ser	Thr	Arg	Met	Pro				
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			325					330					335						
Lys	Gly	Val	Asn	Pro	Asp	Glu	Val	Val	Ala	Val	Gly	Ala	Ala	Leu	Gln				
			340				345						350						
Ala	Gly	Val	Leu	Arg	Gly	Glu	Val	Lys	Asp	Val	Leu	Leu	Leu	Asp	Val				
		355				360						365							
Thr	Pro	Leu	Ser	Leu	Gly	Ile	Glu	Thr	Lys	Gly	Gly	Val	Met	Thr	Lys				
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Leu	Ile	Glu	Arg	Asn	Thr	Thr	Ile	Pro	Thr	Lys	Arg	Ser	Glu	Thr	Phe				

385		390		395		400
Thr Thr Ala Glu Asp Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln						
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Gly Glu Arg Glu Ile Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu						
	420		425			430
Leu Gly Gly Ile Ala Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val						
	435		440			445
Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp						
	450		455		460	
Lys Gly Thr Gly Lys Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly						
465		470		475		480
Leu Ser Gln Asp Glu Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His						
	485		490			495
Ala Asp Glu Asp Lys Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn						
	500		505			510
Ala Glu Ser Leu Val Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser						
	515		520		525	
Glu Lys Val Ser Glu Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys						
	530		535		540	
Gly Val Glu Glu Ala Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala						
545		550		555		560
Ala Val Glu Lys Leu Asn Thr Glu Ser Gln Glu Met Gly Lys Xaa Ile						
	565		570			575
Xaa Glu Ala Asp Ala Xaa Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala						
	580		585			590
Glu Gly Ala Ala Asp Asp Asn Val Val Asp Ala Glu Val Val Glu Asp						
	595		600		605	
Asp Ala Ala Asp Asn Gly Glu Asp Lys Lys						
	610		615			

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<211> 1947

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1924)

<223> RXN02280

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Met Gln Glu Ser Ser	
1 5	
cgat gat aat ttc caa gtt gac ctc ggc ggc gtt gtt gat ctt ttg agt	163
Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val Val Asp Leu Leu Ser	
10 15 20	
cgc cac att tat tcc ggt ccg agg gtg tat gtg cgt gag ttg ctg cag	211
Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val Arg Glu Leu Leu Gln	
25 30 35	
aat gcg gtt gat gct tgt act gca cgt tct gaa cag ggt gag gag ggc	259
Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu Gln Gly Glu Glu Gly	
40 45 50	
tac gag ccg agt att cgt att ccg ccg gtg acc aag gat cgt gcc acg	307
Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr Lys Asp Arg Ala Thr	
55 60 65	
ttt tca ctg gtt gat aat ggt acg ggc ctg acc gcg cag gag gcg cgg	355
Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr Ala Gln Glu Ala Arg	
70 75 80 85	
gaa ttg ctg gcg acg gtg ggg ccg acg tcg aaa cgc gat gaa ttc ggt	403
Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys Arg Asp Glu Phe Gly	
90 95 100	
ctg cag ccg gaa ggt cgc ctg ggg caa ttt ggc atc ggc ctg ctt agt	451
Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly Ile Gly Leu Leu Ser	
105 110 115	
tgt ttc atg gtg gcg gat gag atc acc atg gtg tcg cat gcg gag ggt	499
Cys Phe Met Val Ala Asp Glu Ile Thr Met Val Ser His Ala Glu Gly	
120 125 130	
gcg tcg gcg att ccg tgg act ggt cat gcg gat ggc acc ttt aac ctg	547
Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp Gly Thr Phe Asn Leu	
135 140 145	
gag att ctt ggg gat gac gca acg gat gtc att ccg gtg ggc acg act	595
Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile Pro Val Gly Thr Thr	
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gtg cac ctg act ccg cgc cct gat gag cgc acg ttg ctg acg gaa aat	643
Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr Leu Leu Thr Glu Asn	
170 175 180	
tcc gtg gtc acc att gct agt aat tat ggc cgc tac ctg ccg att cct	691
Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg Tyr Leu Pro Ile Pro	
185 190 195	
att gtg gtg cag ggt gag aaa aac acc acc atc act aca tcg ccg gtg	739
Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile Thr Thr Ser Pro Val	
200 205 210	

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Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu Tyr Ala Gly Arg Glu	
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cgc ctt ggt aaa act cct ttt gat gtc atc gat ctc acc ggt cct ggc	835
Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp Leu Thr Gly Pro Gly	
230 235 240 245	
atc gag ggt gtg gct tat gta ttg ccg gag gcc cag gct ccg cat atg	883
Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala Gln Ala Pro His Met	
250 255 260	
tcc agg cgt cac agt att tat gtc aac cgc atg ttg gtc tct gat ggg	931
Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met Leu Val Ser Asp Gly	
265 270 275	
cct tcc acg gtg ctg ccc aac tgg gcg ttc ttt gtg gaa tgt gaa atc	979
Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe Val Glu Cys Glu Ile	
280 285 290	
aat tca acc gat ttg gaa ccc acc gca tcg cgt gaa gcg ctc atg gat	1027
Asn Ser Thr Asp Leu Glu Pro Thr Ala Ser Arg Glu Ala Leu Met Asp	
295 300 305	
gac acc gcg ttc gcg gca acc agg gaa cat atc ggt gag tgc att aaa	1075
Asp Thr Ala Phe Ala Ala Thr Arg Glu His Ile Gly Glu Cys Ile Lys	
310 315 320 325	
tcg tgg ctg att aat ctc gcc atg acc aag cct cac cgc gtg cgg gaa	1123
Ser Trp Leu Ile Asn Leu Ala Met Thr Lys Pro His Arg Val Arg Glu	
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Phe Thr Ala Ile His Asp Leu Ala Leu Arg Glu Leu Cys Gln Ser Asp	
345 350 355	
gcg gac ctg gct gaa acc atg ttg ggt ctt ctc acc ttg gag acc tcc	1219
Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu Thr Leu Glu Thr Ser	
360 365 370	
cgt ggt cgc atc tcg atc ggt gag atc acc acg ttg tcc atc acc gag	1267
Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu	
375 380 385	
gat gtg tcg ctg cag ctg gct acc acg ttg gat gat ttc agg cag ctc	1315
Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu	
390 395 400 405	
aac acc att gcg cgc ccg gac acc ttg att att aat ggc ggc tac att	1363
Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Ile	
410 415 420	
cac gac agc gat ctg gct cgg ctc att ccc gtt cac tac cca ccg ctt	1411
His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu	
425 430 435	
acg gta tct act gct gac ctg cgc gaa tcc atg gat ctg atg gag ctt	1459

Thr	Val	Ser	Thr	Ala	Asp	Leu	Arg	Glu	Ser	Met	Asp	Leu	Met	Glu	Leu		
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ccg	ccg	ctg	cag	gac	att	gag	aaa	gcc	aag	gca	ctg	gat	gcg	cag	gtc	1507	
Pro	Pro	Leu	Gln	Asp	Ile	Glu	Lys	Ala	Lys	Ala	Leu	Asp	Ala	Gln	Val		
		455					460				465						
acg	gaa	tca	ttg	aag	gat	ttt	cag	atc	aag	ggc	gca	acg	agg	gtt	ttt	1555	
Thr	Glu	Ser	Leu	Lys	Asp	Phe	Gln	Ile	Lys	Gly	Ala	Thr	Arg	Val	Phe		
470						475				480					485		
gaa	ccc	gca	gat	gtt	cct	gcc	gtg	gtg	atc	att	gat	tcc	aag	gcg	cag	1603	
Glu	Pro	Ala	Asp	Val	Pro	Ala	Val	Val	Ile	Ile	Asp	Ser	Lys	Ala	Gln		
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gcc	tca	cgg	gat	cgc	aat	gaa	aca	caa	agc	gca	acc	act	gat	cgt	tgg	1651	
Ala	Ser	Arg	Asp	Arg	Asn	Glu	Thr	Gln	Ser	Ala	Thr	Thr	Asp	Arg	Trp		
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gct	gac	att	ttg	gca	acg	gtg	gat	aac	acg	ttg	agc	cgt	caa	aca	gcc	1699	
Ala	Asp	Ile	Leu	Ala	Thr	Val	Asp	Asn	Thr	Leu	Ser	Arg	Gln	Thr	Ala		
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aac	att	cca	cag	gat	cag	gga	ctg	tcg	gcg	ttg	tgc	ttg	aat	tgg	aac	1747	
Asn	Ile	Pro	Gln	Asp	Gln	Gly	Leu	Ser	Ala	Leu	Cys	Leu	Asn	Trp	Asn		
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aat	tcg	ctg	gtc	agg	aaa	ttg	gcg	tcc	act	gat	gac	acc	gcc	gtg	gtg	1795	
Asn	Ser	Leu	Val	Arg	Lys	Leu	Ala	Ser	Thr	Asp	Asp	Thr	Ala	Val	Val		
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tcg	cgc	acg	gtg	cgt	ttg	ctc	tac	gtt	cag	gca	ttg	ttg	tcc	agc	aag	1843	
Ser	Arg	Thr	Val	Arg	Leu	Leu	Tyr	Val	Gln	Ala	Leu	Leu	Ser	Ser	Lys		
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agg	cca	ctg	cgg	gtg	aag	gaa	cgc	gcg	ctg	ctt	aat	gat	tcg	ctg	gca	1891	
Arg	Pro	Leu	Arg	Val	Lys	Glu	Arg	Ala	Leu	Leu	Asn	Asp	Ser	Leu	Ala		
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gat	ctg	gtt	tct	ttg	tct	ttg	tca	tcc	gat	atc	taagacaatc	ctccgcta	aat			1944	
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ctt																1947	

<210> 36

<211> 608

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

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 Gln Gly Glu Glu Gly Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr
 50 55 60
 Lys Asp Arg Ala Thr Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr
 65 70 75 80
 Ala Gln Glu Ala Arg Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys
 85 90 95
 Arg Asp Glu Phe Gly Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly
 100 105 110
 Ile Gly Leu Leu Ser Cys Phe Met Val Ala Asp Glu Ile Thr Met Val
 115 120 125
 Ser His Ala Glu Gly Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp
 130 135 140
 Gly Thr Phe Asn Leu Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile
 145 150 155 160
 Pro Val Gly Thr Thr Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr
 165 170 175
 Leu Leu Thr Glu Asn Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg
 180 185 190
 Tyr Leu Pro Ile Pro Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile
 195 200 205
 Thr Thr Ser Pro Val Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu
 210 215 220
 Tyr Ala Gly Arg Glu Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp
 225 230 235 240
 Leu Thr Gly Pro Gly Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala
 245 250 255
 Gln Ala Pro His Met Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met
 260 265 270
 Leu Val Ser Asp Gly Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe
 275 280 285
 Val Glu Cys Glu Ile Asn Ser Thr Asp Leu Glu Pro Thr Ala Ser Arg
 290 295 300
 Glu Ala Leu Met Asp Asp Thr Ala Phe Ala Ala Thr Arg Glu His Ile
 305 310 315 320
 Gly Glu Cys Ile Lys Ser Trp Leu Ile Asn Leu Ala Met Thr Lys Pro
 325 330 335

His Arg Val Arg Glu Phe Thr Ala Ile His Asp Leu Ala Leu Arg Glu
 340 345 350
 Leu Cys Gln Ser Asp Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu
 355 360 365
 Thr Leu Glu Thr Ser Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr
 370 375 380
 Leu Ser Ile Thr Glu Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp
 385 390 395 400
 Asp Phe Arg Gln Leu Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile
 405 410 415
 Asn Gly Gly Tyr Ile His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val
 420 425 430
 His Tyr Pro Pro Leu Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met
 435 440 445
 Asp Leu Met Glu Leu Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala
 450 455 460
 Leu Asp Ala Gln Val Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly
 465 470 475 480
 Ala Thr Arg Val Phe Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile
 485 490 495
 Asp Ser Lys Ala Gln Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala
 500 505 510
 Thr Thr Asp Arg Trp Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu
 515 520 525
 Ser Arg Gln Thr Ala Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu
 530 535 540
 Cys Leu Asn Trp Asn Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp
 545 550 555 560
 Asp Thr Ala Val Val Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala
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 Asn Asp Ser Leu Ala Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile
 595 600 605

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<211> 436
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(436)
 <223> FRXA02282

<400> 37

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               1               5

cgt gat aat ttc caa gtt gac ctc ggc ggc gtt gtt gat ctt ttg agt 163
Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val Val Asp Leu Leu Ser
               10               15               20

cgc cac att tat tcc ggt ccg agg gtg tat gtg cgt gag ttg ctg cag 211
Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val Arg Glu Leu Leu Gln
               25               30               35

aat gcg gtt gat gct tgt act gca cgt tct gaa cag ggt gag gag ggc 259
Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu Gln Gly Glu Glu Gly
               40               45               50

tac gag ccg agt att cgt att ccg ccg gtg acc aag gat cgt gcc acg 307
Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr Lys Asp Arg Ala Thr
               55               60               65

ttt tca ctg gtt gat aat ggt acg ggc ctg acc gcg cag gag gcg ccg 355
Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr Ala Gln Glu Ala Arg
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gaa ttg ctg gcg acg gtg ggg ccg acg tcg aaa cgc gat gaa ttc ggt 403
Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys Arg Asp Glu Phe Gly
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<210> 38
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 <213> Corynebacterium glutamicum

<400> 38

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Phe Gly Gly Ser Gly Gly Leu Gly Asp Ile Phe Asp Ala Phe Phe Gly	
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Gly Gly Ala Gly Gly Ser Arg Gly Pro Arg Ser Arg Val Gln Pro Gly	
105 110 115	
agt gac acc ttg tgg cgc acc tcc atc acc ttg gaa gag gct tac aag	499
Ser Asp Thr Leu Trp Arg Thr Ser Ile Thr Leu Glu Glu Ala Tyr Lys	
120 125 130	
ggc gct aag aaa gat ctc acc ctt gac acc gca gtg ctg tgt acc aag	547
Gly Ala Lys Lys Asp Leu Thr Leu Asp Thr Ala Val Leu Cys Thr Lys	
135 140 145	
tgt cat ggt tct gga tct gca tcc gac aag aag cct gtt acc tgt ggc	595
Cys His Gly Ser Gly Ser Ala Ser Asp Lys Lys Pro Val Thr Cys Gly	
150 155 160 165	
acc tgt aat ggc gct ggt gaa att cag gaa gtg cag cgc agc ttc ctg	643
Thr Cys Asn Gly Ala Gly Glu Ile Gln Glu Val Gln Arg Ser Phe Leu	
170 175 180	
ggc aac gtc atg acg tcc cgc cca tgc cac acc tgc gat ggc acc ggt	691
Gly Asn Val Met Thr Ser Arg Pro Cys His Thr Cys Asp Gly Thr Gly	
185 190 195	
gag atc atc cca gat cct tgc act gag tgt gca gca gat ggt cgt gtg	739
Glu Ile Ile Pro Asp Pro Cys Thr Glu Cys Ala Ala Asp Gly Arg Val	
200 205 210	
cgt gct cgc cgc gac atc gtg gcc aac atc cca gct ggc atc cag tcc	787
Arg Ala Arg Arg Asp Ile Val Ala Asn Ile Pro Ala Gly Ile Gln Ser	
215 220 225	
ggc atg cgc atc cgc atg gca ggc caa ggt gag gtt ggc gct ggt ggc	835
Gly Met Arg Ile Arg Met Ala Gly Gln Gly Glu Val Gly Ala Gly Gly	
230 235 240 245	
ggt cct gcg ggt gac ctc tac att gaa gtc atg gtg cgc ccg cac gcc	883
Gly Pro Ala Gly Asp Leu Tyr Ile Glu Val Met Val Arg Pro His Ala	
250 255 260	
atc ttc acc cgc gat ggc gac gat ctg cac gcc agc atc aag gtt cca	931
Ile Phe Thr Arg Asp Gly Asp Asp Leu His Ala Ser Ile Lys Val Pro	
265 270 275	
atg ttc gat gca gcg ctt ggc acc gaa ttg gac gtg gaa tcc ctc acc	979
Met Phe Asp Ala Ala Leu Gly Thr Glu Leu Asp Val Glu Ser Leu Thr	
280 285 290	
ggc gaa gag gtg aaa att acc atc cct gca ggt act cag ccc aac gat	1027
Gly Glu Glu Val Lys Ile Thr Ile Pro Ala Gly Thr Gln Pro Asn Asp	
295 300 305	
gtg atc acc ttg gat ggt gaa ggc atg ccg aag ctg cgc gca gaa ggc	1075
Val Ile Thr Leu Asp Gly Glu Gly Met Pro Lys Leu Arg Ala Glu Gly	

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cac ggc aac ctc atg gcg cat gtc gat cta ttt gtg cca acc gat ttg				1123
His Gly Asn Leu Met Ala His Val Asp Leu Phe Val Pro Thr Asp Leu				
330		335	340	
gat gac cgc acc cgc gaa ttg ctt gaa gaa atc cgc aac cat cgc agc				1171
Asp Asp Arg Thr Arg Glu Leu Leu Glu Glu Ile Arg Asn His Arg Ser				
345		350	355	
gac aac gct tcc gtg cat cgc gaa ggc gga gaa gaa tcc ggt ttc ttt				1219
Asp Asn Ala Ser Val His Arg Glu Gly Gly Glu Glu Ser Gly Phe Phe				
360		365	370	
gac aag ctc cga aac aag ttc cgc aaa taatgtcact gccagtattt				1266
Asp Lys Leu Arg Asn Lys Phe Arg Lys				
375		380		
atc				1269
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Pro Asp Val Asn Pro Gly Glu Glu Ala Ala Glu Lys Phe Arg Glu Ala				
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Ser Val Ala His Glu Val Leu Thr Asp Pro Asp Lys Arg Arg Ile Val				
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Asp Met Gly Gly Asp Pro Met Glu Gln Gly Gly Gly Ala Gly Ala Gly				
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Gly Phe Gly Gly Gly Phe Gly Gly Ser Gly Gly Leu Gly Asp Ile Phe				
85	90	95		
Asp Ala Phe Phe Gly Gly Gly Ala Gly Gly Ser Arg Gly Pro Arg Ser				
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Arg Val Gln Pro Gly Ser Asp Thr Leu Trp Arg Thr Ser Ile Thr Leu				
115	120	125		
Glu Glu Ala Tyr Lys Gly Ala Lys Lys Asp Leu Thr Leu Asp Thr Ala				
130	135	140		
Val Leu Cys Thr Lys Cys His Gly Ser Gly Ser Ala Ser Asp Lys Lys				
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 Gln Arg Ser Phe Leu Gly Asn Val Met Thr Ser Arg Pro Cys His Thr
 180 185 190
 Cys Asp Gly Thr Gly Glu Ile Ile Pro Asp Pro Cys Thr Glu Cys Ala
 195 200 205
 Ala Asp Gly Arg Val Arg Ala Arg Arg Asp Ile Val Ala Asn Ile Pro
 210 215 220
 Ala Gly Ile Gln Ser Gly Met Arg Ile Arg Met Ala Gly Gln Gly Glu
 225 230 235 240
 Val Gly Ala Gly Gly Gly Pro Ala Gly Asp Leu Tyr Ile Glu Val Met
 245 250 255
 Val Arg Pro His Ala Ile Phe Thr Arg Asp Gly Asp Asp Leu His Ala
 260 265 270
 Ser Ile Lys Val Pro Met Phe Asp Ala Ala Leu Gly Thr Glu Leu Asp
 275 280 285
 Val Glu Ser Leu Thr Gly Glu Glu Val Lys Ile Thr Ile Pro Ala Gly
 290 295 300
 Thr Gln Pro Asn Asp Val Ile Thr Leu Asp Gly Glu Gly Met Pro Lys
 305 310 315 320
 Leu Arg Ala Glu Gly His Gly Asn Leu Met Ala His Val Asp Leu Phe
 325 330 335
 Val Pro Thr Asp Leu Asp Asp Arg Thr Arg Glu Leu Leu Glu Glu Ile
 340 345 350
 Arg Asn His Arg Ser Asp Asn Ala Ser Val His Arg Glu Gly Gly Glu
 355 360 365
 Glu Ser Gly Phe Phe Asp Lys Leu Arg Asn Lys Phe Arg Lys
 370 375 380

<210> 41

<211> 1470

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1447)

<223> RXS00568

<400> 41

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ctgaaacttt ccctttcccg atcatccagg agatttactc gtg aag agt tct gtc 115

															Val	Lys	Ser	Ser	Val	
															1				5	
gag aag ctg agc gac acc cgt tca aag atc acc gtt gag gtt cca ttt	163																			
Glu Lys Leu Ser Asp Thr Arg Ser Lys Ile Thr Val Glu Val Pro Phe																				
	10	15	20																	
tct gaa ctg aag cca gag atc gac cag gca tac gcc gct cta gcg cag	211																			
Ser Glu Leu Lys Pro Glu Ile Asp Gln Ala Tyr Ala Ala Leu Ala Gln																				
	25	30	35																	
caa gtc cag atc cct ggt ttc cgt aag ggc aag gca ccg cgt cag ctt	259																			
Gln Val Gln Ile Pro Gly Phe Arg Lys Gly Lys Ala Pro Arg Gln Leu																				
	40	45	50																	
atc gac gca cgc ttc ggc cgt ggt gcg gtt ctg gag cag gtt gtc aac	307																			
Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu Glu Gln Val Val Asn																				
	55	60	65																	
gac atg ctt cct aac cgc tac gca cag gca atc gaa gct gag ggc atc	355																			
Asp Met Leu Pro Asn Arg Tyr Ala Gln Ala Ile Glu Ala Glu Gly Ile																				
	70	75	80	85																
aag gca atc ggc cag cct aac gta gag gtc acc aag atc gaa gac aac	403																			
Lys Ala Ile Gly Gln Pro Asn Val Glu Val Thr Lys Ile Glu Asp Asn																				
	90	95	100																	
gag ctc gtt gag ttc gtc gct gag gtt gac gtt cgc cca gag ttc gag	451																			
Glu Leu Val Glu Phe Val Ala Glu Val Asp Val Arg Pro Glu Phe Glu																				
	105	110	115																	
ctt cct aag ttc gag gac atc act gtt gag gtc cca gct atc aag gct	499																			
Leu Pro Lys Phe Glu Asp Ile Thr Val Glu Val Pro Ala Ile Lys Ala																				
	120	125	130																	
gac gaa gag gca atc gaa gca gag ctc gag acc ctg cgt gca cgt ttc	547																			
Asp Glu Glu Ala Ile Glu Ala Glu Leu Glu Thr Leu Arg Ala Arg Phe																				
	135	140	145																	
tcc acc ttg aag gat cac aac cac aag ctg aag aag ggt gag ttc gtc	595																			
Ser Thr Leu Lys Asp His Asn His Lys Leu Lys Lys Gly Glu Phe Val																				
	150	155	160	165																
acc atc aac atc acc gca agc att gac ggt gag aag att gaa gag gca	643																			
Thr Ile Asn Ile Thr Ala Ser Ile Asp Gly Glu Lys Ile Glu Glu Ala																				
	170	175	180																	
acc act gag ggt ctg tcc tac gaa atc gga tct gac gat ctg att gac	691																			
Thr Thr Glu Gly Leu Ser Tyr Glu Ile Gly Ser Asp Asp Leu Ile Asp																				
	185	190	195																	
ggc ctg gac aag gct ctg atc ggc gct aag aag gat gaa acc gta gag	739																			
Gly Leu Asp Lys Ala Leu Ile Gly Ala Lys Lys Asp Glu Thr Val Glu																				
	200	205	210																	
ttc acc tct gag ctg gca aac ggc gag cac aag ggc aag gaa gct caa	787																			
Phe Thr Ser Glu Leu Ala Asn Gly Glu His Lys Gly Lys Glu Ala Gln																				

215	220	225	
atc agc gtt gag atc acc gca acc aag cag cgc gag ctg cct gag ctg			835
Il Ser Val Glu Ile Thr Ala Thr Lys Gln Arg Glu Leu Pro Glu Leu			
230	235	240	245
gat gat gag ttc gca cag ctg gct tct gag ttc gac acc atc gaa gag			883
Asp Asp Glu Phe Ala Gln Leu Ala Ser Glu Phe Asp Thr Ile Glu Glu			
	250	255	260
ctt cgt gag tcc acc gtg tct gac gtt gag gct aag cag aag aac gag			931
Leu Arg Glu Ser Thr Val Ser Asp Val Glu Ala Lys Gln Lys Asn Glu			
	265	270	275
cag gct gct gca atc cgc gac gaa gtt ctc gct gcg gct ctt ggc gag			979
Gln Ala Ala Ala Ile Arg Asp Glu Val Leu Ala Ala Leu Gly Glu			
	280	285	290
gct gac ttc gct ctg cca cag tcc atc gtt gac gag cag gca cac tcc			1027
Ala Asp Phe Ala Leu Pro Gln Ser Ile Val Asp Glu Gln Ala His Ser			
	295	300	305
cag ctg cac cag ctc ctc ggc gag ctt gca cac gac gat gct gca ctg			1075
Gln Leu His Gln Leu Leu Gly Glu Leu Ala His Asp Asp Ala Ala Leu			
	310	315	320
aac tcc ctc ctt gag gct cag ggc acc act cgt gaa gag ttc gac aag			1123
Asn Ser Leu Leu Glu Ala Gln Gly Thr Thr Arg Glu Glu Phe Asp Lys			
	330	335	340
aag aac gtc gaa gat gct gag aag gct gtt cgc acc cag ctg ttc ctg			1171
Lys Asn Val Glu Asp Ala Glu Lys Ala Val Arg Thr Gln Leu Phe Leu			
	345	350	355
gac acc ctc tct gag gtt gag gag cct gag gtt tcc cag cag gag ctc			1219
Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val Ser Gln Gln Glu Leu			
	360	365	370
acc gac cac atc ctg ttc acc gca cag tct tac ggc atg gac cca aac			1267
Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr Gly Met Asp Pro Asn			
	375	380	385
cag ttc atc ggt cag ctg cag cag tcc ggc cag atc gcg aac ctc ttc			1315
Gln Phe Ile Gly Gln Leu Gln Gln Ser Gly Gln Ile Ala Asn Leu Phe			
	390	395	400
tcc gac gtt cgc cgt ggc aag gct ctt gca cag gct atc tgc cgc gta			1363
Ser Asp Val Arg Arg Gly Lys Ala Leu Ala Gln Ala Ile Cys Arg Val			
	410	415	420
aac gtg aag gac tcc gag ggt aac gag atc gac cct aag gaa tac ttc			1411
Asn Val Lys Asp Ser Glu Gly Asn Glu Ile Asp Pro Lys Glu Tyr Phe			
	425	430	435
ggt gaa gaa gaa gta gct gag act gag tct gaa gct taaaaacttt			1457
Gly Glu Glu Glu Val Ala Glu Thr Glu Ser Glu Ala			
	440	445	

aaagaaataa cgc

1470

<210> 42

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

Val Lys Ser Ser Val Glu Lys Leu Ser Asp Thr Arg Ser Lys Ile Thr
 1 5 10 15

Val Glu Val Pro Phe Ser Glu Leu Lys Pro Glu Ile Asp Gln Ala Tyr
 20 25 30

Ala Ala Leu Ala Gln Gln Val Gln Ile Pro Gly Phe Arg Lys Gly Lys
 35 40 45

Ala Pro Arg Gln Leu Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu
 50 55 60

Glu Gln Val Val Asn Asp Met Leu Pro Asn Arg Tyr Ala Gln Ala Ile
 65 70 75 80

Glu Ala Glu Gly Ile Lys Ala Ile Gly Gln Pro Asn Val Glu Val Thr
 85 90 95

Lys Ile Glu Asp Asn Glu Leu Val Glu Phe Val Ala Glu Val Asp Val
 100 105 110

Arg Pro Glu Phe Glu Leu Pro Lys Phe Glu Asp Ile Thr Val Glu Val
 115 120 125

Pro Ala Ile Lys Ala Asp Glu Glu Ala Ile Glu Ala Glu Leu Glu Thr
 130 135 140

Leu Arg Ala Arg Phe Ser Thr Leu Lys Asp His Asn His Lys Leu Lys
 145 150 155 160

Lys Gly Glu Phe Val Thr Ile Asn Ile Thr Ala Ser Ile Asp Gly Glu
 165 170 175

Lys Ile Glu Glu Ala Thr Thr Glu Gly Leu Ser Tyr Glu Ile Gly Ser
 180 185 190

Asp Asp Leu Ile Asp Gly Leu Asp Lys Ala Leu Ile Gly Ala Lys Lys
 195 200 205

Asp Glu Thr Val Glu Phe Thr Ser Glu Leu Ala Asn Gly Glu His Lys
 210 215 220

Gly Lys Glu Ala Gln Ile Ser Val Glu Ile Thr Ala Thr Lys Gln Arg
 225 230 235 240

Glu Leu Pro Glu Leu Asp Asp Glu Phe Ala Gln Leu Ala Ser Glu Phe
 245 250 255

Asp Thr Ile Glu Glu Leu Arg Glu Ser Thr Val Ser Asp Val Glu Ala
 260 265 270
 Lys Gln Lys Asn Glu Gln Ala Ala Ala Ile Arg Asp Glu Val Leu Ala
 275 280 285
 Ala Ala Leu Gly Glu Ala Asp Phe Ala Leu Pro Gln Ser Ile Val Asp
 290 295 300
 Glu Gln Ala His Ser Gln Leu His Gln Leu Leu Gly Glu Leu Ala His
 305 310 315 320
 Asp Asp Ala Ala Leu Asn Ser Leu Leu Glu Ala Gln Gly Thr Thr Arg
 325 330 335
 Glu Glu Phe Asp Lys Lys Asn Val Glu Asp Ala Glu Lys Ala Val Arg
 340 345 350
 Thr Gln Leu Phe Leu Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val
 355 360 365
 Ser Gln Gln Glu Leu Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr
 370 375 380
 Gly Met Asp Pro Asn Gln Phe Ile Gly Gln Leu Gln Gln Ser Gly Gln
 385 390 395 400
 Ile Ala Asn Leu Phe Ser Asp Val Arg Arg Gly Lys Ala Leu Ala Gln
 405 410 415
 Ala Ile Cys Arg Val Asn Val Lys Asp Ser Glu Gly Asn Glu Ile Asp
 420 425 430
 Pro Lys Glu Tyr Phe Gly Glu Glu Glu Val Ala Glu Thr Glu Ser Glu
 435 440 445

Ala

<210> 43
 <211> 826
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(826)
 <223> RXN03038

<400> 43
 gcgcggaata caccaagtaa gccttacagt ccgacagcct catagcggat gggataagtt 60
 ccaaacacgt tcaaatccgt taaagtgcct gtttaaaact atg cat tca aag gaa 115
 Met His Ser Lys Glu
 1 5

gag tta aca gtg cgt aaa gga att tcc cgc gtc ctc tcg gta gcg gtt	163
Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val Leu Ser Val Ala Val	
10 15 20	
gct agt tca atc gga ttc gga act gta ctg aca ggc acc ggc atc gca	211
Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr Gly Thr Gly Ile Ala	
25 30 35	
gca gct caa gac tct gca ttt gac tac ggt atg gat cca aac atg aac	259
Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Asn Met Asn	
40 45 50	
tac aac ccg atc gat gac atc aag gat cgt ccc gaa gga ttg tcc aat	307
Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro Glu Gly Leu Ser Asn	
55 60 65	
ctt ccc tac ttc gga agt aaa ttg acc agc tgg ggc tca tca tat gcc	355
Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Tyr Ala	
70 75 80 85	
acc gcc tca tcc ggc gtc gtg acc tcc gcg ctc ccg cag tac acc gat	403
Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu Pro Gln Tyr Thr Asp	
90 95 100	
ccg cgc tac ccc ctc ggc aaa gac gac ctg ccc aag gca acc atc gac	451
Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr Ile Asp	
105 110 115	
atg gag cca gaa gtt ctt gcg cgc ctt gag cga ttc gtc ggc gtt gac	499
Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg Phe Val Gly Val Asp	
120 125 130	
ggt gat cgc atc cgc caa atc aac gcg tac tcg cca tca atg gga cgc	547
Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met Gly Arg	
135 140 145	
acc att cct cta gtc tgg gtt gtt cca gaa gac aac acc gtg cct ggc	595
Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp Asn Thr Val Pro Gly	
150 155 160 165	
cca acg gtc tac gca ctc gga ggc ggt gac ggt gga caa ggc ggc cag	643
Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly Gly Gln Gly Gly Gln	
170 175 180	
aac tgg gtc acc cgc acc gac ctt gag gaa tta acc agt gac aac aac	691
Asn Trp Val Thr Arg Thr Asp Leu Glu Glu Leu Thr Ser Asp Asn Asn	
185 190 195	
atc aac ctc atc atg ccg atg ctc gga tct ttt agt ttc tac tct gac	739
Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe Ser Phe Tyr Ser Asp	
200 205 210	
tgg gca cgc gaa agc caa tcc atg ggt tgt gcg caa cag tgg gaa aca	787
Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala Gln Gln Trp Glu Thr	
215 220 225	

ttg ctc atg cac gaa ctg cct gag ccg ctt gta gcg gcc
 Leu Leu Met His Glu Leu Pro Glu Pro Leu Val Ala Ala
 230 235 240

<210> 44

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

Met His Ser Lys Glu Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val
 1 5 10 15

Leu Ser Val Ala Val Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr
 20 25 30

Gly Thr Gly Ile Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met
 35 40 45

Asp Pro Asn Met Asn Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro
 50 55 60

Glu Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp
 65 70 75 80

Gly Ser Ser Tyr Ala Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu
 85 90 95

Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro
 100 105 110

Lys Ala Thr Ile Asp Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg
 115 120 125

Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser
 130 135 140

Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp
 145 150 155 160

Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly
 165 170 175

Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Glu Glu Leu
 180 185 190

Thr Ser Asp Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe
 195 200 205

Ser Phe Tyr Ser Asp Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala
 210 215 220

Gln Gln Trp Glu Thr Leu Leu Met His Glu Leu Pro Glu Pro Leu Val
 225 230 235 240

Ala Ala

<210> 45
 <211> 653
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(630)
 <223> RXN03039

<400> 45
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 Ala Leu Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp
 1 5 10 15

ctg ccc aaa gca acc atc gac atg gag cca gaa gct ctt gcg cgc ctt 96
 Leu Pro Lys Ala Thr Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu
 20 25 30

gag cga ttc gtc ggc gtt gac ggt gat cgc atc cgc caa atc aac gcg 144
 Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala
 35 40 45

tac tcg cca tca atg gga cgc acc att cct cta gtc tgg gtc gtg cca 192
 Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro
 50 55 60

gaa gac aac acc gtg cct ggc cca acg gtc tac gca ctc ggc ggc ggc 240
 Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly
 65 70 75 80

gac ggt ggc caa ggc ggc caa aac tgg gtc acc cgc acc gac ctt gat 288
 Asp Gly Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp
 85 90 95

gag ttg acc agt gaa aac aac atc aac ctc atc atg ccc atg ctc gga 336
 Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly
 100 105 110

tct ttt agt ttc tac gct gac tgg gca ggc gaa agc gaa tcc atg ggt 384
 Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly
 115 120 125

ggt gcg caa cag tgg gaa aca ttc ctc atg cac gaa ctr ccm gag ccg 432
 Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro
 130 135 140

cta gaa gcg gcc atc ggc gca gac ggg caa cgc agc atc gtc ggc atg 480
 Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met
 145 150 155 160

tcc atg tcc ggg gga tcr gtg ctg aac ttt gcg acg cat gac ccc aac 528
 Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn
 165 170 175

ttt tay tcc tck gtc ggc tca ttt tct gga tgt gcc gaa acc aac tcc 576
 Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser
 180 185 190

tgg atg ggr cgc cgn tgg cat cgc agc cac tgc cta caa cgg caa tgt 624
 Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Gln Arg Gln Cys
 195 200 205

cgt gcc tgagcaaadc tttggtgaag tag 653
 Arg Ala
 210

<210> 46

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

Ala Leu Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp
 1 5 10 15

Leu Pro Lys Ala Thr Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu
 20 25 30

Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala
 35 40 45

Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro
 50 55 60

Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly
 65 70 75 80

Asp Gly Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp
 85 90 95

Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly
 100 105 110

Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly
 115 120 125

Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro
 130 135 140

Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met
 145 150 155 160

Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn
 165 170 175

Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser
 180 185 190

Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Gln Arg Gln Cys

195

200

205

Arg Ala
210

<210> 47

<211> 432

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(409)

<223> RXN03040

<400> 47

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ctctacatct tcgccgggtc cgggtgtgttc tctgaactag atg tca tnc ggt gac 115
Met Ser Xaa Gly Asp
1 5

aac gca ccg att gat gag gat gcg ttc aaa aac cgc gtc ttg gtt ggg 163
Asn Ala Pro Ile Asp Glu Asp Ala Phe Lys Asn Arg Val Leu Val Gly
10 15 20

ttt gaa atc gaa gct atg tcc aac acc tgc acc cat aac ctc aag gct 211
Phe Glu Ile Glu Ala Met Ser Asn Thr Cys Thr His Asn Leu Lys Ala
25 30 35

gcg acc gat caa atg ggc atc gac aac atc aac tac gat ttc cga cca 259
Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn Tyr Asp Phe Arg Pro
40 45 50

acc gga acc cac gcc tgg gat tac tgg aac gaa gcg ctc cac cgc ttc 307
Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu Ala Leu His Arg Phe
55 60 65

ttc ccg ttg atg atg cag ggc ttc ggc ctc gac ggt ggt ccc atc ccg 355
Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp Gly Gly Pro Ile Pro
70 75 80 85

atc tat aac cct aac ggt gtg acc tcc agc gag tct tct ntc aga act 403
Ile Tyr Asn Pro Asn Gly Val Thr Ser Ser Glu Ser Ser Xaa Arg Thr
90 95 100

gtc ttc tgatgtgagc cttggcaccn gtg 432
Val Phe

<210> 48

<211> 103

<212> PRT

<213> Corynebacterium glutamicum

<400> 48

Met Ser Xaa Gly Asp Asn Ala Pro Ile Asp Glu Asp Ala Phe Lys Asn
 1 5 10 15
 Arg Val Leu Val Gly Phe Glu Ile Glu Ala Met Ser Asn Thr Cys Thr
 20 25 30
 His Asn Leu Lys Ala Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn
 35 40 45
 Tyr Asp Phe Arg Pro Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu
 50 55 60
 Ala Leu His Arg Phe Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp
 65 70 75 80
 Gly Gly Pro Ile Pro Ile Tyr Asn Pro Asn Gly Val Thr Ser Ser Glu
 85 90 95
 Ser Ser Xaa Arg Thr Val Phe
 100

<210> 49

<211> 835

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(835)

<223> RXN03051

<400> 49

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 ggaactcccg ctgcctaagc gggacatagt tgcagggggac atg cgt tca gat gtt 115
 Met Arg Ser Asp Val
 1 5
 atc gag tta ccg gag ggg gta agc aag gag aaa gct gac cag cta gaa 163
 Ile Glu Leu Pro Glu Gly Val Ser Lys Glu Lys Ala Asp Gln Leu Glu
 10 15 20
 gtt gcg gaa gcg cga ctt aac gag ggt gca cga ctg atg gca acc acc 211
 Val Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg Leu Met Ala Thr Thr
 25 30 35
 ggg tgt gag gtt atg tgg cca acg ggc ttc tca gtt tgt ggc cga att 259
 Gly Cys Glu Val Met Trp Pro Thr Gly Phe Ser Val Cys Gly Arg Ile
 40 45 50
 ctt gac acc tat cgc cag gtt gga ggt cag ttg tca tgg ctt ggg cca 307
 Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu Ser Trp Leu Gly Pro
 55 60 65
 ccg aag tca aac gag ttg acc aat ccc gac ggt gtt ggc aaa aga agt 355

Pro	Lys	Ser	Asn	Glu	Leu	Thr	Asn	Pro	Asp	Gly	Val	Gly	Lys	Arg	Ser		
70					75					80					85		
gaa ttt ttt ggt gga gcc atc tat tgg cac cca gac aca ggc gct tat 403																	
Glu	Phe	Phe	Gly	Gly	Ala	Ile	Tyr	Trp	His	Pro	Asp	Thr	Gly	Ala	Tyr		
			90					95					100				
gca gtg acc ttg gac ggt ttg cga cag tgg ggg acc ttg aac tgg gaa 451																	
Ala	Val	Thr	Leu	Asp	Gly	Leu	Arg	Gln	Trp	Gly	Thr	Leu	Asn	Trp	Glu		
			105					110					115				
tca ggg cca ttg ggg tac cca acc tct ggt ccg atg gat aca aac tat 499																	
Ser	Gly	Pro	Leu	Gly	Tyr	Pro	Thr	Ser	Gly	Pro	Met	Asp	Thr	Asn	Tyr		
		120					125					130					
ccc ctt act cag cga cag act ttt caa ggt ggt gac aac tac tac aac 547																	
Pro	Leu	Thr	Gln	Arg	Gln	Thr	Phe	Gln	Gly	Gly	Asp	Asn	Tyr	Tyr	Asn		
		135				140					145						
cca ttg act ggc ggt gct gtg tgg ggc gat att aaa cag cgc tac gaa 595																	
Pro	Leu	Thr	Gly	Gly	Ala	Val	Trp	Gly	Asp	Ile	Lys	Gln	Arg	Tyr	Glu		
		150			155				160						165		
gaa ctt ggc ggc tcg aat cat gcc att ggc atc ccg atc act aat gag 643																	
Glu	Leu	Gly	Gly	Ser	Asn	His	Ala	Ile	Gly	Ile	Pro	Ile	Thr	Asn	Glu		
			170					175						180			
cta cct agc ggt act gag tat ttt tac aat aat ttc tcc aat gga aca 691																	
Leu	Pro	Ser	Gly	Thr	Glu	Tyr	Phe	Tyr	Asn	Asn	Phe	Ser	Asn	Gly	Thr		
			185					190					195				
att tcg tgg cga aat gat cgt cag aca cgg ttt atg tat ttg gct acg 739																	
Ile	Ser	Trp	Arg	Asn	Asp	Arg	Gln	Thr	Arg	Phe	Met	Tyr	Leu	Ala	Thr		
		200					205					210					
cag cgg gtg tgg gat gcg ttg ggt cgg gag acg ggt cgt tta ggt ttt 787																	
Gln	Arg	Val	Trp	Asp	Ala	Leu	Gly	Arg	Glu	Thr	Gly	Arg	Leu	Gly	Phe		
		215				220					225						
cct gaa gca gat gaa aca cct gag gtt tct ggt cta ttc cat gtg gcg 835																	
Pro	Glu	Ala	Asp	Glu	Thr	Pro	Glu	Val	Ser	Gly	Leu	Phe	His	Val	Ala		
		230			235				240					245			

<210> 50

<211> 245

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

Met	Arg	Ser	Asp	Val	Ile	Glu	Leu	Pro	Glu	Gly	Val	Ser	Lys	Glu	Lys		
1				5					10					15			

Ala	Asp	Gln	Leu	Glu	Val	Ala	Glu	Ala	Arg	Leu	Asn	Glu	Gly	Ala	Arg		
		20					25						30				

Leu	Met	Ala	Thr	Thr	Gly	Cys	Glu	Val	Met	Trp	Pro	Thr	Gly	Phe	Ser		
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	--

35	40	45
Val Cys Gly Arg Ile Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu		
50	55	60
Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly		
65	70	75
Val Gly Lys Arg Ser Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro		
85	90	95
Asp Thr Gly Ala Tyr Ala Val Thr Leu Asp Gly Leu Arg Gln Trp Gly		
100	105	110
Thr Leu Asn Trp Glu Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro		
115	120	125
Met Asp Thr Asn Tyr Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly		
130	135	140
Asp Asn Tyr Tyr Asn Pro Leu Thr Gly Gly Ala Val Trp Gly Asp Ile		
145	150	155
Lys Gln Arg Tyr Glu Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile		
165	170	175
Pro Ile Thr Asn Glu Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn		
180	185	190
Phe Ser Asn Gly Thr Ile Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe		
195	200	205
Met Tyr Leu Ala Thr Gln Arg Val Trp Asp Ala Leu Gly Arg Glu Thr		
210	215	220
Gly Arg Leu Gly Phe Pro Glu Ala Asp Glu Thr Pro Glu Val Ser Gly		
225	230	235
Leu Phe His Val Ala		
245		

<210> 51

<211> 1704

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1681)

<223> RXN03054

<400> 51

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cagtttggtc acatcaacta gtaacgaaag gatcatgtga atg aaa ctg ttt tcc 115
Met Lys Leu Phe Ser

	1	5	
aag gct gca ggc gtc att gct gca gca ctt ctt gtt gca ggt ggt ata			163
Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu Val Ala Gly Gly Ile	10	20	
gca cct gtg gca cag ggg caa gct agt cag gtg gtc aca cct gaa gac			211
Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val Val Thr Pro Glu Asp	25	35	
caa gat gcg tat gtt caa cag ttc cac cac gaa ggg aat acc cca cct			259
Gln Asp Ala Tyr Val Gln Gln Phe His His Glu Gly Asn Thr Pro Pro	40	50	
gtg gta gac ggg gtg ggt ggc tac act gag caa gaa atc gcc gag atc			307
Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln Glu Ile Ala Glu Ile	55	65	
cac gag gct atc cga caa gcc caa gaa tct ggc gca cct aat gaa gag			355
His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly Ala Pro Asn Glu Glu	70	85	
ctc att ccg ggt gag atg tgg tca gat aag gtg gag ctg cca gta act			403
Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Val Thr	90	100	
att gat aaa gca gcc gct gat gag gca gag ata gct att gca cag caa			451
Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln	105	115	
caa tct cag cca cag acg cga ggc ctt gct gcg gct gcg gcg tgt cag			499
Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala Ala Ala Cys Gln	120	130	
acg ttt tgg ccg tca cct cat cag gtt tgt ggt gct att tta gag cgc			547
Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly Ala Ile Leu Glu Arg	135	145	
tat att cag cag ggt gcc cag ttt ggg tgg atg ttg ttt ccg agt gaa			595
Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Phe Pro Ser Glu	150	165	
ggc caa acg tta aat cct gat ggt cag ggg tat cgt cag cgg ttt atg			643
Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met	170	180	
aat ggg ttt gtt tat tgg cat ccg aca act ggt gcg cat gct gtt aat			691
Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly Ala His Ala Val Asn	185	195	
aat tac agt gcg cag gtg tgg gag cgt aat ggg tgg gag tct ggg tgg			739
Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly Trp Glu Ser Gly Trp	200	210	
atg ggt tat ccc act ggt ggt gaa gtc cct gtg aat ggt tcc aat ccg			787
Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Asn Gly Ser Asn Pro	215	225	

att gat ggt gag ttg agt ggg tgg gtg caa act ttc caa ggt ggg cga Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr Phe Gln Gly Gly Arg 230 235 240 245	835
gtg tat cgc agt ccg gta ttg gac ggt ttc cag gtg gcc agt att aat Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln Val Ala Ser Ile Asn 250 255 260	883
ggg ctg atc ttg gat aaa tgg ctt gaa ttg ggt ggt cct gat agt gac Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly Gly Pro Asp Ser Asp 265 270 275	931
ctt ggt ttt ccc att gcg gat gag gct gtg aca gct gac ggt gtg ggt Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr Ala Asp Gly Val Gly 280 285 290	979
aga ttt tct gtt ttc cag aac gga gtt gtc tac tgg cat ccg caa cac Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr Trp His Pro Gln His 295 300 305	1027
gga gct cac cct ata tta ggg aat ata tac agt atc tgg aga gaa gaa Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser Ile Trp Arg Glu Glu 310 315 320 325	1075
gga gct gag agt ggg gaa ttc ggt tac cct atc ggc gat cca gaa aag Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile Gly Asp Pro Glu Lys 330 335 340	1123
tat aca gaa aac atg gct aat cag gta ttc gaa aaa ggc gaa ctt gca Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu Lys Gly Glu Leu Ala 345 350 355	1171
gct aac cta tac ccc aat cct ctt gag gct ttt att gag ttt tta ccc Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe Ile Glu Phe Leu Pro 360 365 370	1219
ttt gct aat ctt gag gaa gca ata gag tat ttt gag aac gga ttg tca Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe Glu Asn Gly Leu Ser 375 380 385	1267
aat tct cgt gta gag gcg aat tca ctt aac gcc aag aaa gat tcg att Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala Lys Lys Asp Ser Ile 390 395 400 405	1315
caa tgt caa tcg caa tcc gct aac att cat gtg aga acg aag agt gac Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val Arg Thr Lys Ser Asp 410 415 420	1363
gga gtc ggg att agg gtt cca aag att ggg ttt aag gct agg atg gat Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe Lys Ala Arg Met Asp 425 430 435	1411
tgc gac ctt cct gga act gtc tca gat gta gtg ggg tat gga tgg att Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val Gly Tyr Gly Trp Ile 440 445 450	1459

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 Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala Ala Tyr Ala Gln Gln
 455 460 465

 ttc ttc ggt aat agg aat tct gtt gtg caa acc aat tta gag gcg ggt 1555
 Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr Asn Leu Glu Ala Gly
 470 475 480 485

 tgc agc ggg gag aag aat aca tta ttt tgg ggt act tca tat ttt cag 1603
 Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly Thr Ser Tyr Phe Gln
 490 495 500

 gtg act tat gaa ggt cag ccg tat ttc ggt cag tca gca act aat tac 1651
 Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln Ser Ala Thr Asn Tyr
 505 510 515

 gct tat ctt ccg tgt acg ata gac cgt agt taacataagg aatggaatag 1701
 Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser
 520 525

 gag 1704

<210> 52
 <211> 527
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 52
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 Val Ala Gly Gly Ile Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val
 20 25 30

 Val Thr Pro Glu Asp Gln Asp Ala Tyr Val Gln Gln Phe His His Glu
 35 40 45

 Gly Asn Thr Pro Pro Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln
 50 55 60

 Glu Ile Ala Glu Ile His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly
 65 70 75 80

 Ala Pro Asn Glu Glu Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val
 85 90 95

 Glu Leu Pro Val Thr Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile
 100 105 110

 Ala Ile Ala Gln Gln Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala
 115 120 125

 Ala Ala Ala Cys Gln Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly
 130 135 140

 Ala Ile Leu Glu Arg Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met

145	150	155	160
Leu Phe Pro Ser	Glu Gly Gln Thr	Leu Asn Pro Asp	Gly Gln Gly Tyr
	165	170	175
Arg Gln Arg Phe	Met Asn Gly Phe	Val Tyr Trp His	Pro Thr Thr Gly
	180	185	190
Ala His Ala Val	Asn Asn Tyr Ser	Ala Gln Val Trp	Glu Arg Asn Gly
	195	200	205
Trp Glu Ser Gly	Trp Met Gly Tyr	Pro Thr Gly Gly	Glu Val Pro Val
	210	215	220
Asn Gly Ser Asn	Pro Ile Asp Gly	Glu Leu Ser Gly	Trp Val Gln Thr
	225	230	235
Phe Gln Gly Gly	Arg Val Tyr Arg	Ser Pro Val Leu	Asp Gly Phe Gln
	245	250	255
Val Ala Ser Ile	Asn Gly Leu Ile	Leu Asp Lys Trp	Leu Glu Leu Gly
	260	265	270
Gly Pro Asp Ser	Asp Leu Gly Phe	Pro Ile Ala Asp	Glu Ala Val Thr
	275	280	285
Ala Asp Gly Val	Gly Arg Phe Ser	Val Phe Gln Asn	Gly Val Val Tyr
	290	295	300
Trp His Pro Gln	His Gly Ala His	Pro Ile Leu Gly	Asn Ile Tyr Ser
	305	310	315
Ile Trp Arg Glu	Glu Gly Ala Glu	Ser Gly Glu Phe	Gly Tyr Pro Ile
	325	330	335
Gly Asp Pro Glu	Lys Tyr Thr Glu	Asn Met Ala Asn	Gln Val Phe Glu
	340	345	350
Lys Gly Glu Leu	Ala Ala Asn Leu	Tyr Pro Asn Pro	Leu Glu Ala Phe
	355	360	365
Ile Glu Phe Leu	Pro Phe Ala Asn	Leu Glu Glu Ala	Ile Glu Tyr Phe
	370	375	380
Glu Asn Gly Leu	Ser Asn Ser Arg	Val Glu Ala Asn	Ser Leu Asn Ala
	385	390	395
Lys Lys Asp Ser	Ile Gln Cys Gln	Ser Gln Ser Ala	Asn Ile His Val
	405	410	415
Arg Thr Lys Ser	Asp Gly Val Gly	Ile Arg Val Pro	Lys Ile Gly Phe
	420	425	430
Lys Ala Arg Met	Asp Cys Asp Leu	Pro Gly Thr Val	Ser Asp Val Val
	435	440	445
Gly Tyr Gly Trp	Ile Tyr Tyr Asp	Tyr Trp Gly Arg	Trp Ala Gln Ala

450

455

460

Ala Tyr Ala Gln Gln Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr
465 470 475 480

Asn Leu Glu Ala Gly Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly
485 490 495

Thr Ser Tyr Phe Gln Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln
500 505 510

Ser Ala Thr Asn Tyr Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser
515 520 525

<210> 53

<211> 456

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(433)

<223> RXN02949

<400> 53

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tggtatcgcc cctggatgag tagtgattta gaggagtgtc gtg agc gac gag cag 115
Val Ser Asp Glu Gln
1 5

aat tct ggc gta ggc gga acg tct cgc cca acg ggt aaa cgc cag ctg 163
Asn Ser Gly Val Gly Gly Thr Ser Arg Pro Thr Gly Lys Arg Gln Leu
10 15 20

tcg ggt gct tcc act acc tct acc tct tct tat gag gct aag cag gta 211
Ser Gly Ala Ser Thr Thr Ser Thr Ser Ser Tyr Glu Ala Lys Gln Val
25 30 35

tct aca cag aag aag tca tcc ggt tcg gat tct aag cct ggc ggc ggt 259
Ser Thr Gln Lys Lys Ser Ser Gly Ser Asp Ser Lys Pro Gly Gly Gly
40 45 50

gtt att tct ttt ctg cct gag gtt gtg gga gaa gtc cgt aag gtt att 307
Val Ile Ser Phe Leu Pro Glu Val Val Gly Glu Val Arg Lys Val Ile
55 60 65

tgg cct act gcg cgc cag atg gtc acg tac acc ctt gtc gtt ttg gga 355
Trp Pro Thr Ala Arg Gln Met Val Thr Tyr Thr Leu Val Val Leu Gly
70 75 80 85

ttc ttg att gtt ttg acc gct ttg gtg tct ggt gtg gat ttc cta gct 403
Phe Leu Ile Val Leu Thr Ala Leu Val Ser Gly Val Asp Phe Leu Ala
90 95 100

ggc ctt gga gtt gag aag att ctg act ccg taggtaggat gtgtaacatc 453

Gly Leu Gly Val Glu Lys Ile Leu Thr Pro
 105 110

ttt

456

<210> 54
 <211> 111
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 54
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Gly Lys Arg Gln Leu Ser Gly Ala Ser Thr Thr Ser Thr Ser Ser Tyr
 20 25 30

Glu Ala Lys Gln Val Ser Thr Gln Lys Lys Ser Ser Gly Ser Asp Ser
 35 40 45

Lys Pro Gly Gly Gly Val Ile Ser Phe Leu Pro Glu Val Val Gly Glu
 50 55 60

Val Arg Lys Val Ile Trp Pro Thr Ala Arg Gln Met Val Thr Tyr Thr
 65 70 75 80

Leu Val Val Leu Gly Phe Leu Ile Val Leu Thr Ala Leu Val Ser Gly
 85 90 95

Val Asp Phe Leu Ala Gly Leu Gly Val Glu Lys Ile Leu Thr Pro
 100 105 110

<210> 55
 <211> 1941
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1918)
 <223> RXN02462

<400> 55
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 atcgcagttc tacaacgtct tcgcacagat cgtcccacgc atg acc aag gac gtt 115
 Met Thr Lys Asp Val
 1 5

cac tac gaa gtc gac gaa cgt aaa aag acc gtc ggt gtg aaa gaa gaa 163
 His Tyr Glu Val Asp Glu Arg Lys Lys Thr Val Gly Val Lys Glu Glu
 10 15 20

ggc gtc gaa tac gtc gaa gac caa ctc ggc atc gac aac ctc tac gca 211
 Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile Asp Asn Leu Tyr Ala

25	30	35	
cct gag cac tca cag ctg gtc agc tac ctg aac aac gcc atc aag gca Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn Asn Ala Ile Lys Ala 40 45 50			259
cag gaa ctg ttc acc cgc gac aag gac tac atc gtc cgc aac ggc gaa Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile Val Arg Asn Gly Glu 55 60 65			307
gtt atg atc gtc gac ggc ttc acc ggc cgt gtc ctt gcc ggc cgc cga Val Met Ile Val Asp Gly Phe Thr Gly Arg Val Leu Ala Gly Arg Arg 70 75 80 85			355
tac aac gaa ggc atg cac cag gcg atc gaa gcc aaa gag cgc gta gag Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala Lys Glu Arg Val Glu 90 95 100			403
atc aaa aac gag aac cag acc ctg gcg acc gtt acc ctc cag aac tac Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val Thr Leu Gln Asn Tyr 105 110 115			451
ttc cgc ctc tac acc aaa ctc gcc ggc atg acc ggt acc gca gag acc Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr 120 125 130			499
gaa gca gca gag ctc aac cag atc tac aag ctc gac gtc atc gcg atc Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu Asp Val Ile Ala Ile 135 140 145			547
cca acc aac cga cca aac cag cgc gaa gac ttg acc gac ttg gtg tac Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu Thr Asp Leu Val Tyr 150 155 160 165			595
aaa acc caa gag gct aag ttc gca gca gtc gtc gac gac atc gca gaa Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val Asp Asp Ile Ala Glu 170 175 180			643
cgc acc gaa aag ggc caa cca gtc ctc gtc ggt acc gtc tcc gtc gag Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly Thr Val Ser Val Glu 185 190 195			691
cgc tcc gaa tac ctc tcc cag ctg ttg acc aaa cga ggc atc aag cac Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys Arg Gly Ile Lys His 200 205 210			739
aac gtc ctc aat gcg aag cac cac gag cag gaa gca cag atc gtt gct Asn Val Leu Asn Ala Lys His His Glu Gln Glu Ala Gln Ile Val Ala 215 220 225			787
cag gca ggt ctt cca ggc gcc gtc acc gtt gcc acc aac atg gcg ggc Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala Thr Asn Met Ala Gly 230 235 240 245			835
cgt gga acc gac atc gtg ctc ggc gga aac cca gaa atc ctc ctc gac Arg Gly Thr Asp Ile Val Leu Gly Gly Asn Pro Glu Ile Leu Leu Asp 250 255 260			883

atc aaa ctc cgc gaa cgt gga ctt gat cct ttc gaa gac gaa gaa agc Ile Lys Leu Arg Glu Arg Gly Leu Asp Pro Phe Glu Asp Glu Glu Ser 265 270 275	931
tac cag gaa gcc tgg gac gct gaa ctt cca gca atg aag cag cga tgc Tyr Gln Glu Ala Trp Asp Ala Glu Leu Pro Ala Met Lys Gln Arg Cys 280 285 290	979
gaa gaa cgt ggc gac aaa gtc cgc gaa gcc gga gga ctc tac gtc ctt Glu Glu Arg Gly Asp Lys Val Arg Glu Ala Gly Gly Leu Tyr Val Leu 295 300 305	1027
ggc acc gaa cgc cac gaa tcc cga cgc atc gac aac cag ctg cgc ggt Gly Thr Glu Arg His Glu Ser Arg Arg Ile Asp Asn Gln Leu Arg Gly 310 315 320 325	1075
cgt tct gca cgt cag ggc gac cca gga tcc acc cgc ttc tat ctc tct Arg Ser Ala Arg Gln Gly Asp Pro Gly Ser Thr Arg Phe Tyr Leu Ser 330 335 340	1123
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acc gtc acc aac tcc atc aag ggc gcc caa gct cag gtg gag aac cag Thr Val Thr Asn Ser Ile Lys Gly Ala Gln Ala Gln Val Glu Asn Gln 375 380 385	1267
aac ttc gaa atg cgt aag aac gtt ctg aag tac gac gaa gtc atg aac Asn Phe Glu Met Arg Lys Asn Val Leu Lys Tyr Asp Glu Val Met Asn 390 395 400 405	1315
gaa cag cgc aag gtt atc tac agc gag cga cgc gaa atc ctc gaa tcc Glu Gln Arg Lys Val Ile Tyr Ser Glu Arg Arg Glu Ile Leu Glu Ser 410 415 420	1363
gca gac atc tcc cgc tac atc caa aac atg atc gaa gaa aca gtc agc Ala Asp Ile Ser Arg Tyr Ile Gln Asn Met Ile Glu Glu Thr Val Ser 425 430 435	1411
gca tac gtc gac ggc gcc acc gcc aac ggc tac gtc gaa gac tgg gac Ala Tyr Val Asp Gly Ala Thr Ala Asn Gly Tyr Val Glu Asp Trp Asp 440 445 450	1459
ctc gac aaa ctc tgg aac gcc ctc gaa gcc ctc tac gac cca tcg atc Leu Asp Lys Leu Trp Asn Ala Leu Glu Ala Leu Tyr Asp Pro Ser Ile 455 460 465	1507
aac tgg acc gac ctc gtc gaa ggc agc gaa tac ggc aaa cca ggg gag Asn Trp Thr Asp Leu Val Glu Gly Ser Glu Tyr Gly Lys Pro Gly Glu 470 475 480 485	1555

ctg tcc gcc gaa gat cta cgc acc gca ctc gtc aac gac gcc cac gcc 1603
 Leu Ser Ala Glu Asp Leu Arg Thr Ala Leu Val Asn Asp Ala His Ala
 490 495 500

gaa tac gca aaa ctc gaa gaa gcc gta tcc gca atc ggc ggc gaa gca 1651
 Glu Tyr Ala Lys Leu Glu Glu Ala Val Ser Ala Ile Gly Gly Glu Ala
 505 510 515

cag atc cgc aac atc gaa cga atg gtg ctc atg cca gtc atc gac acc 1699
 Gln Ile Arg Asn Ile Glu Arg Met Val Leu Met Pro Val Ile Asp Thr
 520 525 530

aaa tgg cgc gaa cac ctc tac gaa atg gac tac ctg aaa gaa ggc atc 1747
 Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr Leu Lys Glu Gly Ile
 535 540 545

ggc ctg cgc gca atg gca cag cgc gac cca ctg gtc gaa tac caa aag 1795
 Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu Val Glu Tyr Gln Lys
 550 555 560 565

gaa ggc ggc gac atg ttc aac ggc atg aaa gac ggc atc aag gaa gaa 1843
 Glu Gly Gly Asp Met Phe Asn Gly Met Lys Asp Gly Ile Lys Glu Glu
 570 575 580

acc gtc cgc cag ctc ttc ctc tcc gca agc agt tca tca agc aag acg 1891
 Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser Ser Ser Ser Lys Thr
 585 590 595

cgg aag tcg ctg act aac tca gaa ccc tgaaattcag catccgccac 1938
 Arg Lys Ser Leu Thr Asn Ser Glu Pro
 600 605

atg 1941

<210> 56
 <211> 606
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 56
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 Gly Val Lys Glu Glu Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile
 20 25 30
 Asp Asn Leu Tyr Ala Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn
 35 40 45
 Asn Ala Ile Lys Ala Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile
 50 55 60
 Val Arg Asn Gly Glu Val Met Ile Val Asp Gly Phe Thr Gly Arg Val
 65 70 75 80
 Leu Ala Gly Arg Arg Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala

85										90										95										
Lys	Glu	Arg	Val	Glu	Ile	Lys	Asn	Glu	Asn	Gln	Thr	Leu	Ala	Thr	Val															
			100					105					110																	
Thr	Leu	Gln	Asn	Tyr	Phe	Arg	Leu	Tyr	Thr	Lys	Leu	Ala	Gly	Met	Thr															
		115					120					125																		
Gly	Thr	Ala	Glu	Thr	Glu	Ala	Ala	Glu	Leu	Asn	Gln	Ile	Tyr	Lys	Leu															
	130					135					140																			
Asp	Val	Ile	Ala	Ile	Pro	Thr	Asn	Arg	Pro	Asn	Gln	Arg	Glu	Asp	Leu															
145					150				155						160															
Thr	Asp	Leu	Val	Tyr	Lys	Thr	Gln	Glu	Ala	Lys	Phe	Ala	Ala	Val	Val															
			165					170						175																
Asp	Asp	Ile	Ala	Glu	Arg	Thr	Glu	Lys	Gly	Gln	Pro	Val	Leu	Val	Gly															
		180						185					190																	
Thr	Val	Ser	Val	Glu	Arg	Ser	Glu	Tyr	Leu	Ser	Gln	Leu	Leu	Thr	Lys															
		195					200					205																		
Arg	Gly	Ile	Lys	His	Asn	Val	Leu	Asn	Ala	Lys	His	His	Glu	Gln	Glu															
	210					215					220																			
Ala	Gln	Ile	Val	Ala	Gln	Ala	Gly	Leu	Pro	Gly	Ala	Val	Thr	Val	Ala															
225					230					235					240															
Thr	Asn	Met	Ala	Gly	Arg	Gly	Thr	Asp	Ile	Val	Leu	Gly	Gly	Asn	Pro															
			245					250					255																	
Glu	Ile	Leu	Leu	Asp	Ile	Lys	Leu	Arg	Glu	Arg	Gly	Leu	Asp	Pro	Phe															
		260						265					270																	
Glu	Asp	Glu	Glu	Ser	Tyr	Gln	Glu	Ala	Trp	Asp	Ala	Glu	Leu	Pro	Ala															
	275						280					285																		
Met	Lys	Gln	Arg	Cys	Glu	Glu	Arg	Gly	Asp	Lys	Val	Arg	Glu	Ala	Gly															
	290					295					300																			
Gly	Leu	Tyr	Val	Leu	Gly	Thr	Glu	Arg	His	Glu	Ser	Arg	Arg	Ile	Asp															
305					310					315				320																
Asn	Gln	Leu	Arg	Gly	Arg	Ser	Ala	Arg	Gln	Gly	Asp	Pro	Gly	Ser	Thr															
			325					330					335																	
Arg	Phe	Tyr	Leu	Ser	Met	Arg	Asp	Asp	Leu	Met	Val	Arg	Phe	Val	Gly															
		340						345					350																	
Pro	Thr	Met	Glu	Asn	Met	Met	Asn	Arg	Leu	Asn	Val	Pro	Asp	Asp	Val															
		355					360					365																		
Pro	Ile	Glu	Ser	Lys	Thr	Val	Thr	Asn	Ser	Ile	Lys	Gly	Ala	Gln	Ala															
	370					375					380																			
Gln	Val	Glu	Asn	Gln	Asn	Phe	Glu	Met	Arg	Lys	Asn	Val	Leu	Lys	Tyr															

385	390	395	400
Asp Glu Val Met	Asn Glu Gln Arg Lys Val Ile Tyr Ser Glu Arg Arg		
	405	410	415
Glu Ile Leu Glu Ser Ala Asp Ile Ser Arg Tyr Ile Gln Asn Met Ile			
	420	425	430
Glu Glu Thr Val Ser Ala Tyr Val Asp Gly Ala Thr Ala Asn Gly Tyr			
	435	440	445
Val Glu Asp Trp Asp Leu Asp Lys Leu Trp Asn Ala Leu Glu Ala Leu			
	450	455	460
Tyr Asp Pro Ser Ile Asn Trp Thr Asp Leu Val Glu Gly Ser Glu Tyr			
	465	470	475
Gly Lys Pro Gly Glu Leu Ser Ala Glu Asp Leu Arg Thr Ala Leu Val			
	485	490	495
Asn Asp Ala His Ala Glu Tyr Ala Lys Leu Glu Glu Ala Val Ser Ala			
	500	505	510
Ile Gly Gly Glu Ala Gln Ile Arg Asn Ile Glu Arg Met Val Leu Met			
	515	520	525
Pro Val Ile Asp Thr Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr			
	530	535	540
Leu Lys Glu Gly Ile Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu			
	545	550	555
Val Glu Tyr Gln Lys Glu Gly Gly Asp Met Phe Asn Gly Met Lys Asp			
	565	570	575
Gly Ile Lys Glu Glu Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser			
	580	585	590
Ser Ser Ser Lys Thr Arg Lys Ser Leu Thr Asn Ser Glu Pro			
	595	600	605

<210> 57

<211> 1965

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1942)

<223> RXN01559

<400> 57

gtctggttga ttggaattga aggagacttt cttggctcgg caaaaaaaga gtgccgctag 60

cgcctgggaa cgatggccaa aacgcgcaat agcgttggtt gtg ctc atc gtc gtt 115
 Val Leu Ile Val Val

1

5

ggt gtt tat gcg ttg gtg ctg ttg aca ggc gat cgt tct gcc aca cca	163
Gly Val Tyr Ala Leu Val Leu Leu Thr Gly Asp Arg Ser Ala Thr Pro	
10 15 20	
aaa ttg ggt att gat ctg caa ggc gga acc cga gtg acc ctc gtg ccg	211
Lys Leu Gly Ile Asp Leu Gln Gly Gly Thr Arg Val Thr Leu Val Pro	
25 30 35	
cag ggg cag gat cca act cag gac cag ctg aat cag gca cgc acc att	259
Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu Asn Gln Ala Arg Thr Ile	
40 45 50	
ctg gaa aac cgt gtg aac ggc atg ggc gtt tca ggt gca agc gtg gtc	307
Leu Glu Asn Arg Val Asn Gly Met Gly Val Ser Gly Ala Ser Val Val	
55 60 65	
gct gac ggt aac acg ctg gtg atc act gtt ccc ggg gaa aat acc gca	355
Ala Asp Gly Asn Thr Leu Val Ile Thr Val Pro Gly Glu Asn Thr Ala	
70 75 80 85	
cag gcg caa tcc cta gga cag acc tcc cag ctg ctg ttc cgt ccc gtt	403
Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln Leu Leu Phe Arg Pro Val	
90 95 100	
ggt cag gca gga atg ccc gat atg acc acg ttg atg cca gag ctg gaa	451
Gly Gln Ala Gly Met Pro Asp Met Thr Thr Leu Met Pro Glu Leu Glu	
105 110 115	
gag atg gcc aac agg tgg gtt gaa tac ggc gtc atc acc gaa gag cag	499
Glu Met Ala Asn Arg Trp Val Glu Tyr Gly Val Ile Thr Glu Glu Gln	
120 125 130	
gca aat gcc tcc ttg gag gaa atg aac acc gct gtt gca tcg acc act	547
Ala Asn Ala Ser Leu Glu Glu Met Asn Thr Ala Val Ala Ser Thr Thr	
135 140 145	
gcg gtg gaa ggc gaa gaa gca act gag cca gaa ccc gtc acc gtg tcg	595
Ala Val Glu Gly Glu Glu Ala Thr Glu Pro Glu Pro Val Thr Val Ser	
150 155 160 165	
gcg acc cct atg gat gag cca gcc aac tcc att gag gca aca cag cga	643
Ala Thr Pro Met Asp Glu Pro Ala Asn Ser Ile Glu Ala Thr Gln Arg	
170 175 180	
cgc cag gaa atc acg gac atg ctg cgc acc gac cgc cag tcc acc gat	691
Arg Gln Glu Ile Thr Asp Met Leu Arg Thr Asp Arg Gln Ser Thr Asp	
185 190 195	
ccc act gtc cag atc gct gca agt tct ttg atg cag tgc acc act gat	739
Pro Thr Val Gln Ile Ala Ala Ser Ser Leu Met Gln Cys Thr Thr Asp	
200 205 210	
gag atg gat cct ttg gcc ggc acc gat gat cca cgc ctg cca ttg gtg	787
Glu Met Asp Pro Leu Ala Gly Thr Asp Asp Pro Arg Leu Pro Leu Val	
215 220 225	

gca tgt gat cca gct gta ggt ggc gtg tat gta ctt gat cct gca cct Ala Cys Asp Pro Ala Val Gly Gly Val Tyr Val Leu Asp Pro Ala Pro 230 235 240 245	835
ttg ctc aac ggc gaa acc gat gag gaa aat ggt gcg cgc cta acc ggt Leu Leu Asn Gly Glu Thr Asp Glu Glu Asn Gly Ala Arg Leu Thr Gly 250 255 260	883
aat gag atc gat acc aac cgt ccc atc acc ggt gga ttc aac gcc cag Asn Glu Ile Asp Thr Asn Arg Pro Ile Thr Gly Gly Phe Asn Ala Gln 265 270 275	931
tcc ggc cag atg gaa atc agc ttt gcc ttc aaa tcc ggc gat ggg gaa Ser Gly Gln Met Glu Ile Ser Phe Ala Phe Lys Ser Gly Asp Gly Glu 280 285 290	979
gaa ggc tct gca act tgg tcc tct ctg acc agc cag tac ctg cag cag Glu Gly Ser Ala Thr Trp Ser Ser Leu Thr Ser Gln Tyr Leu Gln Gln 295 300 305	1027
cag atc gcc atc acc ctg gac tct cag gtg att tct gca ccc gtg att Gln Ile Ala Ile Thr Leu Asp Ser Gln Val Ile Ser Ala Pro Val Ile 310 315 320 325	1075
cag tca gca acc cct gtg ggt tct gca aca tcc atc acc ggt gac ttc Gln Ser Ala Thr Pro Val Gly Ser Ala Thr Ser Ile Thr Gly Asp Phe 330 335 340	1123
act caa act gaa gcc caa gat ctg gcg aac aac ctg cgc tac ggt gca Thr Gln Thr Glu Ala Gln Asp Leu Ala Asn Asn Leu Arg Tyr Gly Ala 345 350 355	1171
ttg ccc ctg agc ttc gca ggt gaa aac ggc gag cgc ggc gga act acc Leu Pro Leu Ser Phe Ala Gly Glu Asn Gly Glu Arg Gly Gly Thr Thr 360 365 370	1219
acc acc gtt ccg cca tca cta ggc gca gca tcc ttg aag gcc gga ctg Thr Thr Val Pro Pro Ser Leu Gly Ala Ala Ser Leu Lys Ala Gly Leu 375 380 385	1267
atc gca ggc atc gtc ggc atc gcg ctg gtc gcc atc ttc gtg ttc gcc Ile Ala Gly Ile Val Gly Ile Ala Leu Val Ala Ile Phe Val Phe Ala 390 395 400 405	1315
tac tac cgc gtc ttc gga ttc gtt tcc ctg ttc acc ctg ttt gcc gca Tyr Tyr Arg Val Phe Gly Phe Val Ser Leu Phe Thr Leu Phe Ala Ala 410 415 420	1363
ggc gtg ttg gtc tac ggc ctt ctg gta ctg ctg gga cgc tgg atc gga Gly Val Leu Val Tyr Gly Leu Leu Val Leu Leu Gly Arg Trp Ile Gly 425 430 435	1411
tat tcc cta gac ctt gct ggt atc gcc ggt ttg atc atc ggt atc ggt Tyr Ser Leu Asp Leu Ala Gly Ile Ala Gly Leu Ile Ile Gly Ile Gly 440 445 450	1459

acc acc gcc gac tcc ttc gtg gtg ttc tat gag cgc atc aag gat gag 1507
 Thr Thr Ala Asp Ser Phe Val Val Phe Tyr Glu Arg Ile Lys Asp Glu
 455 460 465

atc cgt gaa gga aga tcc ttt aga tct gca gta cct cgt gca tgg gaa 1555
 Ile Arg Glu Gly Arg Ser Phe Arg Ser Ala Val Pro Arg Ala Trp Glu
 470 475 480 485

agc gcc aag cgc acc atc gtc aca ggc aac atg gtc act ttg ctc ggc 1603
 Ser Ala Lys Arg Thr Ile Val Thr Gly Asn Met Val Thr Leu Leu Gly
 490 495 500

gct atc gtg att tac ttg ctc gcg gtc ggc gaa gtc aag ggc ttt gcc 1651
 Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu Val Lys Gly Phe Ala
 505 510 515

ttc acc ctg ggt ctg acc acc gta ttc gat ctc gtt gtc acc ttc ctg 1699
 Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu Val Val Thr Phe Leu
 520 525 530

atc acg gca cca ctg gtt atc ctg gca tca cgc aac cca ttc ttt gcc 1747
 Ile Thr Ala Pro Leu Val Ile Leu Ala Ser Arg Asn Pro Phe Phe Ala
 535 540 545

aag tca tcg gtc aac ggc atg gga cga gtg atg aag ctc gtt gaa gaa 1795
 Lys Ser Ser Val Asn Gly Met Gly Arg Val Met Lys Leu Val Glu Glu
 550 555 560 565

cgc cgc gcc aac ggt gaa ttg gat gag cct gag tac ctg aaa aag atc 1843
 Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu Tyr Leu Lys Lys Ile
 570 575 580

cat gcc aag aat gcg gca gct gat aag gct tcc act gac aat tct tcc 1891
 His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser
 585 590 595

act gac aat tct gaa gca cct ggc acc gat acg aac caa gag gag gag 1939
 Thr Asp Asn Ser Glu Ala Pro Gly Thr Asp Thr Asn Gln Glu Glu Glu
 600 605 610

aag tagccatgac tgattcccag act 1965
 Lys

<210> 58

<211> 614

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

Val Leu Ile Val Val Gly Val Tyr Ala Leu Val Leu Leu Thr Gly Asp
 1 5 10 15

Arg Ser Ala Thr Pro Lys Leu Gly Ile Asp Leu Gln Gly Gly Thr Arg
 20 25 30

Val Thr Leu Val Pro Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu Asn
 35 40 45
 Gln Ala Arg Thr Ile Leu Glu Asn Arg Val Asn Gly Met Gly Val Ser
 50 55 60
 Gly Ala Ser Val Val Ala Asp Gly Asn Thr Leu Val Ile Thr Val Pro
 65 70 75 80
 Gly Glu Asn Thr Ala Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln Leu
 85 90 95
 Leu Phe Arg Pro Val Gly Gln Ala Gly Met Pro Asp Met Thr Thr Leu
 100 105 110
 Met Pro Glu Leu Glu Glu Met Ala Asn Arg Trp Val Glu Tyr Gly Val
 115 120 125
 Ile Thr Glu Glu Gln Ala Asn Ala Ser Leu Glu Glu Met Asn Thr Ala
 130 135 140
 Val Ala Ser Thr Thr Ala Val Glu Gly Glu Glu Ala Thr Glu Pro Glu
 145 150 155 160
 Pro Val Thr Val Ser Ala Thr Pro Met Asp Glu Pro Ala Asn Ser Ile
 165 170 175
 Glu Ala Thr Gln Arg Arg Gln Glu Ile Thr Asp Met Leu Arg Thr Asp
 180 185 190
 Arg Gln Ser Thr Asp Pro Thr Val Gln Ile Ala Ala Ser Ser Leu Met
 195 200 205
 Gln Cys Thr Thr Asp Glu Met Asp Pro Leu Ala Gly Thr Asp Asp Pro
 210 215 220
 Arg Leu Pro Leu Val Ala Cys Asp Pro Ala Val Gly Gly Val Tyr Val
 225 230 235 240
 Leu Asp Pro Ala Pro Leu Leu Asn Gly Glu Thr Asp Glu Glu Asn Gly
 245 250 255
 Ala Arg Leu Thr Gly Asn Glu Ile Asp Thr Asn Arg Pro Ile Thr Gly
 260 265 270
 Gly Phe Asn Ala Gln Ser Gly Gln Met Glu Ile Ser Phe Ala Phe Lys
 275 280 285
 Ser Gly Asp Gly Glu Glu Gly Ser Ala Thr Trp Ser Ser Leu Thr Ser
 290 295 300
 Gln Tyr Leu Gln Gln Gln Ile Ala Ile Thr Leu Asp Ser Gln Val Ile
 305 310 315 320
 Ser Ala Pro Val Ile Gln Ser Ala Thr Pro Val Gly Ser Ala Thr Ser
 325 330 335

Ile Thr Gly Asp Phe Thr Gln Thr Glu Ala Gln Asp Leu Ala Asn Asn
 340 345 350
 Leu Arg Tyr Gly Ala Leu Pro Leu Ser Phe Ala Gly Glu Asn Gly Glu
 355 360 365
 Arg Gly Gly Thr Thr Thr Thr Val Pro Pro Ser Leu Gly Ala Ala Ser
 370 375 380
 Leu Lys Ala Gly Leu Ile Ala Gly Ile Val Gly Ile Ala Leu Val Ala
 385 390 395 400
 Ile Phe Val Phe Ala Tyr Tyr Arg Val Phe Gly Phe Val Ser Leu Phe
 405 410 415
 Thr Leu Phe Ala Ala Gly Val Leu Val Tyr Gly Leu Leu Val Leu Leu
 420 425 430
 Gly Arg Trp Ile Gly Tyr Ser Leu Asp Leu Ala Gly Ile Ala Gly Leu
 435 440 445
 Ile Ile Gly Ile Gly Thr Thr Ala Asp Ser Phe Val Val Phe Tyr Glu
 450 455 460
 Arg Ile Lys Asp Glu Ile Arg Glu Gly Arg Ser Phe Arg Ser Ala Val
 465 470 475 480
 Pro Arg Ala Trp Glu Ser Ala Lys Arg Thr Ile Val Thr Gly Asn Met
 485 490 495
 Val Thr Leu Leu Gly Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu
 500 505 510
 Val Lys Gly Phe Ala Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu
 515 520 525
 Val Val Thr Phe Leu Ile Thr Ala Pro Leu Val Ile Leu Ala Ser Arg
 530 535 540
 Asn Pro Phe Phe Ala Lys Ser Ser Val Asn Gly Met Gly Arg Val Met
 545 550 555 560
 Lys Leu Val Glu Glu Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu
 565 570 575
 Tyr Leu Lys Lys Ile His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser
 580 585 590
 Thr Asp Asn Ser Ser Thr Asp Asn Ser Glu Ala Pro Gly Thr Asp Thr
 595 600 605
 Asn Gln Glu Glu Glu Lys
 610

<210> 59

<211> 819

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(796)

<223> RXN00046

<400> 59

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acctaaaacg	ctgttctcaa	cacaggagtt	tccttaaata	atg	gac	tta	aat	act	115
				Met	Asp	Leu	Asn	Thr	
				1				5	

caa	cgc	tca	aag	ctc	tac	gca	cag	ctt	caa	ggc	cag	ctc	att	ggt	tcc	163
Gln	Arg	Ser	Lys	Leu	Tyr	Ala	Gln	Leu	Gln	Gly	Gln	Leu	Ile	Val	Ser	
			10					15						20		

gtg	caa	gct	ccc	gac	ggc	cat	gcc	atg	cga	gat	acc	cat	acg	ctc	acc	211
Val	Gln	Ala	Pro	Asp	Gly	His	Ala	Met	Arg	Asp	Thr	His	Thr	Leu	Thr	
			25					30					35			

cat	gtg	gcc	gca	gcc	tgt	gtc	gat	ggc	ggg	gct	cct	gcc	att	cgc	tgt	259
His	Val	Ala	Ala	Ala	Cys	Val	Asp	Gly	Gly	Ala	Pro	Ala	Ile	Arg	Cys	
		40					45				50					

ggc	ggg	tac	ggc	ggg	ttg	gaa	gat	atc	cgt	tca	atc	tcc	aac	cgt	gtc	307
Gly	Gly	Tyr	Gly	Gly	Leu	Glu	Asp	Ile	Arg	Ser	Ile	Ser	Asn	Arg	Val	
		55			60						65					

gac	ggt	ccc	ggt	ttc	gga	ctc	acc	aaa	gaa	ggc	tcc	gaa	gga	ggt	tac	355
Asp	Val	Pro	Val	Phe	Gly	Leu	Thr	Lys	Glu	Gly	Ser	Glu	Gly	Val	Tyr	
	70				75					80					85	

atc	acc	cca	acc	agg	gat	tcc	ggt	cga	gca	gtg	gca	gaa	tcc	ggc	gcc	403
Ile	Thr	Pro	Thr	Arg	Asp	Ser	Val	Arg	Ala	Val	Ala	Glu	Ser	Gly	Ala	
				90					95					100		

act	gta	gtc	tgc	gcg	gat	gca	act	ttc	cga	cct	agg	cct	gac	ggc	tcc	451
Thr	Val	Val	Cys	Ala	Asp	Ala	Thr	Phe	Arg	Pro	Arg	Pro	Asp	Gly	Ser	
			105					110					115			

acc	ttt	gca	gag	ctg	gtc	act	ggt	gcc	cac	gat	tcc	gga	att	ctc	atc	499
Thr	Phe	Ala	Glu	Leu	Val	Thr	Val	Ala	His	Asp	Ser	Gly	Ile	Leu	Ile	
		120					125					130				

atg	gcg	gac	tgc	gca	act	ccc	gaa	gaa	ggt	ctc	agt	gcg	cat	aag	gct	547
Met	Ala	Asp	Cys	Ala	Thr	Pro	Glu	Glu	Val	Leu	Ser	Ala	His	Lys	Ala	
	135					140					145					

ggc	gcg	gat	ttt	gtg	tcc	acc	acg	ctt	gct	gga	tac	acc	gaa	cac	cgc	595
Gly	Ala	Asp	Phe	Val	Ser	Thr	Thr	Leu	Ala	Gly	Tyr	Thr	Glu	His	Arg	
150					155				160						165	

gag	aaa	aca	gtc	ggt	cca	gat	ttc	gat	tgc	ctc	cgc	gaa	gca	cgt	gag	643
Glu	Lys	Thr	Val	Gly	Pro	Asp	Phe	Asp	Cys	Leu	Arg	Glu	Ala	Arg	Glu	

	170	175	180	
tta gtt ccc gat gcg ttc ctc att ggc gaa ggt cgc ttc tcc aac cct				691
Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly Arg Phe Ser Asn Pro				
	185	190	195	
gcg gat gtg gcg cac ggt cgt ctc att ggt gcc aac gcg atc atc gtg				739
Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala Asn Ala Ile Ile Val				
	200	205	210	
ggc acc gca atc act gac cct ggt ttc atc act gga cag ttc gcg tca				787
Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr Gly Gln Phe Ala Ser				
	215	220	225	
ctg ttg cac tagcacttag tccagcgctg cac				819
Leu Leu His				
230				
<210> 60				
<211> 232				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 60				
Met Asp Leu Asn Thr Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly				
1 5 10 15				
Gln Leu Ile Val Ser Val Gln Ala Pro Asp Gly His Ala Met Arg Asp				
20 25 30				
Thr His Thr Leu Thr His Val Ala Ala Ala Cys Val Asp Gly Gly Ala				
35 40 45				
Pro Ala Ile Arg Cys Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser				
50 55 60				
Ile Ser Asn Arg Val Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly				
65 70 75 80				
Ser Glu Gly Val Tyr Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val				
85 90 95				
Ala Glu Ser Gly Ala Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro				
100 105 110				
Arg Pro Asp Gly Ser Thr Phe Ala Glu Leu Val Thr Val Ala His Asp				
115 120 125				
Ser Gly Ile Leu Ile Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu				
130 135 140				
Ser Ala His Lys Ala Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly				
145 150 155 160				
Tyr Thr Glu His Arg Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu				
165 170 175				

Arg Glu Ala Arg Glu Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly
 180 185 190

Arg Phe Ser Asn Pro Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala
 195 200 205

Asn Ala Ile Ile Val Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr
 210 215 220

Gly Gln Phe Ala Ser Leu Leu His
 225 230

<210> 61

<211> 1219

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (48)..(1196)

<223> RXN01863

<400> 61

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 Met Asn Ser
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gtc aaa ttg aag caa cct gtt agc att tac aat gat cca tgg gaa tca 104
 Val Lys Leu Lys Gln Pro Val Ser Ile Tyr Asn Asp Pro Trp Glu Ser
 5 10 15

tat aac gat gtt aaa gaa cat ggc caa tta act tta agt aac atc gaa 152
 Tyr Asn Asp Val Lys Glu His Gly Gln Leu Thr Leu Ser Asn Ile Glu
 20 25 30 35

ttt aca act aca aat ctt tgt aat atg cgt tgt agc cac tgt gca gtt 200
 Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His Cys Ala Val
 40 45 50

ggt tat act tta caa act gtc gac ccc gag cct tta gat atg gac tta 248
 Gly Tyr Thr Leu Gln Thr Val Asp Pro Glu Pro Leu Asp Met Asp Leu
 55 60 65

att tat cgt aga ctt gat gaa att cca aat ctg cga acg atg tca att 296
 Ile Tyr Arg Arg Leu Asp Glu Ile Pro Asn Leu Arg Thr Met Ser Ile
 70 75 80

aca ggt ggc gaa cca atg ttt tct aaa aag tct att aga aat gtt gtt 344
 Thr Gly Gly Glu Pro Met Phe Ser Lys Lys Ser Ile Arg Asn Val Val
 85 90 95

aaa cct cta tta aag tat gca cat cat cga ggt ata tat aca caa atg 392
 Lys Pro Leu Leu Lys Tyr Ala His His Arg Gly Ile Tyr Thr Gln Met
 100 105 110 115

aat tca aac cta aca ttg cct caa gat cgt tat tta gat att gct gaa	440
Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp Ile Ala Glu	
120 125 130	
tat atc gat gtt atg cat atc tca cat aac tgg gga aca act gat gaa	488
Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr Thr Asp Glu	
135 140 145	
ttc gca aat gtt ggc ttt ggc gca atg aag aag caa cca ccg tta aaa	536
Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro Pro Leu Lys	
150 155 160	
gct aag tta aaa tta tat gaa caa atg att tcg aat gca cgt aca tta	584
Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala Arg Thr Leu	
165 170 175	
tca gaa caa gga atg ttt gta tct gcg gaa aca atg ctc aat caa agt	632
Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu Asn Gln Ser	
180 185 190 195	
acg cta cca cat tta cga aaa ata cat caa gaa gtc gtt cat gat atg	680
Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val His Asp Met	
200 205 210	
aaa tgt agc aga cac gag att cac cct atg tat cca gct gac ttt gca	728
Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala Asp Phe Ala	
215 220 225	
agt caa tta aat gtg tta act cta gcg gaa atg aaa aag aca att cat	776
Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys Thr Ile His	
230 235 240	
gat ata ttg gat ttc aga gat gaa gat att tgg atg tta ttt ggt act	824
Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu Phe Gly Thr	
245 250 255	
ttg cct gtg ttt cca tgc tta aag gat gat gaa gat caa aag tta cta	872
Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln Lys Leu Leu	
260 265 270 275	
tca cgt tta aga aat gct aac aat gta acg act aga aat gac ccg gat	920
Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn Asp Pro Asp	
280 285 290	
ggc cgt agt cgt tta aat gtc aat gta ttt aca ggt aat gta atc gta	968
Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn Val Ile Val	
295 300 305	
act gat ttc gga gat gaa aca ggt aca att tcg aat ata caa aaa gat	1016
Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile Gln Lys Asp	
310 315 320	
aaa tta aca gat gta ttt gat aaa tgg tta tcc tct gat ctt gct aaa	1064
Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp Leu Ala Lys	
325 330 335	
tca tta aat tgt cat tgt tcc gag ttt agt tgt tta gga cca aat gtt	1112

Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly Pro Asn Val
 340 345 350 355

ctt gtt aaa aat atg tac tat ccg aat atg gat ttt aaa gat aat gag 1160
 Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys Asp Asn Glu
 360 365 370

cgt cat atg cac aaa caa cca caa att ata caa ttt taaaaactct 1206
 Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe
 375 380

taattatgcg gag 1219

<210> 62

<211> 383

<212> PRT

<213> Corynebacterium glutamicum

<400> 62

Met Asn Ser Val Lys Leu Lys Gln Pro Val Ser Ile Tyr Asn Asp Pro
 1 5 10 15

Trp Glu Ser Tyr Asn Asp Val Lys Glu His Gly Gln Leu Thr Leu Ser
 20 25 30

Asn Ile Glu Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His
 35 40 45

Cys Ala Val Gly Tyr Thr Leu Gln Thr Val Asp Pro Glu Pro Leu Asp
 50 55 60

Met Asp Leu Ile Tyr Arg Arg Leu Asp Glu Ile Pro Asn Leu Arg Thr
 65 70 75 80

Met Ser Ile Thr Gly Gly Glu Pro Met Phe Ser Lys Lys Ser Ile Arg
 85 90 95

Asn Val Val Lys Pro Leu Leu Lys Tyr Ala His His Arg Gly Ile Tyr
 100 105 110

Thr Gln Met Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp
 115 120 125

Ile Ala Glu Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr
 130 135 140

Thr Asp Glu Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro
 145 150 155 160

Pro Leu Lys Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala
 165 170 175

Arg Thr Leu Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu
 180 185 190

Asn Gln Ser Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val

195	200	205
His Asp Met Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala 210 215 220		
Asp Phe Ala Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys 225 230 235 240		
Thr Ile His Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu 245 250 255		
Phe Gly Thr Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln 260 265 270		
Lys Leu Leu Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn 275 280 285		
Asp Pro Asp Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn 290 295 300		
Val Ile Val Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile 305 310 315 320		
Gln Lys Asp Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp 325 330 335		
Leu Ala Lys Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly 340 345 350		
Pro Asn Val Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys 355 360 365		
Asp Asn Glu Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe 370 375 380		

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 <213> Corynebacterium glutamicum

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 <223> RXN00833

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 Met Ala Lys Thr His
 1 5
 ttt caa ggc aac gaa act gct acc tcc ggc gaa ctg cca cag gtc ggc 163
 Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu Leu Pro Gln Val Gly
 10 15 20

gac aac ctc gca gag ttc aac ctc gtc aac acc gaa ctg ggc gag gtc 211
 Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr Glu Leu Gly Glu Val
 25 30 35

tcc tca aag gac ttc cag ggc cgc aag ctt gtc ctg aac atc ttc cca 259
 Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val Leu Asn Ile Phe Pro
 40 45 50

tcc gtt gac acc ggc gtt tgt gca aca tca gtc cgc aag ttc aac gag 307
 Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val Arg Lys Phe Asn Glu
 55 60 65

gca gca gca agc ctg gaa aac acc acc gtg ctg tgc atc tcc aag gat 355
 Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu Cys Ile Ser Lys Asp
 70 75 80 85

ctt cca ttc gca ctg ggc cgt ttc tgc tcc gca gaa ggc atc gag aac 403
 Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala Glu Gly Ile Glu Asn
 90 95 100

gtc acc cca gta tcc gca ttc cgt tcc acc ttc ggt gaa gac aac ggc 451
 Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe Gly Glu Asp Asn Gly
 105 110 115

atc gtg ctc gaa ggc tca cca ctt aag ggt ctt ctt gca cgc agc gtc 499
 Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu Leu Ala Arg Ser Val
 120 125 130

atc gtc gtc gat gaa aac ggc aag gtt gct tac acc cag ttg gtt gat 547
 Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr Thr Gln Leu Val Asp
 135 140 145

gag atc ttc act gaa cct gat tac gac gct gca ctt gct ggg ctg aac 595
 Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala Leu Ala Gly Leu Asn
 150 155 160 165

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<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

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Glu Leu Gly Glu Val Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val
 35 40 45

Leu Asn Ile Phe Pro Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val
 50 55 60

Arg Lys Phe Asn Glu Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu
 65 70 75 80
 Cys Ile Ser Lys Asp Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala
 85 90 95
 Glu Gly Ile Glu Asn Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe
 100 105 110
 Gly Glu Asp Asn Gly Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu
 115 120 125
 Leu Ala Arg Ser Val Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr
 130 135 140
 Thr Gln Leu Val Asp Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala
 145 150 155 160
 Leu Ala Gly Leu Asn
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 <222> (101)..(856)
 <223> RXN01676

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 Met Ile Leu His Gly
 1 5
 gtt gtg ttc tac gca gga ctt cta gta ctt ctc gtg cca ctt ggc ctt 163
 Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu Val Pro Leu Gly Leu
 10 15 20
 ggt gcg gga atc ctc ggc gag ctg ttt atc acc caa cgc cag acc atc 211
 Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr Gln Arg Gln Thr Ile
 25 30 35
 atc gtg gtt tca tcg atc gtg ctg att atc cta ggt ttt gtc cag atc 259
 Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu Gly Phe Val Gln Ile
 40 45 50
 ttc ggc ggc gga ttc gac ttc gga aaa gca ctc cca gga tta gat cgt 307
 Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu Pro Gly Leu Asp Arg
 55 60 65
 ctg caa tct aag gcc act gtg acc tca ggt cta gga aag agc ttt tta 355
 Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu Gly Lys Ser Phe Leu

70	75	80	85	
cta gga atg acc agt agt att gcc ggt ttt tgt tcc gga cca atc ctc				403
Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys Ser Gly Pro Ile Leu				
	90	95	100	
ggc gcc gtt ctt act ttg gct gcc acc agt gga aac tcc atc acc tca				451
Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly Asn Ser Ile Thr Ser				
	105	110	115	
gca ctc att ttg agt gct tat ggt gcg gga atg gtg ctg ccc ctg atg				499
Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met Val Leu Pro Leu Met				
	120	125	130	
gct att gca gcg ctc tgg gcc aaa ctc gga cag cgt gga cag cag atg				547
Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln Arg Gly Gln Gln Met				
	135	140	145	
ctc cgc ggc cgg gaa ttc acc ttc ttg ggc agg cag tgg cac att gtt				595
Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg Gln Trp His Ile Val				
	150	155	160	165
tct gtc att agc ggt gcc ctg atc atc gct gtc gga atc ctc ttt tgg				643
Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val Gly Ile Leu Phe Trp				
	170	175	180	
tcc acg aac ggc ctt gtc agc atg ccg gag ctc gtt cca atg gac acc				691
Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu Val Pro Met Asp Thr				
	185	190	195	
cag atc tgg cta cag gaa gcc aca ttc tca ctc ggg tca cca ctc ttt				739
Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu Gly Ser Pro Leu Phe				
	200	205	210	
gac atc gca ttg atc att gtc gcc gct ggc ttg ttc ttg tac ttc tgg				787
Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu Phe Leu Tyr Phe Trp				
	215	220	225	
aac aaa cga caa aag cga aaa gaa gaa gct cag cga ccc aaa gaa agt				835
Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln Arg Pro Lys Glu Ser				
	230	235	240	245
gga tgg gtt att aac cct cgc taattattag ttttgagcgc agg				879
Gly Trp Val Ile Asn Pro Arg				
	250			

<210> 66

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

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<210> 67
<211> 744
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(721)  
<223> RXN00380
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Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser Gly Leu Ala Leu Val		
10 15 20		
gcc tgc agc agt gac agt acc gct ggt act gac gct gtt gct gtc ggc	211	
Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp Ala Val Ala Val Gly		
25 30 35		
gga acc ttc caa ttc cac tcc ccg gat gga aag atg gaa att ttc tac	259	
Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys Met Glu Ile Phe Tyr		
40 45 50		
gac gag gct gac cgt caa caa ctc ccc gac att ggt gga gat tcc ctc	307	
Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile Gly Gly Asp Ser Leu		
55 60 65		
atg gaa gag ggc aca cag atc aac ctg tct gat ttc gaa aac caa gtt	355	
Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp Phe Glu Asn Gln Val		
70 75 80 85		
gtc atc ctc aat gcg tgg ggg cag tgg tgt gca ccg tgc cgc tcc gaa	403	
Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala Pro Cys Arg Ser Glu		
90 95 100		
tcc gat gat ctc cag att atc cat gag gaa ctc caa gct gcc gga aac	451	
Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu Gln Ala Ala Gly Asn		
105 110 115		
ggc gac acc cct ggt ggc acc gtg ttg ggt atc aat gtg cgt gat tac	499	
Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile Asn Val Arg Asp Tyr		
120 125 130		
tcc cgc gac atc gcc caa gac ttt gtc acc gac aac ggc ctt gat tac	547	
Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp Asn Gly Leu Asp Tyr		
135 140 145		
cca agc att tac gat cca cca ttt atg aca gca gca tcc ctc ggt ggt	595	
Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala Ala Ser Leu Gly Gly		
150 155 160 165		
gtt ccc gca tcg gtg atc cca acc acc atc gtg ctg gat aaa cag cac	643	
Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val Leu Asp Lys Gln His		
170 175 180		
cgc ccc gca gca gtg ttc ttg cgc gaa gtc acc tcc aaa gat gtg ttg	691	
Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr Ser Lys Asp Val Leu		
185 190 195		
gat gtt gcg ttg cca ttg gta gat gag gcc taaatgtctg agattgtggt	741	
Asp Val Ala Leu Pro Leu Val Asp Glu Ala		
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744

<210> 68

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

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			20					25					30		

Ala	Val	Ala	Val	Gly	Gly	Thr	Phe	Gln	Phe	His	Ser	Pro	Asp	Gly	Lys
		35					40					45			

Met	Glu	Ile	Phe	Tyr	Asp	Glu	Ala	Asp	Arg	Gln	Gln	Leu	Pro	Asp	Ile
	50					55					60				

Gly	Gly	Asp	Ser	Leu	Met	Glu	Glu	Gly	Thr	Gln	Ile	Asn	Leu	Ser	Asp
65					70					75					80

Phe	Glu	Asn	Gln	Val	Val	Ile	Leu	Asn	Ala	Trp	Gly	Gln	Trp	Cys	Ala
			85						90					95	

Pro	Cys	Arg	Ser	Glu	Ser	Asp	Asp	Leu	Gln	Ile	Ile	His	Glu	Glu	Leu
			100					105					110		

Gln	Ala	Ala	Gly	Asn	Gly	Asp	Thr	Pro	Gly	Gly	Thr	Val	Leu	Gly	Ile
		115					120					125			

Asn	Val	Arg	Asp	Tyr	Ser	Arg	Asp	Ile	Ala	Gln	Asp	Phe	Val	Thr	Asp
	130					135					140				

Asn	Gly	Leu	Asp	Tyr	Pro	Ser	Ile	Tyr	Asp	Pro	Pro	Phe	Met	Thr	Ala
145					150					155					160

Ala	Ser	Leu	Gly	Gly	Val	Pro	Ala	Ser	Val	Ile	Pro	Thr	Thr	Ile	Val
			165						170					175	

Leu	Asp	Lys	Gln	His	Arg	Pro	Ala	Ala	Val	Phe	Leu	Arg	Glu	Val	Thr
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Ser	Lys	Asp	Val	Leu	Asp	Val	Ala	Leu	Pro	Leu	Val	Asp	Glu	Ala	
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<211> 495

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(472)

<223> RXN00937

<400> 69

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                                   Met Ala Thr Ile Asp
                                   1       5

gta acc gaa gaa aca ttt gag agc aca gtt acc ggc gac gga att gtc 163
Val Thr Glu Glu Thr Phe Glu Ser Thr Val Thr Gly Asp Gly Ile Val
              10              15              20

ctc gta gac gca tgg gca tcc tgg tgc gga cct tgc cgc cag ttc gcc 211
Leu Val Asp Ala Trp Ala Ser Trp Cys Gly Pro Cys Arg Gln Phe Ala
              25              30              35

cca acc tac gag aag gtt tcc gaa acc cac acc gac gca acc ttc gcc 259
Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr Asp Ala Thr Phe Ala
              40              45              50

aag ctt gat acc gaa gca aac cag ggc ctg gct gca gca ctg cag atc 307
Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala Ala Ala Leu Gln Ile
              55              60              65

cag tcc atc cca act ctg atg gtt ttc cgc gac ggc atc atg gtc tac 355
Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp Gly Ile Met Val Tyr
              70              75              80              85

cgc gaa gcc ggc acc atg cca gct cct gca ctg gat gat ctg gtc aac 403
Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu Asp Asp Leu Val Asn
              90              95              100

cag gtt aag gca ctc gac atg gat gac gtt cgt cgc cag gtc gca gag 451
Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg Arg Gln Val Ala Glu
              105              110              115

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<210> 70

<211> 124

<212> PRT

<213> *Corynebacterium glutamicum*

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      20           25           30

Cys Arg Gln Phe Ala Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr
      35           40           45

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Asp Ala Thr Phe Ala Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala
 50 55 60

Ala Ala Leu Gln Ile Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp
 65 70 75 80

Gly Ile Met Val Tyr Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu
 85 90 95

Asp Asp Leu Val Asn Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg
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Arg Gln Val Ala Glu Gln Gln Gly Ser Ala Glu Ala
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<210> 71

<211> 990

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (101)..(967)

<223> RXN02325

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 Met Asp His Ala His
 1 5

gat tcc tgc tca cca act ctg cgc cgt gat ttg gag gtc act ggc cag 163
 Asp Ser Cys Ser Pro Thr Leu Arg Arg Asp Leu Glu Val Thr Gly Gln
 10 15 20

ctc caa cct gag aaa gct gtc gat tta gca gcg ccg cac gaa ggg aag 211
 Leu Gln Pro Glu Lys Ala Val Asp Leu Ala Ala Pro His Glu Gly Lys
 25 30 35

gtt gcc aat ata acg aag gtg acc tcc tca aat atg gag cac acc atc 259
 Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn Met Glu His Thr Ile
 40 45 50

acg cag gcc tca aaa gct aag gag gtg gtg gtg ctc att ggt cac tcc 307
 Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val Leu Ile Gly His Ser
 55 60 65

ctg ctg ccc aca ttt cag gat ttg gaa aaa gac att ctg cac ttt cag 355
 Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp Ile Leu His Phe Gln
 70 75 80 85

gca ggt aat aaa ggg cga ttt tct gta gcg att gtt gat cct gat cgc 403
 Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile Val Asp Pro Asp Arg
 90 95 100

agt gca gat gtg gtt gcc aga ttt agg cca aaa cag att ccg gtg gca 451
 Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys Gln Ile Pro Val Ala
 105 110 115

tac gtg gtg aaa gat ggc gcc agc att gcg gag ttc aac tcg ctc aac 499
 Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu Phe Asn Ser Leu Asn
 120 125 130

aag gag ccg gtt gca caa tgg ctt gat cat ttt gtg tcg cgg gaa acg 547
 Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe Val Ser Arg Glu Thr
 135 140 145

atc ccc aat gaa aaa gag ggg gac gtc gat aag caa ata gac ccg cgc 595
 Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys Gln Ile Asp Pro Arg
 150 155 160 165

ctg tgg ccg gca gcg gaa ttg gtg aac gcc ggt gat ttt cgc gcg gcg 643
 Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly Asp Phe Arg Ala Ala
 170 175 180

ttg gcg ttg tat gag cag ttg ccg cag gat gcg acg gtg aag ccg gcg 691
 Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala Thr Val Lys Arg Ala
 185 190 195

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 His Ala Ala Val Ser Val Leu Ala Arg Met Ser Val Ala Asp Arg Gly
 200 205 210

gag gat ccg atc gag aag tcg cgc ccg gat cca gac gat gtg aac aag 787
 Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro Asp Asp Val Asn Lys
 215 220 225

gcg ctg gcg gcg gcg gat atg tat gtg ttg atg aat cag ccg gac aca 835
 Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met Asn Gln Pro Asp Thr
 230 235 240 245

gcg ctc gcg cac ctt gca gca cta ttg cca aaa ccg gag gct gcc ccg 883
 Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys Pro Glu Ala Ala Arg
 250 255 260

ccg atc gtg gag ttg ctg aac ttg ttt gat ccg ctg gac ctg gtc gca 931
 Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro Leu Asp Leu Val Ala
 265 270 275

ttg gaa atc agg gcg cag gtg ggg aat gca atg agc taagaaaaca 977
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 280 285

ctttaaatat tct 990

<210> 72

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

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 20 25 30
 Pro His Glu Gly Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn
 35 40 45
 Met Glu His Thr Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val
 50 55 60
 Leu Ile Gly His Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp
 65 70 75 80
 Ile Leu His Phe Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile
 85 90 95
 Val Asp Pro Asp Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys
 100 105 110
 Gln Ile Pro Val Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu
 115 120 125
 Phe Asn Ser Leu Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe
 130 135 140
 Val Ser Arg Glu Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys
 145 150 155 160
 Gln Ile Asp Pro Arg Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly
 165 170 175
 Asp Phe Arg Ala Ala Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala
 180 185 190
 Thr Val Lys Arg Ala His Ala Ala Val Ser Val Leu Ala Arg Met Ser
 195 200 205
 Val Ala Asp Arg Gly Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro
 210 215 220
 Asp Asp Val Asn Lys Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met
 225 230 235 240
 Asn Gln Pro Asp Thr Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys
 245 250 255
 Pro Glu Ala Ala Arg Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro
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 Ser

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Val Ser Thr Asn Lys																5
1																
gaa cga cgc caa cag gcg ctt tcc cag ctg gag aaa gaa atc aaa agc																163
Glu Arg Arg Gln Gln Ala Leu Ser Gln Leu Glu Lys Glu Ile Lys Ser																20
10 15																
cgg gac cgc aaa gaa aag acc aag cca cta acc gtg gtc ttt gct tcc																211
Arg Asp Arg Lys Glu Lys Thr Lys Pro Leu Thr Val Val Phe Ala Ser																35
25 30																
ctg gct gtc atc ctg gtt gtc gtt ggc ggt atc tgg tac gca gct acc																259
Leu Ala Val Ile Leu Val Val Val Gly Gly Ile Trp Tyr Ala Ala Thr																50
40 45																
cgc agc acc gaa gac gaa gtc atc acc gct gat gaa aca tcc acc acc																307
Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp Glu Thr Ser Thr Thr																65
55 60																
gca gag acc cct gac tac cag cca ctg gcg ctg acc cgc acc acc gcg																355
Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu Thr Arg Thr Thr Ala																85
70 75 80																
ctc ggc gac tcc gtg acc tgt gag tac cca gat gct ggc gag gct tcc																403
Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp Ala Gly Glu Ala Ser																100
90 95																
aag gat gtc tcc aag cct gct act gaa aac gtg cca gca acc ggc acc																451
Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val Pro Ala Thr Gly Thr																115
105 110																
gtg acc gtc aac ctg acc acc gcc cag ggc aac atc ggc atg gaa ctt																499
Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn Ile Gly Met Glu Leu																130
120 125																
gat cgc tcc gta tcc cct tgt acc gtc aac gct gtt gag cac atg gct																547
Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala Val Glu His Met Ala																145
135 140																
tcc gag ggc tac tac aac gat act gtc tgc cac cgc atc acc acc tct																595
Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His Arg Ile Thr Thr Ser																165
150 155 160																

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 Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser Ser Thr Gly Ala Gly
 170 175 180

ggc cca ggg ttc agc ttc gcc aac gaa tac cca acc gac gaa gca act 691
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 185 190 195

gac cta acc acc cca gtc atc tac gag cgc ggc acc atc gcc atg gcc 739
 Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly Thr Ile Ala Met Ala
 200 205 210

aac gct ggc gct gac acc aac ggg ctc cca gtt ctt cct caa cta cga 787
 Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val Leu Pro Gln Leu Arg
 215 220 225

gga ttc ccc act ggc acc gaa cta cac cta ctt cgg cca gat cac cga 835
 Gly Phe Pro Thr Gly Thr Glu Leu His Leu Arg Pro Asp His Arg
 230 235 240 245

aga agg cct tgc aac cct cga cgc cat cgc aga agt tgg cac 877
 Arg Arg Pro Cys Asn Pro Arg Arg His Arg Arg Ser Trp His
 250 255

tgaaggtgga accggcgacg gag 900

<210> 74

<211> 259

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 74

Val Ser Thr Asn Lys Glu Arg Arg Gln Gln Ala Leu Ser Gln Leu Glu
 1 5 10 15

Lys Glu Ile Lys Ser Arg Asp Arg Lys Glu Lys Thr Lys Pro Leu Thr
 20 25 30

Val Val Phe Ala Ser Leu Ala Val Ile Leu Val Val Val Gly Gly Ile
 35 40 45

Trp Tyr Ala Ala Thr Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp
 50 55 60

Glu Thr Ser Thr Thr Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu
 65 70 75 80

Thr Arg Thr Thr Ala Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp
 85 90 95

Ala Gly Glu Ala Ser Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val
 100 105 110

Pro Ala Thr Gly Thr Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn
 115 120 125

Ile Gly Met Glu Leu Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala
 130 135 140
 Val Glu His Met Ala Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His
 145 150 155 160
 Arg Ile Thr Thr Ser Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser
 165 170 175
 Ser Thr Gly Ala Gly Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro
 180 185 190
 Thr Asp Glu Ala Thr Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly
 195 200 205
 Thr Ile Ala Met Ala Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val
 210 215 220
 Leu Pro Gln Leu Arg Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu
 225 230 235 240
 Arg Pro Asp His Arg Arg Arg Pro Cys Asn Pro Arg Arg His Arg Arg
 245 250 255
 Ser Trp His

<210> 75
 <211> 741
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(741)
 <223> RXN01926

<400> 75
 ctg cga agc ttc tac acc cca gaa caa gcc atc gaa cgc gaa ggc gac 48
 Leu Arg Ser Phe Tyr Thr Pro Glu Gln Ala Ile Glu Arg Glu Gly Asp
 1 5 10 15
 gtc tgg aaa gcc gcc acc gaa gaa gca gaa ctc ctc gca gct gac ggc 96
 Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly
 20 25 30
 gcc gtc cac gac cag gaa ctc ttc ctc aac tgc acc acc tcc cca ctg 144
 Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu
 35 40 45
 atc ttc gcc tcc gcg atg ctc aac ttc ggc gtc cac caa atc ctg gac 192
 Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp
 50 55 60
 acc ctc tgc caa ctc gca cca tcc ccc gcc ggc cgc gac gca gac ccc 240

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Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro
65          70          75          80

aaa gcc ctc gaa gcc gcc acc tcc gca atg gac gac cac cgc gac acc 288
Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr
      85          90          95

acc gac gac ttc tcc ggc gtc gtc ttc aaa gtc caa gcc ggc atg gac 336
Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp
      100          105          110

aaa aac cac cgc gat acc ctc gcc ttc atg cgc gtc gtc tcc ggc gaa 384
Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu
      115          120          125

ttc gac cgc ggc atg caa gtc acc cac tcc caa tcc ggc cgc agc ttc 432
Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe
      130          135          140

tcc acc aaa tac gcc ctc acc gtc ttc ggc cgc acc cgc tct acc gtc 480
Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val
      145          150          155          160

gaa acc gcc ttc ccc ggc gac atc gtc ggc ctc gtc aac gcc ggc gcc 528
Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala
      165          170          175

ctc gca cca ggc gac acc atc ttc gaa ggc cga aaa atc caa tac cca 576
Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro
      180          185          190

cca atg cca aaa ttc gcg cca gaa cac ttc cgc atc ctg cgc gcc aaa 624
Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys
      195          200          205

tca ctc ggc aaa tac aaa cag ttc cgc aaa gcc ctc gag cag ctg gac 672
Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp
      210          215          220

tcc gaa ggt gtc gtc cag atc ctc aag aac gac ctg cgt ggc gac gcc 720
Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala
      225          230          235          240

aac cca ggt cat ggc cgg tgt 741
Asn Pro Gly His Gly Arg Cys
      245

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<210> 76

<211> 247

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

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Leu Arg Ser Phe Tyr Thr Pro Glu Gln Ala Ile Glu Arg Glu Gly Asp
1          5          10          15

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Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly
 20 25 30
 Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu
 35 40 45
 Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp
 50 55 60
 Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro
 65 70 75 80
 Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr
 85 90 95
 Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp
 100 105 110
 Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu
 115 120 125
 Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe
 130 135 140
 Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val
 145 150 155 160
 Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala
 165 170 175
 Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro
 180 185 190
 Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys
 195 200 205
 Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp
 210 215 220
 Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala
 225 230 235 240
 Asn Pro Gly His Gly Arg Cys
 245

<210> 77

<211> 478

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(478)

<223> RXN02002

<400> 77

aagtggcaaa aaacgtttca agcaggcaac gccggcgtag aacttcgctg agctggggcg 60
attatggccc agcgcccaca acccgctatt cttaatacccc atg agc aac gcc aat 115
Met Ser Asn Ala Asn
1 5
tcc gac acc acc gcc gcc gag gca cat cgc cgc aga aca ttc gcc gta 163
Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg Thr Phe Ala Val
10 15 20
atc gca cac ccc gac gcc ggt aaa tcc acc ctc acc gag gca ttg gcg 211
Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu Thr Glu Ala Leu Ala
25 30 35
ctg cat gca cac atc atc tcc gaa gcc ggc gcc acc cac ggc aaa gca 259
Leu His Ala His Ile Ile Ser Glu Ala Gly Ala Thr His Gly Lys Ala
40 45 50
ggc cgc aaa gcc acc gtt tcc gac tgg atg gaa atg gaa aaa gac cgc 307
Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu Met Glu Lys Asp Arg
55 60 65
ggc atc tcc atc gcc tcc tcc gca ctc caa ttc gag tac gca cca gaa 355
Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe Glu Tyr Ala Pro Glu
70 75 80 85
ggc cac gca ggc gag ccc ttc atg atc aac ctc gtg gac acc cca ggc 403
Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu Val Asp Thr Pro Gly
90 95 100
cac gcc gac ttc tcc gaa gac acc tac cgc gtc ctc atg gcc gtc gac 451
His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val Leu Met Ala Val Asp
105 110 115
gca gca gtc atg ctt atg cac tcc gtc 478
Ala Ala Val Met Leu Met His Ser Val
120 125

<210> 78

<211> 126

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 78

Met Ser Asn Ala Asn Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg
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Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu
20 25 30
Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser Glu Ala Gly Ala
35 40 45
Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu
50 55 60

Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe
65 70 75 80

Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu
85 90 95

Val Asp Thr Pro Gly His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val
100 105 110

Leu Met Ala Val Asp Ala Ala Val Met Leu Met His Ser Val
115 120 125

<210> 79

<211> 1080

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1057)

<223> RXN02736

<400> 79

cagaggatta cccagcgggt acgtgggggtc caaagagcgc tgatgaaatg ctttcccgca 60

acggtcacac ctggcgcagg ccataattta ggggcaaaaa atg atc ttt gaa ctt 115
Met Ile Phe Glu Leu
1 5

ccg gat acc acc acc cag caa att tcc aag acc cta act cga ctg cgt 163
Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr Leu Thr Arg Leu Arg
10 15 20

gaa tcg ggc acc cag gtc acc acc ggc cga gtg ctc acc ctc atc gtg 211
Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val Leu Thr Leu Ile Val
25 30 35

gtc act gac tcc gaa agc gat gtc gct gca gtt acc gag tcc acc aat 259
Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val Thr Glu Ser Thr Asn
40 45 50

gaa gcc tcg cgc gag cac cca tct cgc gtg atc att ttg gtg gtt ggc 307
Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile Ile Leu Val Val Gly
55 60 65

gat aaa act gca gaa aac aaa gtt gac gca gaa gtc cgt atc ggt ggc 355
Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu Val Arg Ile Gly Gly
70 75 80 85

gac gct ggt gct tcc gag atg atc atc atg cat ctc aac gga cct gtc 403
Asp Ala Gly Ala Ser Glu Met Ile Ile Met His Leu Asn Gly Pro Val
90 95 100

gct gac aag ctc cag tat gtc gtc aca cca ctg ttg ctt cct gac acc 451
Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu Leu Leu Pro Asp Thr
105 110 115

ccc atc gtt gct tgg tgg cca ggt gaa tca cca aag aat cct tcc cag 499
Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro Lys Asn Pro Ser Gln
120 125 130

gac cca att gga cgc atc gca caa cga cgc atc act gat gct ttg tac 547
Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile Thr Asp Ala Leu Tyr
135 140 145

gac cgt gat gac gca cta gaa gat cgt gtt gag aac tat cac cca ggt 595
Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu Asn Tyr His Pro Gly
150 155 160 165

gat acc gac atg acg tgg gcg cgc ctt acc cag tgg cgg gga ctt gtt 643
Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln Trp Arg Gly Leu Val
170 175 180

gcc tcc tca ttg gat cac cca cca cac agc gaa atc act tcc gtg agg 691
Ala Ser Ser Leu Asp His Pro Pro His Ser Glu Ile Thr Ser Val Arg
185 190 195

ctg acc ggt gca agc ggc agt acc tcg gtg gat ttg gct gca ggc tgg 739
Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp Leu Ala Ala Gly Trp
200 205 210

ttg gcg cgg agg ctg aaa gtg cct gtg atc cgc gag gtg aca gat gct 787
Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg Glu Val Thr Asp Ala
215 220 225

ccc acc gtg cca acc gat gag ttt ggt act cca ctg ctg gct atc cag 835
Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro Leu Leu Ala Ile Gln
230 235 240 245

cgc ctg gag atc gtt cgc acc acc ggc tcg atc atc atc acc atc tat 883
Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile Ile Ile Thr Ile Tyr
250 255 260

gac gct cat acc ctt cag gta gag atg ccg gaa tcc ggc aat gcc cca 931
Asp Ala His Thr Leu Gln Val Glu Met Pro Glu Ser Gly Asn Ala Pro
265 270 275

tcg ctg gtg gct att ggt cgt cga agt gag tcc gac tgc ttg tct gag 979
Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser Asp Cys Leu Ser Glu
280 285 290

gag ctt cgc cac atg gat cca gat ttg ggc tac cag cac gca cta tcc 1027
Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr Gln His Ala Leu Ser
295 300 305

ggc ttg tcc agc gtc aag ctg gaa acc gtc taaggagaaa tacaacacta 1077
Gly Leu Ser Ser Val Lys Leu Glu Thr Val
310 315

tgg 1080

<210> 80

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

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Met Ile Ph  Glu Leu Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr
 1              5              10              15

Leu Thr Arg  Leu Arg Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val
      20              25              30

Leu Thr Leu Ile Val Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val
      35              40              45

Thr Glu Ser Thr Asn Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile
      50              55              60

Ile Leu Val Val Gly Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu
 65              70              75              80

Val Arg Ile Gly Gly Asp Ala Gly Ala Ser Glu Met Ile Ile Met His
      85              90              95

Leu Asn Gly Pro Val Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu
      100              105              110

Leu Leu Pro Asp Thr Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro
      115              120              125

Lys Asn Pro Ser Gln Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile
      130              135              140

Thr Asp Ala Leu Tyr Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu
 145              150              155              160

Asn Tyr His Pro Gly Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln
      165              170              175

Trp Arg Gly Leu Val Ala Ser Ser Leu Asp His Pro Pro His Ser Glu
      180              185              190

Ile Thr Ser Val Arg Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp
      195              200              205

Leu Ala Ala Gly Trp Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg
      210              215              220

Glu Val Thr Asp Ala Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro
 225              230              235              240

Leu Leu Ala Ile Gln Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile
      245              250              255

Ile Ile Thr Ile Tyr Asp Ala His Thr Leu Gln Val Glu Met Pro Glu
      260              265              270

Ser Gly Asn Ala Pro Ser Leu Val Ala Il  Gly Arg Arg Ser Glu Ser

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275

280

285

Asp Cys Leu Ser Glu Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr
 290 295 300

Gln His Ala Leu Ser Gly Leu Ser Ser Val Lys Leu Glu Thr Val
 305 310 315

<210> 81

<211> 331

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(301)

<223> RXS03217

<400> 81

tctgtgaagg tagatggttt gacgaggagt tccaacgact cggacgctgg tgaatcatgc 60

tggcgaacgt agcatcacct gattaggaaa aggtacaaat atg gca cag ggt act 115
 Met Ala Gln Gly Thr
 1 5

gtg aaa tgg ttc aac ggc gaa aag gga ttt ggt ttc atc gct ccc aac 163
 Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly Phe Ile Ala Pro Asn
 10 15 20

gat ggc tcc gca gat ctc ttc gtc cac tac tct gag att cag ggc tcc 211
 Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser Glu Ile Gln Gly Ser
 25 30 35

ggt ttc cgt aat ctt gag gaa aac cag cca gtt gaa ttt gag gtc ggc 259
 Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val Glu Phe Glu Val Gly
 40 45 50

gag ggc gcc aag ggc cca cag gct cag cag gtt cgt gct ctc 301
 Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val Arg Ala Leu
 55 60 65

taagctctaa ctgctagcta aaaattccgc 331

<210> 82

<211> 67

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 82

Met Ala Gln Gly Thr Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly
 1 5 10 15

Phe Ile Ala Pro Asn Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser
 20 25 30

Glu Ile Gln Gly Ser Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val
 35 40 45

Glu Phe Glu Val Gly Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val
 50 55 60

Arg Ala Leu
 65

<210> 83

<211> 324

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(301)

<223> FRXA01917

<400> 83

tctgtgaagg tagatgggtt gacgaggagt tccaacgact cggacgctgg tgaatcatgc 60

tggcgaacgt agcatcacct gattaggaaa aggtacaaat atg gca cag ggt act 115
 Met Ala Gln Gly Thr
 1 5

gtg aaa tgg ttc aac ggc gaa aag gga ttt ggt ttc atc gct ccc aac 163
 Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly Phe Ile Ala Pro Asn
 10 15 20

gat ggc tcc gca gat ctc ttc gtc cac tac tct gag att cag ggc tcc 211
 Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser Glu Ile Gln Gly Ser
 25 30 35

ggg ttc cgt aat ctt gag gaa aac cag cca gtt gaa ttt gag gtc ggc 259
 Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val Glu Phe Glu Val Gly
 40 45 50

gag ggc gcc aag ggc cca cag gct cag cag gtt cgt gct ctc 301
 Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val Arg Ala Leu
 55 60 65

taagctctaa ctgctagcta aaa 324

<210> 84

<211> 67

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

Met Ala Gln Gly Thr Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly
 1 5 10 15

Phe Ile Ala Pro Asn Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser
 20 25 30

Glu Ile Gln Gly Ser Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val
 35 40 45

Glu Phe Glu Val Gly Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val
 50 55 60

Arg Ala Leu
 65

<210> 85

<211> 504

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(481)

<223> RXA02184

<400> 85

tttaccgcga tgcttgccgt gtataataat ttcttctggt caaaaatagt tgatcaattt 60

gaatcagcat atgaattagg aatgaaagtg gtgaggacaa gtg cct gtc gga aca 115
 Val Pro Val Gly Thr
 1 5

gtg aag tgg tac gac gcg gag cgt ggt ttc ggc ttt gtc tcc aat cca 163
 Val Lys Trp Tyr Asp Ala Glu Arg Gly Phe Gly Phe Val Ser Asn Pro
 10 15 20

ggt ggt gaa gat tgc ttc gta ggt aag caa gta ctt ccc aag gga gtc 211
 Gly Gly Glu Asp Cys Phe Val Gly Lys Gln Val Leu Pro Lys Gly Val
 25 30 35

acc gaa ttg cac aag gga cag cga atc gat ttt gac ttc gcc gca ggc 259
 Thr Glu Leu His Lys Gly Gln Arg Ile Asp Phe Asp Phe Ala Ala Gly
 40 45 50

cgt aag ggc cct caa gca ctt cga ata aag att ctt gaa act cca cgc 307
 Arg Lys Gly Pro Gln Ala Leu Arg Ile Lys Ile Leu Glu Thr Pro Arg
 55 60 65

agg cgt cca cag cac aaa tac aag cca gaa gag ctc aac gga atg atc 355
 Arg Arg Pro Gln His Lys Tyr Lys Pro Glu Glu Leu Asn Gly Met Ile
 70 75 80 85

tct gac ctc atc acg ctt cta gaa agt gga gtg caa cca ggc ctt gcc 403
 Ser Asp Leu Ile Thr Leu Leu Glu Ser Gly Val Gln Pro Gly Leu Ala
 90 95 100

aaa ggg caa tac ccg gag cac aaa gct gga gcg cag gta gca gaa att 451
 Lys Gly Gln Tyr Pro Glu His Lys Ala Gly Ala Gln Val Ala Glu Ile
 105 110 115

ctt cgc gtt gtt gcg aag gag ctt gag tct taaaacaata aggagaggat 501

Leu Arg Val Val Ala Lys Glu Leu Glu Ser
120 125

ccg

504

<210> 86

<211> 127

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 86

Val Pro Val Gly Thr Val Lys Trp Tyr Asp Ala Glu Arg Gly Phe Gly
1 5 10 15

Phe Val Ser Asn Pro Gly Gly Glu Asp Cys Phe Val Gly Lys Gln Val
20 25 30

Leu Pro Lys Gly Val Thr Glu Leu His Lys Gly Gln Arg Ile Asp Phe
35 40 45

Asp Phe Ala Ala Gly Arg Lys Gly Pro Gln Ala Leu Arg Ile Lys Ile
50 55 60

Leu Glu Thr Pro Arg Arg Arg Pro Gln His Lys Tyr Lys Pro Glu Glu
65 70 75 80

Leu Asn Gly Met Ile Ser Asp Leu Ile Thr Leu Leu Glu Ser Gly Val
85 90 95

Gln Pro Gly Leu Ala Lys Gly Gln Tyr Pro Glu His Lys Ala Gly Ala
100 105 110

Gln Val Ala Glu Ile Leu Arg Val Val Ala Lys Glu Leu Glu Ser
115 120 125

<210> 87

<211> 324

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(301)

<223> RXA00810

<400> 87

tcggcggttcg ttcaagaaac ggccagatgt tgctgttcga gctcatgcaa gagggaaca 60

tcgaacccgg tagtaattcc aatcagtaaa ggtaagacaa atg gca cag ggc act 115
Met Ala Gln Gly Thr
1 5

gtt aag tgg ttc aac cca gag aag ggc ttc ggc ttc atc gct cct tcc 163
Val Lys Trp Phe Asn Pro Glu Lys Gly Phe Gly Phe Ile Ala Pro Ser
10 15 20

gac gga tcc gct gac gtt ttc gtc cac tac tcc gag atc gag ggc aac 211
 Asp Gly Ser Ala Asp Val Phe Val His Tyr Ser Glu Ile Glu Gly Asn
 25 30 35

ggc ttc cgt acc ctc gag gag aac cag ctc gtc gag ttc gaa atc ggc 259
 Gly Phe Arg Thr Leu Glu Glu Asn Gln Leu Val Glu Phe Glu Ile Gly
 40 45 50

gag ggc gct aag ggc ctt cag gct cag gct gtt cgt gca atc 301
 Glu Gly Ala Lys Gly Leu Gln Ala Gln Ala Val Arg Ala Ile
 55 60 65

taattgcac tcgagttcgaa acc 324

<210> 88

<211> 67

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

Met Ala Gln Gly Thr Val Lys Trp Phe Asn Pro Glu Lys Gly Phe Gly
 1 5 10 15

Phe Ile Ala Pro Ser Asp Gly Ser Ala Asp Val Phe Val His Tyr Ser
 20 25 30

Glu Ile Glu Gly Asn Gly Phe Arg Thr Leu Glu Glu Asn Gln Leu Val
 35 40 45

Glu Phe Glu Ile Gly Glu Gly Ala Lys Gly Leu Gln Ala Gln Ala Val
 50 55 60

Arg Ala Ile
 65

<210> 89

<211> 1017

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(994)

<223> RXA01674

<400> 89

cggcgctcgat tccagaaggt ttgtagacat gcttcaaggt tgcgctaatt gaaaagaacg 60

cggtagacgg tactttcata tccaccata taatgttgat atg gat aat ggg tgg 115
 Met Asp Asn Gly Trp
 1 5

ccg aac ctg caa act ctc gca ctc ttt gtg gcg att gtg gaa gag ggg 163
 Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala Ile Val Glu Glu Gly

	10	15	20	
agc ctc ggt gcc ggt gct cga aaa gtc gga atg gcc caa cct aat gcc				211
Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met Ala Gln Pro Asn Ala	25	30	35	
agt cgg gct atc gca gag ctt gag gca gac atg aaa gcc gaa ttg ttg				259
Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met Lys Ala Glu Leu Leu	40	45	50	
gta cgt cat cct cga gga tca cat cca aca gct gct gga ctt gcg ctt				307
Val Arg His Pro Arg Gly Ser His Pro Thr Ala Ala Gly Leu Ala Leu	55	60	65	
gtt gag cat tcg cgc gat ctg ctt caa tct gta caa gaa ttt act gaa				355
Val Glu His Ser Arg Asp Leu Leu Gln Ser Val Gln Glu Phe Thr Glu	70	75	80	85
tgg gtg aca gag gga cga act gag cag ccg ctg aaa ttg cat gtt ggg				403
Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu Lys Leu His Val Gly	90	95	100	
gcc agt atg acc att gcc gag gct cta ctt cca gct tgg gtt gcg gac				451
Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro Ala Trp Val Ala Asp	105	110	115	
atg cgc acg cgt ttt cct gcc tgc cgt gtc gac gtc tct gtg atg aat				499
Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp Val Ser Val Met Asn	120	125	130	
tct tct caa gta att gaa gcc gtc cag aaa ggg cac ttg caa cta ggt				547
Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly His Leu Gln Leu Gly	135	140	145	
ttt att gaa aca ccg cat gtt ccc gta cgg ctt cat gct cgt gtg gtg				595
Phe Ile Glu Thr Pro His Val Pro Val Arg Leu His Ala Arg Val Val	150	155	160	165
caa gag gac aag ctg att gtg gtg att tct cct aat cat gag tgg gct				643
Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro Asn His Glu Trp Ala	170	175	180	
aat cgc acg ggt agg atc agt ctt cgg gag ttg tcg gaa act ccg ctg				691
Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu Ser Glu Thr Pro Leu	185	190	195	
ata gtg agg gaa gtc ggc tca ggt acc cga gaa gca tta caa gaa tta				739
Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu Ala Leu Gln Glu Leu	200	205	210	
ctt gcg gat tat gac atg gct gag ccg att caa gtg tta aac agc aat				787
Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln Val Leu Asn Ser Asn	215	220	225	
gct gcg gta cgt gtt gtt gtt gaa gca ggg gca ggt cct gca gta ctt				835
Ala Ala Val Arg Val Val Val Glu Ala Gly Ala Gly Pro Ala Val Leu	230	235	240	245

ggt gaa tta gcc ttg cgt gat cat ctt gcg ctc ggc agg ctg ttg agt 883
 Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu Gly Arg Leu Leu Ser
 250 255 260

gtg cca ttt gaa ggc agt gga gtt act cgt cct ctt aca gct gtg tgg 931
 Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro Leu Thr Ala Val Trp
 265 270 275

agt gga ccc cgc aga ttg ccg att cta gcg gga gaa tta gtg tcc atc 979
 Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly Glu Leu Val Ser Ile
 280 285 290

gca tcg aac cac atc tgattttgag ccctggctaa cgg 1017
 Ala Ser Asn His Ile
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<210> 90

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

Met Asp Asn Gly Trp Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala
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Ile Val Glu Glu Gly Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met
 20 25 30

Ala Gln Pro Asn Ala Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met
 35 40 45

Lys Ala Glu Leu Leu Val Arg His Pro Arg Gly Ser His Pro Thr Ala
 50 55 60

Ala Gly Leu Ala Leu Val Glu His Ser Arg Asp Leu Leu Gln Ser Val
 65 70 75 80

Gln Glu Phe Thr Glu Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu
 85 90 95

Lys Leu His Val Gly Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro
 100 105 110

Ala Trp Val Ala Asp Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp
 115 120 125

Val Ser Val Met Asn Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly
 130 135 140

His Leu Gln Leu Gly Phe Ile Glu Thr Pro His Val Pro Val Arg Leu
 145 150 155 160

His Ala Arg Val Val Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro
 165 170 175

Asn His Glu Trp Ala Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu
 180 185 190
 Ser Glu Thr Pro Leu Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu
 195 200 205
 Ala Leu Gln Glu Leu Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln
 210 215 220
 Val Leu Asn Ser Asn Ala Ala Val Arg Val Val Val Glu Ala Gly Ala
 225 230 235 240
 Gly Pro Ala Val Leu Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu
 245 250 255
 Gly Arg Leu Leu Ser Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro
 260 265 270
 Leu Thr Ala Val Trp Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly
 275 280 285
 Glu Leu Val Ser Ile Ala Ser Asn His Ile
 290 295

<210> 91
 <211> 1214
 <212> DNA
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<220>
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 <222> (1)..(1191)
 <223> RXA02431

<400> 91
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 Val Val Val Thr Pro Arg His Ile Val Tyr Ser Ala Ala Ser Arg Arg
 1 5 10 15
 gtg ttc caa atc gtg gaa aaa cgc gcc gga att gtc gaa cgc ctc agc 96
 Val Phe Gln Ile Val Glu Lys Arg Ala Gly Ile Val Glu Arg Leu Ser
 20 25 30
 atc gat gaa ggc ttc atg gaa cca gag gct ctc gtt gga gcc acc cca 144
 Ile Asp Glu Gly Phe Met Glu Pro Glu Ala Leu Val Gly Ala Thr Pro
 35 40 45
 gaa gag gtg aaa cag tgg gcg gaa gaa tta cgc gcg gaa att aaa gaa 192
 Glu Glu Val Lys Gln Trp Ala Glu Glu Leu Arg Ala Glu Ile Lys Glu
 50 55 60
 gtt act ggc tta ccc tcc tcg gtt ggt gct ggc tcc ggt aag cag atc 240
 Val Thr Gly Leu Pro Ser Ser Val Gly Ala Gly Ser Gly Lys Gln Ile
 65 70 75 80
 gcc aaa att ggt tca ggc gaa gca aag cca gat ggt gtg ttt gtc gtg 288

Ala Lys Ile Gly Ser Gly Glu Ala Lys Pro Asp Gly Val Ph Val Val	
85 90 95	
cca gta gac aag caa cat gac ttg ctt gat cca ctt cct gtg ggc gca	336
Pro Val Asp Lys Gln His Asp Leu Leu Asp Pro Leu Pro Val Gly Ala	
100 105 110	
ctt tgg gga gtg ggt cct gtg aca ggc tcc aag ctt gcc tca atg ggg	384
Leu Trp Gly Val Gly Pro Val Thr Gly Ser Lys Leu Ala Ser Met Gly	
115 120 125	
gtg gaa aca att ggt gat cta gca gcg cta acc caa aaa gaa gta gaa	432
Val Glu Thr Ile Gly Asp Leu Ala Ala Leu Thr Gln Lys Glu Val Glu	
130 135 140	
atc agc ctc ggt gca acc atc gga ata tca ctg tgg aac ctt gcc cga	480
Ile Ser Leu Gly Ala Thr Ile Gly Ile Ser Leu Trp Asn Leu Ala Arg	
145 150 155 160	
gga atc gac gac cgc cct gtg gaa ccc cgc gcc gaa gca aaa cag atc	528
Gly Ile Asp Asp Arg Pro Val Glu Pro Arg Ala Glu Ala Lys Gln Ile	
165 170 175	
tcc caa gag cac acc tat gaa aaa gac ctc ctc acc agg caa caa gta	576
Ser Gln Glu His Thr Tyr Glu Lys Asp Leu Leu Thr Arg Gln Gln Val	
180 185 190	
gat gct gcc atc att cga tca gcc gaa ggc gca cac cga cgg ctc ctc	624
Asp Ala Ala Ile Ile Arg Ser Ala Glu Gly Ala His Arg Arg Leu Leu	
195 200 205	
aaa gac gga cgc ggt gcc aga act gtc agc gtg aaa ctg cgg atg gcc	672
Lys Asp Gly Arg Gly Ala Arg Thr Val Ser Val Lys Leu Arg Met Ala	
210 215 220	
gac ttt cgt att gag tct cgt tcc tac acc ttg tcc tat gcc acc gat	720
Asp Phe Arg Ile Glu Ser Arg Ser Tyr Thr Leu Ser Tyr Ala Thr Asp	
225 230 235 240	
gat tac gca act ctt gag gca aca gca ttc cga ctt gcc cgc tac ccc	768
Asp Tyr Ala Thr Leu Glu Ala Thr Ala Phe Arg Leu Ala Arg Tyr Pro	
245 250 255	
gga gaa gta ggc ccc atc cgc ctt gtc gga gta agt ttt tct ggt ttg	816
Gly Glu Val Gly Pro Ile Arg Leu Val Gly Val Ser Phe Ser Gly Leu	
260 265 270	
gaa gaa tcc cgc caa gac atc ctc ttc ccg gaa ctt gac caa caa atc	864
Glu Glu Ser Arg Gln Asp Ile Leu Phe Pro Glu Leu Asp Gln Gln Ile	
275 280 285	
atc gta cca cca gca ccc gac acc gat tat gag gta ggc gtg caa tcc	912
Ile Val Pro Pro Ala Pro Asp Thr Asp Tyr Glu Val Gly Val Gln Ser	
290 295 300	
tct tct agt tcc gaa agt act caa gtt gaa gcg ccg caa gat gtc gcg	960
Ser Ser Ser Ser Glu Ser Thr Gln Val Glu Ala Pro Gln Asp Val Ala	

305	310	315	320	
ttg agt atg tgg tgc gca acg caa gat gtc tac cac cca gaa tat ggc				1008
Leu Ser Met Trp Cys Ala Thr Gln Asp Val Tyr His Pro Glu Tyr Gly				
325		330	335	
cac ggt tgg gta caa ggt gcc ggt cac ggt gtt gta tca gta cgt ttt				1056
His Gly Trp Val Gln Gly Ala Gly His Gly Val Val Ser Val Arg Phe				
340	345		350	
gaa acc cgc agc acc aca aaa ggg cga act aaa agt ttt tcc atg gat				1104
Glu Thr Arg Ser Thr Thr Lys Gly Arg Thr Lys Ser Phe Ser Met Asp				
355	360		365	
gac ccg gac ctc acc ccg gca gac cct cta gat agt ttg gat tgg gct				1152
Asp Pro Asp Leu Thr Pro Ala Asp Pro Leu Asp Ser Leu Asp Trp Ala				
370	375		380	
gac tgg ttt gct gaa aat ggt gaa acg ggg gat gac gaa tagggtttca				1201
Asp Trp Phe Ala Glu Asn Gly Glu Thr Gly Asp Asp Glu				
385	390	395		
tcggggtttcg ggg				1214
<210> 92				
<211> 397				
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<213> Corynebacterium glutamicum				
<400> 92				
Val Val Val Thr Pro Arg His Ile Val Tyr Ser Ala Ala Ser Arg Arg				
1	5	10	15	
Val Phe Gln Ile Val Glu Lys Arg Ala Gly Ile Val Glu Arg Leu Ser				
20	25	30		
Ile Asp Glu Gly Phe Met Glu Pro Glu Ala Leu Val Gly Ala Thr Pro				
35	40	45		
Glu Glu Val Lys Gln Trp Ala Glu Glu Leu Arg Ala Glu Ile Lys Glu				
50	55	60		
Val Thr Gly Leu Pro Ser Ser Val Gly Ala Gly Ser Gly Lys Gln Ile				
65	70	75	80	
Ala Lys Ile Gly Ser Gly Glu Ala Lys Pro Asp Gly Val Phe Val Val				
85	90	95		
Pro Val Asp Lys Gln His Asp Leu Leu Asp Pro Leu Pro Val Gly Ala				
100	105	110		
Leu Trp Gly Val Gly Pro Val Thr Gly Ser Lys Leu Ala Ser Met Gly				
115	120	125		
Val Glu Thr Ile Gly Asp Leu Ala Ala Leu Thr Gln Lys Glu Val Glu				
130	135	140		

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Ile Ser Leu Gly Ala Thr Ile Gly Ile Ser Leu Trp Asn Leu Ala Arg
145                      150                      155                      160

Gly Ile Asp Asp Arg Pro Val Glu Pro Arg Ala Glu Ala Lys Gln Ile
                      165                      170                      175

Ser Gln Glu His Thr Tyr Glu Lys Asp Leu Leu Thr Arg Gln Gln Val
                      180                      185                      190

Asp Ala Ala Ile Ile Arg Ser Ala Glu Gly Ala His Arg Arg Leu Leu
195                      200                      205

Lys Asp Gly Arg Gly Ala Arg Thr Val Ser Val Lys Leu Arg Met Ala
210                      215                      220

Asp Phe Arg Ile Glu Ser Arg Ser Tyr Thr Leu Ser Tyr Ala Thr Asp
225                      230                      235                      240

Asp Tyr Ala Thr Leu Glu Ala Thr Ala Phe Arg Leu Ala Arg Tyr Pro
                      245                      250                      255

Gly Glu Val Gly Pro Ile Arg Leu Val Gly Val Ser Phe Ser Gly Leu
260                      265                      270

Glu Glu Ser Arg Gln Asp Ile Leu Phe Pro Glu Leu Asp Gln Gln Ile
275                      280                      285

Ile Val Pro Pro Ala Pro Asp Thr Asp Tyr Glu Val Gly Val Gln Ser
290                      295                      300

Ser Ser Ser Ser Glu Ser Thr Gln Val Glu Ala Pro Gln Asp Val Ala
305                      310                      315                      320

Leu Ser Met Trp Cys Ala Thr Gln Asp Val Tyr His Pro Glu Tyr Gly
                      325                      330                      335

His Gly Trp Val Gln Gly Ala Gly His Gly Val Val Ser Val Arg Phe
340                      345                      350

Glu Thr Arg Ser Thr Thr Lys Gly Arg Thr Lys Ser Phe Ser Met Asp
355                      360                      365

Asp Pro Asp Leu Thr Pro Ala Asp Pro Leu Asp Ser Leu Asp Trp Ala
370                      375                      380

Asp Trp Phe Ala Glu Asn Gly Glu Thr Gly Asp Asp Glu
385                      390                      395

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<210> 93

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> RXA02446

<400> 93

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gagcgtattc tttgtgttct ctcacgacag gaatactgct atg gcg atc gag tcc 115
Met Ala Ile Glu Ser
1 5

atc gcg tac acc agt gaa gca ctc tca acc ggc agt ggc cgg ctg ggg 163
Ile Ala Tyr Thr Ser Glu Ala Leu Ser Thr Gly Ser Gly Arg Leu Gly
10 15 20

cat gtg cgc tcc aca gat ggt gcg ctc gaa ttt gaa atg aca ccg cca 211
His Val Arg Ser Thr Asp Gly Ala Leu Glu Phe Glu Met Thr Pro Pro
25 30 35

aag gct ttg ggc gga tcc ggt gaa ggc acc aat cca gaa cag ctg ttc 259
Lys Ala Leu Gly Gly Ser Gly Glu Gly Thr Asn Pro Glu Gln Leu Phe
40 45 50

gcg gta ggt tac gca gcc tgt ttc cac tct gcc atg cac tct gtc gca 307
Ala Val Gly Tyr Ala Ala Cys Phe His Ser Ala Met His Ser Val Ala
55 60 65

cgc agc cgc aag atc act ctt gaa gac aca gcg gtt ggt gcc cga gtt 355
Arg Ser Arg Lys Ile Thr Leu Glu Asp Thr Ala Val Gly Ala Arg Val
70 75 80 85

agc atc ggc cca aac ggc gct ggt gga ttt gag att gcc gta gaa ctc 403
Ser Ile Gly Pro Asn Gly Ala Gly Gly Phe Glu Ile Ala Val Glu Leu
90 95 100

gaa gta tcg att cct caa ttg cca caa gca gaa gcc cag gaa ctt gct 451
Glu Val Ser Ile Pro Gln Leu Pro Gln Ala Glu Ala Gln Glu Leu Ala
105 110 115

gat gcc gcg cac cag gtg tgc ccg tat tcc aac gcc aca cga ggc aat 499
Asp Ala Ala His Gln Val Cys Pro Tyr Ser Asn Ala Thr Arg Gly Asn
120 125 130

atc tcg gta act gtg tca gtc atc gac gaa gag gct taaaaccaca 545
Ile Ser Val Thr Val Ser Val Ile Asp Glu Glu Ala
135 140 145

ggattaacaa aac 558

<210> 94

<211> 145

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 94

Met Ala Ile Glu Ser Ile Ala Tyr Thr Ser Glu Ala Leu Ser Thr Gly
1 5 10 15

Ser	Gly	Arg	Leu	Gly	His	Val	Arg	Ser	Thr	Asp	Gly	Ala	Leu	Glu	Phe			
						20								25				30
Glu	Met	Thr	Pro	Pro	Lys	Ala	Leu	Gly	Gly	Ser	Gly	Glu	Gly	Thr	Asn			
			35									40					45	
Pro	Glu	Gln	Leu	Phe	Ala	Val	Gly	Tyr	Ala	Ala	Cys	Phe	His	Ser	Ala			
			50							55							60	
Met	His	Ser	Val	Ala	Arg	Ser	Arg	Lys	Ile	Thr	Leu	Glu	Asp	Thr	Ala			
		65						70						75			80	
Val	Gly	Ala	Arg	Val	Ser	Ile	Gly	Pro	Asn	Gly	Ala	Gly	Gly	Phe	Glu			
				85						90							95	
Ile	Ala	Val	Glu	Leu	Glu	Val	Ser	Ile	Pro	Gln	Leu	Pro	Gln	Ala	Glu			
			100					105							110			
Ala	Gln	Glu	Leu	Ala	Asp	Ala	Ala	His	Gln	Val	Cys	Pro	Tyr	Ser	Asn			
			115						120							125		
Ala	Thr	Arg	Gly	Asn	Ile	Ser	Val	Thr	Val	Ser	Val	Ile	Asp	Glu	Glu			
			130						135							140		
Ala																		
145																		

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<210> 95
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1183)  
<223> RXA02861
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gaaggtatta atacttcttt aagggtcggg ggattttcgt atg tct act aga aca 115
Met Ser Thr Arg Thr
1 5

acg cca caa gac cgt tat acc gac gaa tac ggc atc gaa cgc gtc aac 163
Thr Pro Gln Asp Arg Tyr Thr Asp Glu Tyr Gly Ile Glu Arg Val Asn
10 15 20

aag gat gaa ccc ggc ctg gtg gac aaa ctc cgg gac aag cac gac tgg 211
Lys Asp Glu Pro Gly Leu Val Asp Lys Leu Arg Asp Lys His Asp Trp
25 30 35

ttt gat cat ctc atg cgc atg aat gaa cgt ttc ggc gca aaa ggt ggc 259
Phe Asp His Leu Met Arg Met Asn Glu Arg Phe Gly Ala Lys Gly Gly
40 45 50

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aac caa ttg tcg gcg ggt att acg tat ttc tcc gtg ctg tcg atc ttc Asn Gln Leu Ser Ala Gly Ile Thr Tyr Phe Ser Val Leu Ser Ile Phe 55 60 65	307
ccg att gcc atg ctt gtc ttc ggt att gca ggt gtc atc ctt gcc gga Pro Ile Ala Met Leu Val Phe Gly Ile Ala Gly Val Ile Leu Ala Gly 70 75 80 85	355
aac cct gaa gtt ctc aca gat att caa aat cga atc aac gat gct tta Asn Pro Glu Val Leu Thr Asp Ile Gln Asn Arg Ile Asn Asp Ala Leu 90 95 100	403
gaa ggc gag atc ggt aac acc gtc aac ggc atc att gat tcc gcg att Glu Gly Glu Ile Gly Asn Thr Val Asn Gly Ile Ile Asp Ser Ala Ile 105 110 115	451
gcg cag cgt ggt gct gtg ttg ggc att ggt ggt gta act gcc ctg tgg Ala Gln Arg Gly Ala Val Leu Gly Ile Gly Gly Val Thr Ala Leu Trp 120 125 130	499
tct gga ctg ggg tgg atg gcg aac ctg cgc ttt gga gtt tcc cgc atg Ser Gly Leu Gly Trp Met Ala Asn Leu Arg Phe Gly Val Ser Arg Met 135 140 145	547
tgg gcc att gac cca act gaa ggc aac ttc att caa aag aag ctc acc Trp Ala Ile Asp Pro Thr Glu Gly Asn Phe Ile Gln Lys Lys Leu Thr 150 155 160 165	595
gac ttg gtc gcg ctg atc gtc ttg ctg ctg gcc atg ggc gta gcc ttc Asp Leu Val Ala Leu Ile Val Leu Leu Leu Ala Met Gly Val Ala Phe 170 175 180	643
ggt atc acg gcg ctc ggt gct tcc gga cta acc aaa aac ctg ctg gac Gly Ile Thr Ala Leu Gly Ala Ser Gly Leu Thr Lys Asn Leu Leu Asp 185 190 195	691
ttt gtg ggc ctg ggg gag att ccg ggc att agc tac atc acc tgg gtg Phe Val Gly Leu Gly Glu Ile Pro Gly Ile Ser Tyr Ile Thr Trp Val 200 205 210	739
gtc gca gca ctt gtt ggt gtc ttg gct aac ttc ctg gtg ttc atg tgg Val Ala Ala Leu Val Gly Val Leu Ala Asn Phe Leu Val Phe Met Trp 215 220 225	787
ctg att ttc tcc ctg cca cgt acc aaa gtt ccc atg aaa ccg ggt ctt Leu Ile Phe Ser Leu Pro Arg Thr Lys Val Pro Met Lys Pro Gly Leu 230 235 240 245	835
cag gca gca ctg ctt ggc gca atc ggt ttt gag gtg gtc aag cag gtt Gln Ala Ala Leu Leu Gly Ala Ile Gly Phe Glu Val Val Lys Gln Val 250 255 260	883
gga tcg ctg ttg gct tca aat gca ttg agt aac ccc gcg ggt gca gca Gly Ser Leu Leu Ala Ser Asn Ala Leu Ser Asn Pro Ala Gly Ala Ala 265 270 275	931

ttc ggt ccg atc atc ggc atc atg gtt gtg ctg tat ttg atc tgg cgc 979
 Phe Gly Pro Ile Ile Gly Ile Met Val Val Leu Tyr Leu Ile Trp Arg
 280 285 290

atc ctc atg tat tgc tct gcg tgg gct gcc acc agt gaa gaa gcg ttg 1027
 Ile Leu Met Tyr Cys Ser Ala Trp Ala Ala Thr Ser Glu Glu Ala Leu
 295 300 305

cgt ctt gcg act gtt cca gca cca gag cct gcg atc att cgg gtt cgc 1075
 Arg Leu Ala Thr Val Pro Ala Pro Glu Pro Ala Ile Ile Arg Val Arg
 310 315 320 325

cat gaa att gat cca ggt gaa gaa gtc tcc caa tct gct cga aaa gtg 1123
 His Glu Ile Asp Pro Gly Glu Glu Val Ser Gln Ser Ala Arg Lys Val
 330 335 340

ggc att gga gtg gcc gtg ggt gcc gcg act gcg ggt gct ttt gcg ctg 1171
 Gly Ile Gly Val Ala Val Gly Ala Ala Thr Ala Gly Ala Phe Ala Leu
 345 350 355

ttg cgt aaa aaa tagtttttat taagggcatt ccc 1206
 Leu Arg Lys Lys
 360

<210> 96
 <211> 361
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 96
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 Ile Glu Arg Val Asn Lys Asp Glu Pro Gly Leu Val Asp Lys Leu Arg
 20 25 30
 Asp Lys His Asp Trp Phe Asp His Leu Met Arg Met Asn Glu Arg Phe
 35 40 45
 Gly Ala Lys Gly Gly Asn Gln Leu Ser Ala Gly Ile Thr Tyr Phe Ser
 50 55 60
 Val Leu Ser Ile Phe Pro Ile Ala Met Leu Val Phe Gly Ile Ala Gly
 65 70 75 80
 Val Ile Leu Ala Gly Asn Pro Glu Val Leu Thr Asp Ile Gln Asn Arg
 85 90 95
 Ile Asn Asp Ala Leu Glu Gly Glu Ile Gly Asn Thr Val Asn Gly Ile
 100 105 110
 Ile Asp Ser Ala Ile Ala Gln Arg Gly Ala Val Leu Gly Ile Gly Gly
 115 120 125
 Val Thr Ala Leu Trp Ser Gly Leu Gly Trp Met Ala Asn Leu Arg Phe
 130 135 140

Gly Val Ser Arg Met Trp Ala Ile Asp Pro Thr Glu Gly Asn Phe Ile
 145 150 155 160
 Gln Lys Lys Leu Thr Asp Leu Val Ala Leu Ile Val Leu Leu Leu Ala
 165 170 175
 Met Gly Val Ala Phe Gly Ile Thr Ala Leu Gly Ala Ser Gly Leu Thr
 180 185 190
 Lys Asn Leu Leu Asp Phe Val Gly Leu Gly Glu Ile Pro Gly Ile Ser
 195 200 205
 Tyr Ile Thr Trp Val Val Ala Ala Leu Val Gly Val Leu Ala Asn Phe
 210 215 220
 Leu Val Phe Met Trp Leu Ile Phe Ser Leu Pro Arg Thr Lys Val Pro
 225 230 235 240
 Met Lys Pro Gly Leu Gln Ala Ala Leu Leu Gly Ala Ile Gly Phe Glu
 245 250 255
 Val Val Lys Gln Val Gly Ser Leu Leu Ala Ser Asn Ala Leu Ser Asn
 260 265 270
 Pro Ala Gly Ala Ala Phe Gly Pro Ile Ile Gly Ile Met Val Val Leu
 275 280 285
 Tyr Leu Ile Trp Arg Ile Leu Met Tyr Cys Ser Ala Trp Ala Ala Thr
 290 295 300
 Ser Glu Glu Ala Leu Arg Leu Ala Thr Val Pro Ala Pro Glu Pro Ala
 305 310 315 320
 Ile Ile Arg Val Arg His Glu Ile Asp Pro Gly Glu Glu Val Ser Gln
 325 330 335
 Ser Ala Arg Lys Val Gly Ile Gly Val Ala Val Gly Ala Ala Thr Ala
 340 345 350
 Gly Ala Phe Ala Leu Leu Arg Lys Lys
 355 360

<210> 97

<211> 753

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(730)

<223> RXA00981

<400> 97

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Met Ser Glu Asn Leu	
1 5	
cca gcg ccc gag aat ctc ctg gac gcc gag aga att cag atg atc aag	163
Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg Ile Gln Met Ile Lys	
10 15 20	
aac ttc cgc aac gaa tta acg ggg ttc atg ctc aac tac caa ttt ggc	211
Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu Asn Tyr Gln Phe Gly	
25 30 35	
att gat gag atc ctg acc aag atc aac atc ctg aaa act gaa ttc agc	259
Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu Lys Thr Glu Phe Ser	
40 45 50	
cag ctg cac gaa tac gca cct atc gag cac gta tct tca cga ttg aag	307
Gln Leu His Glu Tyr Ala Pro Ile Glu His Val Ser Ser Arg Leu Lys	
55 60 65	
aca cca gaa agc atc gtc aaa aag gtc atc cga aaa gga gac gag ctc	355
Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg Lys Gly Asp Glu Leu	
70 75 80 85	
tcc ctc gca gct atc aaa gac aca gtg ttt gat atc gca ggc att cga	403
Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp Ile Ala Gly Ile Arg	
90 95 100	
atc gtc tgc agt ttc ctc aaa gat gcc tac gca atc gcc gat atg ctg	451
Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala Ile Ala Asp Met Leu	
105 110 115	
acc aac caa aaa gac gtc acg gtc atc gag gcc aaa gac tac atc gct	499
Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala Lys Asp Tyr Ile Ala	
120 125 130	
aac cca aag ccg aac ggc tac aag agt ttg cac ctt atc ctc caa gtg	547
Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His Leu Ile Leu Gln Val	
135 140 145	
cct gtc ttc ctg tct aac tcc gtg gaa aag gtc aat gtt gaa gtc cag	595
Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val Asn Val Glu Val Gln	
150 155 160 165	
atc cgc acc att gcc atg gac ttc tgg gca agc ctc gag cac aaa atc	643
Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser Leu Glu His Lys Ile	
170 175 180	
tac tac aaa ttt gaa caa gaa gtt cct cag tca atc ctt gat gag ctc	691
Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu	
185 190 195	
agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca	740
Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu Val Thr	
200 205 210	
gttgaaacca ctg	753

<210> 98
 <211> 210
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 98

Met Ser Glu Asn Leu Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg
 1 5 10 15

Ile Gln Met Ile Lys Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu
 20 25 30

Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu
 35 40 45

Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val
 50 55 60

Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg
 65 70 75 80

Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp
 85 90 95

Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala
 100 105 110

Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala
 115 120 125

Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His
 130 135 140

Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val
 145 150 155 160

Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser
 165 170 175

Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser
 180 185 190

Ile Leu Asp Glu Leu Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu
 195 200 205

Val Thr
 210

<210> 99
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<220>

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<223> RXN00786

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 Met Ser Ser Pro Val
 1 5

atc agc ccc gaa acc aaa acc gga aag aag atc ctg ctt gca gcc cct 163
 Ile Ser Pro Glu Thr Lys Thr Gly Lys Lys Ile Leu Leu Ala Ala Pro
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cgc gga tac tgt gcc ggc gta gac cgt gca gtg gaa acc gtc gag cgc 211
 Arg Gly Tyr Cys Ala Gly Val Asp Arg Ala Val Glu Thr Val Glu Arg
 25 30 35

gcg ctc gag gaa tac ggc gcc cca att tat gtc cgt aaa gaa atc gtg 259
 Ala Leu Glu Glu Tyr Gly Ala Pro Ile Tyr Val Arg Lys Glu Ile Val
 40 45 50

cac aac cgt tac gtt gtg gac acc ctg gca gaa aag ggc gcg att ttt 307
 His Asn Arg Tyr Val Val Asp Thr Leu Ala Glu Lys Gly Ala Ile Phe
 55 60 65

gtc aac gaa gca tct gaa gca cca gaa ggt gcc aac atg gtg ttc tct 355
 Val Asn Glu Ala Ser Glu Ala Pro Glu Gly Ala Asn Met Val Phe Ser
 70 75 80 85

gca cac ggc gtg agc cca atg gtc cac gaa gaa gct gca gct aaa aac 403
 Ala His Gly Val Ser Pro Met Val His Glu Glu Ala Ala Lys Asn
 90 95 100

atc aag gct att gac gcg gcc tgc ccg ctg gtc acc aaa gtg cac aag 451
 Ile Lys Ala Ile Asp Ala Ala Cys Pro Leu Val Thr Lys Val His Lys
 105 110 115

gaa gtc cag cgc ttt gat aag cag gga ttc cac att ctc ttc atc ggt 499
 Glu Val Gln Arg Phe Asp Lys Gln Gly Phe His Ile Leu Phe Ile Gly
 120 125 130

cac gaa ggc cat gaa gaa gta gag ggc acc atg ggt cat tcc gtt gag 547
 His Glu Gly His Glu Glu Val Glu Gly Thr Met Gly His Ser Val Glu
 135 140 145

aaa acc cac ctg gtt gac ggc gtt gct ggc att gcc acc ctg cct gaa 595
 Lys Thr His Leu Val Asp Gly Val Ala Gly Ile Ala Thr Leu Pro Glu
 150 155 160 165

ttc tta aac gat gaa cca aac ctg atc tgg ctg tct cag acc acg ctt 643
 Phe Leu Asn Asp Glu Pro Asn Leu Ile Trp Leu Ser Gln Thr Thr Leu
 170 175 180

tct gtg gac gag acc atg gag atc gtc cgc gag ctg aag gtg aag ttc 691
 Ser Val Asp Glu Thr Met Glu Ile Val Arg Glu Leu Lys Val Lys Phe

185										190										195										
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Pro	Gln	Leu	Gln	Asp	Pro	Pro	Ser	Asp	Asp	Ile	Cys	Tyr	Ala	Thr	Gln															
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Asn	Arg	Gln	Val	Ala	Val	Lys	Ala	Ile	Ala	Glu	Arg	Cys	Glu	Leu	Met															
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att	gtg	gtc	ggg	tcc	cgc	aac	tcc	tcc	aac	tgc	gtt	cgt	ctg	gtt	gag	835														
Il	Val	Val	Gly	Ser	Arg	Asn	Ser	Ser	Asn	Ser	Val	Arg	Leu	Val	Glu															
230					235					240					245															
gtc	gct	aag	caa	aac	ggg	gcc	gat	aac	gcc	tac	ctg	gtg	gat	tac	gcc	883														
Val	Ala	Lys	Gln	Asn	Gly	Ala	Asp	Asn	Ala	Tyr	Leu	Val	Asp	Tyr	Ala															
250					255					260																				
cgc	gaa	atc	gac	cca	gca	tgg	ttc	gaa	ggc	gta	gag	acc	atc	ggg	atc	931														
Arg	Glu	Ile	Asp	Pro	Ala	Trp	Phe	Glu	Gly	Val	Glu	Thr	Ile	Gly	Ile															
265					270					275																				
tcc	tcc	ggc	gct	tcc	gtg	cct	gag	atc	ctc	gtc	cag	ggc	gtc	att	gag	979														
Ser	Ser	Gly	Ala	Ser	Val	Pro	Glu	Ile	Leu	Val	Gln	Gly	Val	Ile	Glu															
280					285					290																				
cgc	ctg	gct	gag	ttc	ggc	tac	gac	gac	gtc	gag	gaa	gtc	acc	tcc	gcc	1027														
Arg	Leu	Ala	Glu	Phe	Gly	Tyr	Asp	Asp	Val	Glu	Glu	Val	Thr	Ser	Ala															
295					300					305																				
gct	gag	aag	att	gtt	ttc	gcg	ctg	cct	cgc	gtg	ctg	cgc	cac	aag	aat	1075														
Ala	Glu	Lys	Ile	Val	Phe	Ala	Leu	Pro	Arg	Val	Leu	Arg	His	Lys	Asn															
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<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

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Leu	Leu	Ala	Ala	Pro	Arg	Gly	Tyr	Cys	Ala	Gly	Val	Asp	Arg	Ala	Val
		20						25					30		

Glu	Thr	Val	Glu	Arg	Ala	Leu	Glu	Glu	Tyr	Gly	Ala	Pro	Ile	Tyr	Val
	35						40					45			

Arg	Lys	Glu	Ile	Val	His	Asn	Arg	Tyr	Val	Val	Asp	Thr	Leu	Ala	Glu
	50					55					60				

Lys	Gly	Ala	Ile	Phe	Val	Asn	Glu	Ala	Ser	Glu	Ala	Pro	Glu	Gly	Ala
65					70					75					80

Asn Met Val Phe Ser Ala His Gly Val Ser Pro Met Val His Glu Glu
 85 90 95
 Ala Ala Ala Lys Asn Ile Lys Ala Ile Asp Ala Ala Cys Pro Leu Val
 100 105 110
 Thr Lys Val His Lys Glu Val Gln Arg Phe Asp Lys Gln Gly Phe His
 115 120 125
 Ile Leu Phe Ile Gly His Glu Gly His Glu Glu Val Glu Gly Thr Met
 130 135 140
 Gly His Ser Val Glu Lys Thr His Leu Val Asp Gly Val Ala Gly Ile
 145 150 155 160
 Ala Thr Leu Pro Glu Phe Leu Asn Asp Glu Pro Asn Leu Ile Trp Leu
 165 170 175
 Ser Gln Thr Thr Leu Ser Val Asp Glu Thr Met Glu Ile Val Arg Glu
 180 185 190
 Leu Lys Val Lys Phe Pro Gln Leu Gln Asp Pro Pro Ser Asp Asp Ile
 195 200 205
 Cys Tyr Ala Thr Gln Asn Arg Gln Val Ala Val Lys Ala Ile Ala Glu
 210 215 220
 Arg Cys Glu Leu Met Ile Val Val Gly Ser Arg Asn Ser Ser Asn Ser
 225 230 235 240
 Val Arg Leu Val Glu Val Ala Lys Gln Asn Gly Ala Asp Asn Ala Tyr
 245 250 255
 Leu Val Asp Tyr Ala Arg Glu Ile Asp Pro Ala Trp Phe Glu Gly Val
 260 265 270
 Glu Thr Ile Gly Ile Ser Ser Gly Ala Ser Val Pro Glu Ile Leu Val
 275 280 285
 Gln Gly Val Ile Glu Arg Leu Ala Glu Phe Gly Tyr Asp Asp Val Glu
 290 295 300
 Glu Val Thr Ser Ala Ala Glu Lys Ile Val Phe Ala Leu Pro Arg Val
 305 310 315 320
 Leu Arg His Lys Asn
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<210> 101

<211> 1131

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1108)

<223> RXS01027

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gaactgtgtg caccacaacg cggaaggtga atcgcaccca atg gca aat aag aac 115
 Met Ala Asn Lys Asn
 1 5

aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc 163
 Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile
 10 15 20

aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc 211
 Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr
 25 30 35

cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc 259
 Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr
 40 45 50

aac ccg gac agc atc gag gtc gct gtc atc cac cgc ccg cac tat gat 307
 Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp
 55 60 65

gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg 355
 Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro
 70 75 80 85

aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt 403
 Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg
 90 95 100

ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc 451
 Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr
 105 110 115

aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc 499
 Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val
 120 125 130

ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca 547
 Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala
 135 140 145

tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca 595
 Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala
 150 155 160 165

gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc 643
 Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg
 170 175 180

cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag 691
 His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys
 185 190 195

cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc 739
 Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro
 200 205 210

atg ttg ttg ccc ttc aaa ccc acc gca att tac tcg gcg gtg ccc gat 787
 Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr Ser Ala Val Pro Asp
 215 220 225

cgc tgc caa gcc acc gcg ctc ccc ctt gcc gat gag ctc ggc ctc gac 835
 Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp Glu Leu Gly Leu Asp
 230 235 240 245

gtg tcc gtc aac cga ctg ttc ggc gac gac gcc tgg gaa acc gat ccc 883
 Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala Trp Glu Thr Asp Pro
 250 255 260

gag gcc tgc aag aag cgc ttc acc gac gtg gtc gcg caa ggt ggc gtg 931
 Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln Gly Gly Val
 265 270 275

ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg atc aaa tgg 979
 Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp
 280 285 290

ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa 1027
 Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys
 295 300 305

aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc 1075
 Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly
 310 315 320 325

gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg tttaaggcct 1128
 Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 330 335

cca 1131

<210> 102

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

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Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp
35 40 45

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
50 55 60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
 65 70 75 80
 Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr
 85 90 95
 Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
 100 105 110
 Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
 115 120 125
 Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
 130 135 140
 Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
 145 150 155 160
 Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
 165 170 175
 Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
 180 185 190
 Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
 195 200 205
 Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr
 210 215 220
 Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp
 225 230 235 240
 Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala
 245 250 255
 Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val
 260 265 270
 Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro
 275 280 285
 Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu
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 Lys Ile Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp
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 Gly Val Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
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 <223> RXS01528

<400> 103

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                                   Val Asn Gln Ala Trp
                                   1 5

cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163
Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu
                                   10 15 20

gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat 211
Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp
                                   25 30 35

ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt 259
Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly
                                   40 45 50

cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat 307
Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Pro Gly Glu Asp
                                   55 60 65

aag gct gcg act gct gag cgt gag gtg tgg gag gag acc ggc atc cac 355
Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His
                                   70 75 80 85

ggt gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg 403
Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser
                                   90 95 100

gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat 451
Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr
                                   105 110 115

gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg 499
Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala
                                   120 125 130

tgg att ccg gcg aat cag ttg att gag cat ttg gct ttt gcg gat gag 547
Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu
                                   135 140 145

cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg 595
Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu
                                   150 155 160 165

aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaaccg 648

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aac

651

<210> 104

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

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20 25 30

Asn Asn Glu Val Asp Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg
35 40 45

Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val
50 55 60

Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu
65 70 75 80

Glu Thr Gly Ile His Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp
85 90 95

Tyr Trp Phe Val Ser Glu Gly Lys Arg Ile His Lys Thr Val His His
100 105 110

His Leu Leu Arg Tyr Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu
115 120 125

Val Thr Glu Val Ala Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu
130 135 140

Ala Phe Ala Asp Glu Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu
145 150 155 160

Pro Glu Phe Ala Leu Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg
165 170 175

<210> 105

<211> 509

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(486)

<223> RXS01716

<400> 105

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ggt cgc ctg ggc aaa ggc gtc gac gcc acc ggt cag cta gac ccc gag	96
Val Arg Leu Gly Lys Gly Val Asp Ala Thr Gly Gln Leu Asp Pro Glu	
20 25 30	
gca atc gag cgc act cgt gtc gct ttg gaa aac tac gtt gaa ctc atg	144
Ala Ile Glu Arg Thr Arg Val Ala Leu Glu Asn Tyr Val Glu Leu Met	
35 40 45	
gaa acc cat ggg gta gag gcc gta cga atg gtt gcc acc tcc gca acc	192
Glu Thr His Gly Val Glu Ala Val Arg Met Val Ala Thr Ser Ala Thr	
50 55 60	
cgc gat gcg tcc aac cgc gat gaa ttc ttt tcg atg acc cgc cag ctt	240
Arg Asp Ala Ser Asn Arg Asp Glu Phe Phe Ser Met Thr Arg Gln Leu	
65 70 75 80	
ctg tcc aag atc cgt cct gga tac caa gct gaa gta att tcc ggc gaa	288
Leu Ser Lys Ile Arg Pro Gly Tyr Gln Ala Glu Val Ile Ser Gly Glu	
85 90 95	
gag gaa gct ctg ctg tcc ttc cga ggt gca atc gtt gac ctg cct gaa	336
Glu Glu Ala Leu Leu Ser Phe Arg Gly Ala Ile Val Asp Leu Pro Glu	
100 105 110	
gac caa ggt cct ttc tgt gtt atc gac ctt ggc ggt gga tcc act gag	384
Asp Gln Gly Pro Phe Cys Val Ile Asp Leu Gly Gly Gly Ser Thr Glu	
115 120 125	
ttc atc gtt ggc acc tac gac ggt gaa atc cta ggc tcc cac tca acc	432
Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr	
130 135 140	
caa atg gga tgc gtg cgc ctg acc gaa cga atc atg cgc agc gac cca	480
Gln Met Gly Cys Val Arg Leu Thr Glu Arg Ile Met Arg Ser Asp Pro	
145 150 155 160	
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Pro Asp	

<210> 106

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

Glu Val Thr Pro Glu Gly Phe Lys Glu Ile Thr Arg Glu Asn Thr Ile
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 20 25 30
 Ala Ile Glu Arg Thr Arg Val Ala Leu Glu Asn Tyr Val Glu Leu Met
 35 40 45
 Glu Thr His Gly Val Glu Ala Val Arg Met Val Ala Thr Ser Ala Thr
 50 55 60
 Arg Asp Ala Ser Asn Arg Asp Glu Phe Phe Ser Met Thr Arg Gln Leu
 65 70 75 80
 Leu Ser Lys Ile Arg Pro Gly Tyr Gln Ala Glu Val Ile Ser Gly Glu
 85 90 95
 Glu Glu Ala Leu Leu Ser Phe Arg Gly Ala Ile Val Asp Leu Pro Glu
 100 105 110
 Asp Gln Gly Pro Phe Cys Val Ile Asp Leu Gly Gly Gly Ser Thr Glu
 115 120 125
 Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr
 130 135 140
 Gln Met Gly Cys Val Arg Leu Thr Glu Arg Ile Met Arg Ser Asp Pro
 145 150 155 160
 Pro Asp

<210> 107
 <211> 654
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(631)
 <223> RXS01835

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 ttctgcgtg aatacacttt cccgcgcct tcgcaaagct atg aat act gcc gcg 115
 Met Asn Thr Ala Ala
 1 5
 tgg gca cac cgc cac cac gta cgc aaa ggc ggt gga att ccg tat gtc 163
 Trp Ala His Arg His His Val Arg Lys Gly Gly Gly Ile Pro Tyr Val
 10 15 20
 agc cat ctt tat tca gtg atg tac ttg ctg gcc agc gtc act aat gat 211
 Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala Ser Val Thr Asn Asp
 25 30 35
 gaa gat gtg ctc atc gcc ggg ctg ctc cac gac acc ctc gaa gac gta 259

Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val
 40 45 50

ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg 307
 Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg
 55 60 65

gtg cgc gag ttg gtg gaa gag ctc acc aaa cag ccc tta aaa agc tgg 355
 Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp
 70 75 80 85

aaa gcg cgt gcc gac gct tac ctc ctg cac ctc agc gca ggt gcc agc 403
 Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser
 90 95 100

tta gag gct gtc tta atc tcc acc gca gat aaa ctg cat aat ctc atg 451
 Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys Leu His Asn Leu Met
 105 110 115

tcc atc ttg gat gac ctt gaa ata cac ggt gaa gat tta tgg caa cgc 499
 Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu Asp Leu Trp Gln Arg
 120 125 130

ttt aac gct ggc aaa gag cag caa atc tgg tgg tat agc gag gtt tat 547
 Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr
 135 140 145

cag ata tct ctc cag cgc tta ggg ttc aat gag ttg aat aaa caa ctg 595
 Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu
 150 155 160 165

ggg ttg tgc gtc gaa aag ctc tta aag caa agc gcc taggcgctcg 641
 Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser Ala
 170 175

gcggcgctcga taa 654

<210> 108
 <211> 177
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 108
 Met Asn Thr Ala Ala Trp Ala His Arg His His Val Arg Lys Gly Gly
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Gly Ile Pro Tyr Val Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala
 20 25 30

Ser Val Thr Asn Asp Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp
 35 40 45

Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala
 50 55 60

Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln

65	70	75	80
Pro Leu Lys Ser Trp	Lys Ala Arg Ala Asp	Ala Tyr Leu Leu His Leu	
	85	90	95
Ser Ala Gly Ala Ser	Leu Glu Ala Val Leu Ile Ser Thr	Ala Asp Lys	
	100	105	110
Leu His Asn Leu Met Ser	Ile Leu Asp Asp Leu Glu Ile His Gly Glu		
	115	120	125
Asp Leu Trp Gln Arg Phe	Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp		
	130	135	140
Tyr Ser Glu Val Tyr	Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu		
	145	150	155
Leu Asn Lys Gln Leu Gly	Leu Cys Val Glu Lys Leu Leu Lys Gln Ser		
	165	170	175

Ala

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 <222> (101)..(1027)
 <223> RXS02497

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gattcacact ttgccaccct agaccgtcta accttttaggt gtg aga tta ggt gta 115
 Val Arg Leu Gly Val
 1 5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163
 Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg
 10 15 20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211
 Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg
 25 30 35

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259
 Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile
 40 45 50

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307
 Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr
 55 60 65

ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser 70 75 80 85	355
gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly 90 95 100	403
gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe 105 110 115	451
ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn 120 125 130	499
ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu 135 140 145	547
tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr 150 155 160 165	595
cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu 170 175 180	643
ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met 185 190 195	691
cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe 200 205 210	739
cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro 215 220 225	787
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agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu 265 270 275	931
gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp 280 285 290	979
gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag	1027

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1050

<210> 110

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

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 20 25 30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
 35 40 45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
 50 55 60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
 65 70 75 80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
 85 90 95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
 100 105 110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
 115 120 125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
 130 135 140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly
 145 150 155 160

Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg
 165 170 175

Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu
 180 185 190

Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly
 195 200 205

Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro
 210 215 220

Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu
 225 230 235 240

Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala
245 250 255

Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly
260 265 270

Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val
275 280 285

Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile
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Asp Lys Gly Leu Glu
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<211> 534

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXS02972

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gaacgaatca tgcgcagcga cccacccgac tgaaaccgaa gtg gaa atc gcc cgc 115
Val Glu Ile Ala Arg
1 5

gac tac gtt gca gaa cgc atc cag gaa gta aaa gcc atc gtc cca att 163
Asp Tyr Val Ala Glu Arg Ile Gln Glu Val Lys Ala Ile Val Pro Ile
10 15 20

tca aag gca aaa acc ttt gtg gga tgc gca ggc acc ttc acc aca atc 211
Ser Lys Ala Lys Thr Phe Val Gly Cys Ala Gly Thr Phe Thr Thr Ile
25 30 35

tcc gcc tgg gtg caa ggc cta gaa agc tac gac cgc gac gcg atc cac 259
Ser Ala Trp Val Gln Gly Leu Glu Ser Tyr Asp Arg Asp Ala Ile His
40 45 50

ctc tct gca ctc aac ttc gat gca ctg cga gtt gtc acc gat gag atc 307
Leu Ser Ala Leu Asn Phe Asp Ala Leu Arg Val Val Thr Asp Glu Ile
55 60 65

att tca gaa tca tca tca cag cgc gcc agc aac cca gtt gtt gat cca 355
Ile Ser Glu Ser Ser Ser Gln Arg Ala Ser Asn Pro Val Val Asp Pro
70 75 80 85

ggg cgc gcc gac gtc atc ggt ggc gga tcc gtt gtt gtc caa gca gcg 403
Gly Arg Ala Asp Val Ile Gly Gly Gly Ser Val Val Val Gln Ala Ala
90 95 100

atc gac tta gcc tcc aaa gaa gcc ggt gta gac tac atc att att tcc 451
 Ile Asp Leu Ala Ser Lys Glu Ala Gly Val Asp Tyr Ile Ile Ile Ser
 105 110 115

gaa aaa gac atc ctc gac ggc ctc atc ctt ggc ctg gta gaa gcc gac 499
 Glu Lys Asp Ile Leu Asp Gly Leu Ile Leu Gly Leu Val Glu Ala Asp
 120 125 130

tct ttg aag aaa taggacccta gttttaaac act 534
 Ser Leu Lys Lys
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<210> 112

<211> 137

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

Val Glu Ile Ala Arg Asp Tyr Val Ala Glu Arg Ile Gln Glu Val Lys
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 20 25 30

Thr Phe Thr Thr Ile Ser Ala Trp Val Gln Gly Leu Glu Ser Tyr Asp
 35 40 45

Arg Asp Ala Ile His Leu Ser Ala Leu Asn Phe Asp Ala Leu Arg Val
 50 55 60

Val Thr Asp Glu Ile Ile Ser Glu Ser Ser Ser Gln Arg Ala Ser Asn
 65 70 75 80

Pro Val Val Asp Pro Gly Arg Ala Asp Val Ile Gly Gly Gly Ser Val
 85 90 95

Val Val Gln Ala Ala Ile Asp Leu Ala Ser Lys Glu Ala Gly Val Asp
 100 105 110

Tyr Ile Ile Ile Ser Glu Lys Asp Ile Leu Asp Gly Leu Ile Leu Gly
 115 120 125

Leu Val Glu Ala Asp Ser Leu Lys Lys
 130 135

<210> 113

<211> 636

<212> DNA

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<220>

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<222> (101)..(613)

<223> RXA02159

<400> 113

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                                         Met Ser Leu Gly Ser
                                         1           5
acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc act gca cgc 163
Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val Thr Arg Thr Ala Arg
                        10                15                20
caa gct ctc att ttg cag att ttg gac aaa caa aaa gtc acc agc cag 211
Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln Lys Val Thr Ser Gln
                        25                30                35
gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat atc acc cag 259
Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly Ile Asp Ile Thr Gln
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gcc acc ttg tcc cga gat ctc gat gaa ctc ggt gca cgc aag gtt cgc 307
Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly Ala Arg Lys Val Arg
                        55                60                65
ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta gat agc atc 355
Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Pro Val Asp Ser Ile
                        70                75                80                85
gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc cgc atg ctt 403
Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys Leu Arg Arg Met Leu
                        90                95                100
gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc gcg atg ctg 451
Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly Asn Ile Ala Met Leu
                        105                110                115
cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc atc gat agg 499
Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala Ser Phe Ile Asp Arg
                        120                125                130
gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggt gat gac acc gtt 547
Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp Asp Thr Val
                        135                140                145
ttc gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta ggt gaa tta 595
Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu Gly Glu Leu
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Leu Ser Gly Arg Thr Thr
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<210> 114

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 114

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Lys Val Thr Ser Gln Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly
 35 40 45

Ile Asp Ile Thr Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly
 50 55 60

Ala Arg Lys Val Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly
 65 70 75 80

Pro Val Asp Ser Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys
 85 90 95

Leu Arg Arg Met Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly
 100 105 110

Asn Ile Ala Met Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala
 115 120 125

Ser Phe Ile Asp Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala
 130 135 140

Gly Asp Asp Thr Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys
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Glu Leu Gly Glu Leu Leu Ser Gly Arg Thr Thr
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<210> 115

<211> 486

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(463)

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 Met Ala Ala Ala Leu
 1 5

gcc aaa aaa cat gcc ggg gac gct ctc aaa gtt tat tca gct ggc aca 163
 Ala Lys Lys His Ala Gly Asp Ala Leu Lys Val Tyr Ser Ala Gly Thr
 10 15 20

aag cca ggt acg aaa tta aat caa cag tcc ctt gat tcc att gct gaa 211

Lys Pro Gly Thr Lys Leu Asn Gln Gln Ser Leu Asp Ser Ile Ala Glu
 25 30 35

gtt ggc gca gat atg tct caa ggg ttt cca aag ggc att gac cag gag 259
 Val Gly Ala Asp Met Ser Gln Gly Phe Pro Lys Gly Ile Asp Gln Glu
 40 45 50

tta att aag cga gta gac cgc gtg gtc att ctt ggt gcc gaa gct caa 307
 Leu Ile Lys Arg Val Asp Arg Val Val Ile Leu Gly Ala Glu Ala Gln
 55 60 65

cta gaa atg cct atc gat gca aac ggc ata cta cag cgc tgg gta act 355
 Leu Glu Met Pro Ile Asp Ala Asn Gly Ile Leu Gln Arg Trp Val Thr
 70 75 80 85

gac gaa ccc tct gaa cgt gga att gaa ggt atg gaa cgc atg cgc ctg 403
 Asp Glu Pro Ser Glu Arg Gly Ile Glu Gly Met Glu Arg Met Arg Leu
 90 95 100

gtc cga gat gat att gac gcc cga gtc caa aac ctc gtc gct gaa cta 451
 Val Arg Asp Asp Ile Asp Ala Arg Val Gln Asn Leu Val Ala Glu Leu
 105 110 115

acc caa aac gca tagcagtttt ctaatctcac aca 486
 Thr Gln Asn Ala
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<210> 116
 <211> 121
 <212> PRT
 <213> *Corynebacterium glutamicum*

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Tyr Ser Ala Gly Thr Lys Pro Gly Thr Lys Leu Asn Gln Gln Ser Leu
 20 25 30

Asp Ser Ile Ala Glu Val Gly Ala Asp Met Ser Gln Gly Phe Pro Lys
 35 40 45

Gly Ile Asp Gln Glu Leu Ile Lys Arg Val Asp Arg Val Val Ile Leu
 50 55 60

Gly Ala Glu Ala Gln Leu Glu Met Pro Ile Asp Ala Asn Gly Ile Leu
 65 70 75 80

Gln Arg Trp Val Thr Asp Glu Pro Ser Glu Arg Gly Ile Glu Gly Met
 85 90 95

Glu Arg Met Arg Leu Val Arg Asp Asp Ile Asp Ala Arg Val Gln Asn
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Leu Val Ala Glu Leu Thr Gln Asn Ala
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<210> 117
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<212> DNA
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<222> (101)..(487)  
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Met Lys Ser Val Leu																	5
1																	
ttt gtg tgc gtc ggt aat ggc gga aaa tca cag atg gcg gcg gcg ctg																	163
Phe Val Cys Val Gly Asn Gly Gly Lys Ser Gln Met Ala Ala Ala Leu																	20
10 15																	
gca cag aag tat gca tca gat tca gta gag atc cat tct gct gga acc																	211
Ala Gln Lys Tyr Ala Ser Asp Ser Val Glu Ile His Ser Ala Gly Thr																	35
25 30																	
aag cct gca cag ggg cta aac caa ttg tct gtg gaa tcc atc gct gag																	259
Lys Pro Ala Gln Gly Leu Asn Gln Leu Ser Val Glu Ser Ile Ala Glu																	50
40 45																	
gtg ggc gct gat atg tcg caa gga att ccc aaa gcg atc gat ccg gag																	307
Val Gly Ala Asp Met Ser Gln Gly Ile Pro Lys Ala Ile Asp Pro Glu																	65
55 60 65																	
ctg ctg cgc act gtc gat cgt gtg gtt att ttg ggc gat gac gca cag																	355
Leu Leu Arg Thr Val Asp Arg Val Val Ile Leu Gly Asp Asp Ala Gln																	85
70 75 80																	
gta gat atg cct gaa tct gca cag ggc gct ctt gag cgt tgg tca att																	403
Val Asp Met Pro Glu Ser Ala Gln Gly Ala Leu Glu Arg Trp Ser Ile																	100
90 95 100																	
gag gaa ccg gat gct caa ggt atg gaa cgt atg cgt att gtg cgg gat																	451
Glu Glu Pro Asp Ala Gln Gly Met Glu Arg Met Arg Ile Val Arg Asp																	115
105 110 115																	
cag atc gat aac cga gtc caa gct ttg cta gcg gga taagcgccga																	497
Gln Ile Asp Asn Arg Val Gln Ala Leu Leu Ala Gly																	125
120 125																	
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<213> Corynebacterium glutamicum

<400> 118

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Met Ala Ala Ala Leu Ala Gln Lys Tyr Ala Ser Asp Ser Val Glu Ile
20 25 30

His Ser Ala Gly Thr Lys Pro Ala Gln Gly Leu Asn Gln Leu Ser Val
35 40 45

Glu Ser Ile Ala Glu Val Gly Ala Asp Met Ser Gln Gly Ile Pro Lys
50 55 60

Ala Ile Asp Pro Glu Leu Leu Arg Thr Val Asp Arg Val Val Ile Leu
65 70 75 80

Gly Asp Asp Ala Gln Val Asp Met Pro Glu Ser Ala Gln Gly Ala Leu
85 90 95

Glu Arg Trp Ser Ile Glu Glu Pro Asp Ala Gln Gly Met Glu Arg Met
100 105 110

Arg Ile Val Arg Asp Gln Ile Asp Asn Arg Val Gln Ala Leu Leu Ala
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Gly

<210> 119

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1198)

<223> RXA00600

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Met Ile Glu Gly Trp
1 5

ctc atg acc ctt act aaa gag cat tcg acä cct cga gcg gct ggc tca 163
Leu Met Thr Leu Thr Lys Glu His Ser Thr Pro Arg Ala Ala Gly Ser
10 15 20

atg tcg ttt ctt gac cgc tgg tta gct gcc tgg att ttc ttg gct atg 211
Met Ser Phe Leu Asp Arg Trp Leu Ala Ala Trp Ile Phe Leu Ala Met
25 30 35

gct gct ggg ttg tta atc ggc aag gtc ttt cca gga att ggg gcg ctt 259

Ala	Ala	Gly	Leu	Leu	Ile	Gly	Lys	Val	Phe	Pro	Gly	Ile	Gly	Ala	Leu		
		40					45					50					
ttg	agc	gcg	gtg	gaa	att	ggg	gga	att	tcc	att	cca	att	gct	atc	ggg	307	
Leu	Ser	Ala	Val	Glu	Ile	Gly	Gly	Ile	Ser	Ile	Pro	Ile	Ala	Ile	Gly		
	55					60					65						
ttg	atc	gtc	atg	atg	tat	cca	cct	ttg	gcc	aag	gtg	cgc	tac	gac	aaa	355	
Leu	Ile	Val	Met	Met	Tyr	Pro	Pro	Leu	Ala	Lys	Val	Arg	Tyr	Asp	Lys		
	70				75				80						85		
act	aaa	gaa	atc	agc	aca	gac	cgc	gct	ctc	atg	gtg	gtg	tcg	att	atg	403	
Thr	Lys	Glu	Ile	Ser	Thr	Asp	Arg	Ala	Leu	Met	Val	Val	Ser	Ile	Met		
				90				95						100			
ttg	aac	tgg	atc	gtt	gga	cca	gca	ctt	atg	ttt	agc	ctg	gcg	tgg	ctg	451	
Leu	Asn	Trp	Ile	Val	Gly	Pro	Ala	Leu	Met	Phe	Ser	Leu	Ala	Trp	Leu		
			105					110					115				
ttt	ctt	cca	gat	caa	cca	gag	ctt	cgc	act	ggg	cta	att	atc	gtg	ggc	499	
Phe	Leu	Pro	Asp	Gln	Pro	Glu	Leu	Arg	Thr	Gly	Leu	Ile	Ile	Val	Gly		
		120					125					130					
ctt	gcg	cgc	tgt	atc	gcg	atg	gtt	ttg	gta	tgg	agt	gat	ctc	gct	tgt	547	
Leu	Ala	Arg	Cys	Ile	Ala	Met	Val	Leu	Val	Trp	Ser	Asp	Leu	Ala	Cys		
	135					140					145						
ggg	gac	cgg	gaa	gca	act	gct	gtg	ctg	gtt	gca	atc	aac	tcg	gtg	ttc	595	
Gly	Asp	Arg	Glu	Ala	Thr	Ala	Val	Leu	Val	Ala	Ile	Asn	Ser	Val	Phe		
	150				155					160					165		
cag	atc	ctt	atg	ttc	ggg	gtg	ctt	ggg	tgg	ttt	tac	ctg	cag	att	ctt	643	
Gln	Ile	Leu	Met	Phe	Gly	Val	Leu	Gly	Trp	Phe	Tyr	Leu	Gln	Ile	Leu		
				170					175					180			
ccc	tcg	tgg	ctg	gga	tta	gac	acc	acg	tcg	gtg	act	ttc	tct	gtg	gta	691	
Pro	Ser	Trp	Leu	Gly	Leu	Asp	Thr	Thr	Ser	Val	Thr	Phe	Ser	Val	Val		
			185					190					195				
tca	atc	gtg	act	tcc	gtt	ctc	gtg	ttc	ttg	ggc	ata	cca	ctt	gta	gct	739	
Ser	Ile	Val	Thr	Ser	Val	Leu	Val	Phe	Leu	Gly	Ile	Pro	Leu	Val	Ala		
		200					205					210					
gga	gtt	tta	tct	cgc	gtc	att	ggg	gaa	aaa	aca	aag	gga	cgg	cgc	tgg	787	
Gly	Val	Leu	Ser	Arg	Val	Ile	Gly	Glu	Lys	Thr	Lys	Gly	Arg	Arg	Trp		
	215					220					225						
tac	gag	gac	acg	ttc	ctg	cct	aag	att	tca	ccc	ttg	gcg	ctg	att	ggc	835	
Tyr	Glu	Asp	Thr	Phe	Leu	Pro	Lys	Ile	Ser	Pro	Leu	Ala	Leu	Ile	Gly		
	230				235					240					245		
ttg	cta	tac	aca	att	gtt	ctg	ctg	ttt	tcg	ttg	cag	ggg	gat	gaa	atc	883	
Leu	Leu	Tyr	Thr	Ile	Val	Leu	Leu	Phe	Ser	Leu	Gln	Gly	Asp	Glu	Ile		
				250					255					260			
aca	gcg	cag	cct	tgg	aca	gta	gct	cgt	ctt	gca	ttg	ccg	ctg	ctg	atg	931	
Thr	Ala	Gln	Pro	Trp	Thr	Val	Ala	Arg	Leu	Ala	Leu	Pro	Leu	Leu	Met		

265	270	275	
tac ttt gtg ggc atg ttt ttc att tcc ctg gtg gta tcc aaa ctg tcc			979
Tyr Phe Val Gly Met Phe Phe Ile Ser Leu Val Val Ser Lys Leu Ser			
280	285	290	
ggg tta act tat gag cga gct gct tcc gtg tct ttt act gca gca gga			1027
Gly Leu Thr Tyr Glu Arg Ala Ala Ser Val Ser Phe Thr Ala Ala Gly			
295	300	305	
aac aac ttt gaa tta gcg att gcg gta tcg atc gga acc ttt ggt gcg			1075
Asn Asn Phe Glu Leu Ala Ile Ala Val Ser Ile Gly Thr Phe Gly Ala			
310	315	320	325
aca tca ccg cag gca tta gct gga acg atc ggc cct ttg att gaa gtc			1123
Thr Ser Pro Gln Ala Leu Ala Gly Thr Ile Gly Pro Leu Ile Glu Val			
330	335		340
cca gta tta gtc gga ttg gtt tat gtc atg ttg tgg ctt gga cca aaa			1171
Pro Val Leu Val Gly Leu Val Tyr Val Met Leu Trp Leu Gly Pro Lys			
345	350		355
atc ttt aaa aag gag aat gca gga tca tgaaatcagt tttgtttgtg			1218
Ile Phe Lys Lys Glu Asn Ala Gly Ser			
360	365		
tgc			1221
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20	25		30
Ile Phe Leu Ala Met Ala Ala Gly Leu Leu Ile Gly Lys Val Phe Pro			
35	40		45
Gly Ile Gly Ala Leu Leu Ser Ala Val Glu Ile Gly Gly Ile Ser Ile			
50	55		60
Pro Ile Ala Ile Gly Leu Ile Val Met Met Tyr Pro Pro Leu Ala Lys			
65	70	75	80
Val Arg Tyr Asp Lys Thr Lys Glu Ile Ser Thr Asp Arg Ala Leu Met			
85	90		95
Val Val Ser Ile Met Leu Asn Trp Ile Val Gly Pro Ala Leu Met Phe			
100	105		110
Ser Leu Ala Trp Leu Phe Leu Pro Asp Gln Pro Glu Leu Arg Thr Gly			

115	120	125
Leu Ile Ile Val Gly Leu Ala Arg Cys Ile Ala Met Val Leu Val Trp 130 135 140		
Ser Asp Leu Ala Cys Gly Asp Arg Glu Ala Thr Ala Val Leu Val Ala 145 150 155 160		
Ile Asn Ser Val Phe Gln Ile Leu Met Phe Gly Val Leu Gly Trp Phe 165 170 175		
Tyr Leu Gln Ile Leu Pro Ser Trp Leu Gly Leu Asp Thr Thr Ser Val 180 185 190		
Thr Phe Ser Val Val Ser Ile Val Thr Ser Val Leu Val Phe Leu Gly 195 200 205		
Ile Pro Leu Val Ala Gly Val Leu Ser Arg Val Ile Gly Glu Lys Thr 210 215 220		
Lys Gly Arg Arg Trp Tyr Glu Asp Thr Phe Leu Pro Lys Ile Ser Pro 225 230 235 240		
Leu Ala Leu Ile Gly Leu Leu Tyr Thr Ile Val Leu Leu Phe Ser Leu 245 250 255		
Gln Gly Asp Glu Ile Thr Ala Gln Pro Trp Thr Val Ala Arg Leu Ala 260 265 270		
Leu Pro Leu Leu Met Tyr Phe Val Gly Met Phe Phe Ile Ser Leu Val 275 280 285		
Val Ser Lys Leu Ser Gly Leu Thr Tyr Glu Arg Ala Ala Ser Val Ser 290 295 300		
Phe Thr Ala Ala Gly Asn Asn Phe Glu Leu Ala Ile Ala Val Ser Ile 305 310 315 320		
Gly Thr Phe Gly Ala Thr Ser Pro Gln Ala Leu Ala Gly Thr Ile Gly 325 330 335		
Pro Leu Ile Glu Val Pro Val Leu Val Gly Leu Val Tyr Val Met Leu 340 345 350		
Trp Leu Gly Pro Lys Ile Phe Lys Lys Glu Asn Ala Gly Ser 355 360 365		

<210> 121

<211> 1233

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1210)

<223> RXA02200

<400> 121
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tttgaatatc gacaggtatc aatataccga aaggtgtcgc atg aca aac tca act 115
Met Thr Asn Ser Thr
1 5
cag acg cgg gcc aag cca gcc cga atc tca ttt ctt gat aaa tac att 163
Gln Thr Arg Ala Lys Pro Ala Arg Ile Ser Phe Leu Asp Lys Tyr Ile
10 15 20
cca ctt tgg att att ttg gcg atg gcg ttt ggg cta ttt tta ggc cgg 211
Pro Leu Trp Ile Ile Leu Ala Met Ala Phe Gly Leu Phe Leu Gly Arg
25 30 35
agc gtt tcg gga ctc tca ggc ttt cta ggc gca atg gaa gtc gga ggg 259
Ser Val Ser Gly Leu Ser Gly Phe Leu Gly Ala Met Glu Val Gly Gly
40 45 50
atc tcc ttg cca atc gct tta ggc ctc ctt gta atg atg tac cca ccg 307
Ile Ser Leu Pro Ile Ala Leu Gly Leu Leu Val Met Met Tyr Pro Pro
55 60 65
ttg gcc aaa gtt cgg tat gac aaa act aaa caa att gcc act gat aag 355
Leu Ala Lys Val Arg Tyr Asp Lys Thr Lys Gln Ile Ala Thr Asp Lys
70 75 80 85
cat ttg atg ggc gtg tca ctc att ctc aat tgg gtg gtg ggt cct gcc 403
His Leu Met Gly Val Ser Leu Ile Leu Asn Trp Val Val Gly Pro Ala
90 95 100
tta atg ttc gcg cta gct tgg ttg ttc ctc cca gac caa ccg gaa tta 451
Leu Met Phe Ala Leu Ala Trp Leu Phe Leu Pro Asp Gln Pro Glu Leu
105 110 115
cga acc ggc ctg att att gta gga ctc gca cga tgt att gcg atg gtc 499
Arg Thr Gly Leu Ile Ile Val Gly Leu Ala Arg Cys Ile Ala Met Val
120 125 130
ttg gtt tgg tct gat atg tcc tgt gga gac cgc gag gct aca gca gtt 547
Leu Val Trp Ser Asp Met Ser Cys Gly Asp Arg Glu Ala Thr Ala Val
135 140 145
ctc gta gcc att aat tca gtt ttt caa gtc gca atg ttt ggt gca ctt 595
Leu Val Ala Ile Asn Ser Val Phe Gln Val Ala Met Phe Gly Ala Leu
150 155 160 165
ggc tgg ttc tat ctg caa gtt tta cca tcc tgg cta gga tta cca act 643
Gly Trp Phe Tyr Leu Gln Val Leu Pro Ser Trp Leu Gly Leu Pro Thr
170 175 180
acc acc gct caa ttc tct ttc tgg tca att gtg act tcg gtt ttg gtg 691
Thr Thr Ala Gln Phe Ser Phe Trp Ser Ile Val Thr Ser Val Leu Val
185 190 195
ttc ctc gga ata cct cta ctt gct gga gtt ttc tcg cga att att ggc 739

Phe	Leu	Gly	Ile	Pro	Leu	Leu	Ala	Gly	Val	Phe	Ser	Arg	Ile	Ile	Gly		
	200						205					210					
gaa	aag	atc	aag	gga	cgt	gag	tgg	tat	gaa	caa	aag	ttc	ctt	ccg	gca	787	
Glu	Lys	Ile	Lys	Gly	Arg	Glu	Trp	Tyr	Glu	Gln	Lys	Phe	Leu	Pro	Ala		
	215					220					225						
atc	tct	cca	ttt	gca	cta	atc	ggg	ctg	ctt	tat	acg	atc	gtc	ttg	ttg	835	
Ile	Ser	Pro	Phe	Ala	Leu	Ile	Gly	Leu	Leu	Tyr	Thr	Ile	Val	Leu	Leu		
	230				235					240					245		
ttt	tca	ttg	caa	ggg	gat	cag	atc	gtc	tct	caa	cca	tgg	gct	gta	gtt	883	
Phe	Ser	Leu	Gln	Gly	Asp	Gln	Ile	Val	Ser	Gln	Pro	Trp	Ala	Val	Val		
			250						255					260			
cgt	ctc	gcg	ata	cca	ttg	gtt	atc	tat	ttc	gtt	gga	atg	ttt	ttc	att	931	
Arg	Leu	Ala	Ile	Pro	Leu	Val	Ile	Tyr	Phe	Val	Gly	Met	Phe	Phe	Ile		
			265					270					275				
tca	ctc	att	gcg	tca	aaa	cta	tct	ggc	atg	aac	tat	gca	aag	tct	gca	979	
Ser	Leu	Ile	Ala	Ser	Lys	Leu	Ser	Gly	Met	Asn	Tyr	Ala	Lys	Ser	Ala		
		280					285					290					
tcc	gtc	tct	ttc	act	gca	gct	ggc	aac	aat	ttt	gaa	ctt	gcg	att	gcg	1027	
Ser	Val	Ser	Phe	Thr	Ala	Ala	Gly	Asn	Asn	Phe	Glu	Leu	Ala	Ile	Ala		
	295					300					305						
gtg	tcg	atc	gga	acg	ttt	ggc	gca	act	tct	gca	cag	gct	atg	gca	gga	1075	
Val	Ser	Ile	Gly	Thr	Phe	Gly	Ala	Thr	Ser	Ala	Gln	Ala	Met	Ala	Gly		
	310				315					320					325		
acg	att	ggg	ccc	ttg	att	gaa	att	cca	gta	ctt	gtc	ggc	ttg	gtc	tac	1123	
Thr	Ile	Gly	Pro	Leu	Ile	Glu	Ile	Pro	Val	Leu	Val	Gly	Leu	Val	Tyr		
			330						335					340			
gcc	atg	ctg	tgg	cta	ggc	ccc	aag	ttg	ttc	cca	aat	gac	ccc	acg	ctg	1171	
Ala	Met	Leu	Trp	Leu	Gly	Pro	Lys	Leu	Phe	Pro	Asn	Asp	Pro	Thr	Leu		
			345				350						355				
cca	tca	tca	gct	cgt	tct	acc	agc	caa	atc	atc	aac	tca	tagcgaagga			1220	
Pro	Ser	Ser	Ala	Arg	Ser	Thr	Ser	Gln	Ile	Ile	Asn	Ser					
			360				365					370					
atcaacttca	tga															1233	

<210> 122
 <211> 370
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 122
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 Leu Asp Lys Tyr Ile Pro Leu Trp Ile Ile Leu Ala Met Ala Phe Gly
 20 25 30

Leu Phe Leu Gly Arg Ser Val Ser Gly Leu Ser Gly Phe Leu Gly Ala
 35 40 45
 Met Glu Val Gly Gly Ile Ser Leu Pro Ile Ala Leu Gly Leu Leu Val
 50 55 60
 Met Met Tyr Pro Pro Leu Ala Lys Val Arg Tyr Asp Lys Thr Lys Gln
 65 70 75 80
 Ile Ala Thr Asp Lys His Leu Met Gly Val Ser Leu Ile Leu Asn Trp
 85 90 95
 Val Val Gly Pro Ala Leu Met Phe Ala Leu Ala Trp Leu Phe Leu Pro
 100 105 110
 Asp Gln Pro Glu Leu Arg Thr Gly Leu Ile Ile Val Gly Leu Ala Arg
 115 120 125
 Cys Ile Ala Met Val Leu Val Trp Ser Asp Met Ser Cys Gly Asp Arg
 130 135 140
 Glu Ala Thr Ala Val Leu Val Ala Ile Asn Ser Val Phe Gln Val Ala
 145 150 155 160
 Met Phe Gly Ala Leu Gly Trp Phe Tyr Leu Gln Val Leu Pro Ser Trp
 165 170 175
 Leu Gly Leu Pro Thr Thr Thr Ala Gln Phe Ser Phe Trp Ser Ile Val
 180 185 190
 Thr Ser Val Leu Val Phe Leu Gly Ile Pro Leu Leu Ala Gly Val Phe
 195 200 205
 Ser Arg Ile Ile Gly Glu Lys Ile Lys Gly Arg Glu Trp Tyr Glu Gln
 210 215 220
 Lys Phe Leu Pro Ala Ile Ser Pro Phe Ala Leu Ile Gly Leu Leu Tyr
 225 230 235 240
 Thr Ile Val Leu Leu Phe Ser Leu Gln Gly Asp Gln Ile Val Ser Gln
 245 250 255
 Pro Trp Ala Val Val Arg Leu Ala Ile Pro Leu Val Ile Tyr Phe Val
 260 265 270
 Gly Met Phe Phe Ile Ser Leu Ile Ala Ser Lys Leu Ser Gly Met Asn
 275 280 285
 Tyr Ala Lys Ser Ala Ser Val Ser Phe Thr Ala Ala Gly Asn Asn Phe
 290 295 300
 Glu Leu Ala Ile Ala Val Ser Ile Gly Thr Phe Gly Ala Thr Ser Ala
 305 310 315 320
 Gln Ala Met Ala Gly Thr Ile Gly Pro Leu Ile Glu Ile Pro Val Leu
 325 330 335

Val Gly Leu Val Tyr Ala Met Leu Trp Leu Gly Pro Lys L u Phe Pro
 340 345 350

Asn Asp Pro Thr Leu Pro Ser Ser Ala Arg Ser Thr Ser Gln Ile Ile
 355 360 365

Asn Ser
 370

<210> 123

<211> 762

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(739)

<223> RXA02202

<400> 123

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aatctattgg tttccccgta aaattcttcga aaggaagaac atg acc ggg caa gct 115
                                     Met Thr Gly Gln Ala
                                     1 5

gca cca aac ttg cat acc aat att ttg aac cgt atc gca aat gaa ctg 163
Ala Pro Asn Leu His Thr Asn Ile Leu Asn Arg Ile Ala Asn Glu Leu
          10 15 20

gcg ttg acc tat caa gga gtt ttc tct gca gag act atc aac cgc tat 211
Ala Leu Thr Tyr Gln Gly Val Phe Ser Ala Glu Thr Ile Asn Arg Tyr
          25 30 35

att ttt gaa tcg tat gtg tcg ttg gcg aga aca gca aaa atc cat acg 259
Ile Phe Glu Ser Tyr Val Ser Leu Ala Arg Thr Ala Lys Ile His Thr
          40 45 50

cac ctg cca att ttg gca gaa ggt ttt gct aaa gac cgg ctg cac gca 307
His Leu Pro Ile Leu Ala Glu Gly Phe Ala Lys Asp Arg Leu His Ala
          55 60 65

ctt gcg gta gct gaa ggt aag gtg gct tca cct gtg cct cag gtc cta 355
Leu Ala Val Ala Glu Gly Lys Val Ala Ser Pro Val Pro Gln Val Leu
          70 75 80 85

ttt att tgc gtc cac aac gca ggt cgt tca caa att gct tcg gcg ttg 403
Phe Ile Cys Val His Asn Ala Gly Arg Ser Gln Ile Ala Ser Ala Leu
          90 95 100

ttg tct cac tat gcc ggt agt tct gta gag gta cgt tct gca ggt tct 451
Leu Ser His Tyr Ala Gly Ser Ser Val Glu Val Arg Ser Ala Gly Ser
          105 110 115

tta cct gct tct gaa att cac cca ctg gtg ttg gaa att ttg tca gag 499
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Leu Pro Ala Ser Glu Ile His Pro Leu Val Leu Glu Il Leu Ser Glu
 120 125 130
 cga gga gtg aac att tct gat gca ttt ccg aaa ccg cta acc gat gat 547
 Arg Gly Val Asn Ile Ser Asp Ala Phe Pro Lys Pro Leu Thr Asp Asp
 135 140 145
 gtt att cgc gca tct gac tat gtc ata aca atg gga tgt gga gat gtg 595
 Val Ile Arg Ala Ser Asp Tyr Val Ile Thr Met Gly Cys Gly Asp Val
 150 155 160
 tgc cca atg tat cca gga aag cac tat ctc gat tgg gag ctc gct gat 643
 Cys Pro Met Tyr Pro Gly Lys His Tyr Leu Asp Trp Glu Leu Ala Asp
 170 175 180
 ccg tca gat gaa ggt gag gac aag ata cag gaa ata att gag gaa att 691
 Pro Ser Asp Glu Gly Glu Asp Lys Ile Gln Glu Ile Ile Glu Glu Ile
 185 190 195
 gac ggt cga atc cgc gag ctt tgg aaa agc att caa tta tcg caa aac 739
 Asp Gly Arg Ile Arg Glu Leu Trp Lys Ser Ile Gln Leu Ser Gln Asn
 200 205 210
 taggcagtca aaggtctggc acc 762

<210> 124

<211> 213

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

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 Ile Ala Asn Glu Leu Ala Leu Thr Tyr Gln Gly Val Phe Ser Ala Glu
 20 25 30
 Thr Ile Asn Arg Tyr Ile Phe Glu Ser Tyr Val Ser Leu Ala Arg Thr
 35 40 45
 Ala Lys Ile His Thr His Leu Pro Ile Leu Ala Glu Gly Phe Ala Lys
 50 55 60
 Asp Arg Leu His Ala Leu Ala Val Ala Glu Gly Lys Val Ala Ser Pro
 65 70 75 80
 Val Pro Gln Val Leu Phe Ile Cys Val His Asn Ala Gly Arg Ser Gln
 85 90 95
 Ile Ala Ser Ala Leu Leu Ser His Tyr Ala Gly Ser Ser Val Glu Val
 100 105 110
 Arg Ser Ala Gly Ser Leu Pro Ala Ser Glu Ile His Pro Leu Val Leu
 115 120 125
 Glu Ile Leu Ser Glu Arg Gly Val Asn Ile Ser Asp Ala Phe Pro Lys

130

135

140

Pro Leu Thr Asp Asp Val Ile Arg Ala Ser Asp Tyr Val Ile Thr Met
 145 150 155 160

Gly Cys Gly Asp Val Cys Pro Met Tyr Pro Gly Lys His Tyr Leu Asp
 165 170 175

Trp Glu Leu Ala Asp Pro Ser Asp Glu Gly Glu Asp Lys Ile Gln Glu
 180 185 190

Ile Ile Glu Glu Ile Asp Gly Arg Ile Arg Glu Leu Trp Lys Ser Ile
 195 200 205

Gln Leu Ser Gln Asn
 210

<210> 125

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(979)

<223> RXA02205

<400> 125

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caccacacta ctgaggtcat aaggtagtac ggtagatcgg gtg aat gaa gag ata 115
 Val Asn Glu Glu Ile
 1 5

acc ctc cta gcc gca gca gca gat cct gcc gca act gaa aat att ggc 163
 Thr Leu Leu Ala Ala Ala Ala Asp Pro Ala Ala Thr Glu Asn Ile Gly
 10 15 20

tgg gta caa acc att gtg ctc tcc atc gtt caa ggc ctc aca gag ttc 211
 Trp Val Gln Thr Ile Val Leu Ser Ile Val Gln Gly Leu Thr Glu Phe
 25 30 35

ctg ccg atc agc tcc agc gga cac ctc cga atc atc tct gag ctg ttc 259
 Leu Pro Ile Ser Ser Ser Gly His Leu Arg Ile Ile Ser Glu Leu Phe
 40 45 50

tgg ggt gcc gat gcc ggc gcg tcc ttt acc gcc gtg gtt cag ctt ggt 307
 Trp Gly Ala Asp Ala Gly Ala Ser Phe Thr Ala Val Val Gln Leu Gly
 55 60 65

acc gaa gcc gca gtg ctg gtg ttt ttt gcc aag gaa atc tgg caa atc 355
 Thr Glu Ala Ala Val Leu Val Phe Phe Ala Lys Glu Ile Trp Gln Ile
 70 75 80 85

atc aca ggt tgg ttc gct ggc gta ttc aat aag gaa cgc cgc gga ttt 403
 Ile Thr Gly Trp Phe Ala Gly Val Phe Asn Lys Glu Arg Arg Gly Phe

	90	95	100	
gaa tac cgc atg ggc tgg atg atc att gtt gcc acc att ccc gtc gtg				451
Glu Tyr Arg Met Gly Trp Met Ile Ile Val Ala Thr Ile Pro Val Val				
	105	110	115	
atc ttg ggt gtg ttg ggc aag gac ctg atc cgt gag gcg ctg cga aat				499
Ile Leu Gly Val Leu Gly Lys Asp Leu Ile Arg Glu Ala Leu Arg Asn				
	120	125	130	
atg tgg atc act gca tcc gtg ctg atc ctg ttc tcc ctg gtg ttc att				547
Met Trp Ile Thr Ala Ser Val Leu Ile Leu Phe Ser Leu Val Phe Ile				
	135	140	145	
ttg gcc gag aag atg ggc aag aag gaa cgc gac tac gac aaa ctg acc				595
Leu Ala Glu Lys Met Gly Lys Lys Glu Arg Asp Tyr Asp Lys Leu Thr				
	150	155	160	165
atg aaa gat gcc atc atc atg ggt ctt gca cag tgt ctt gcg ctg atc				643
Met Lys Asp Ala Ile Ile Met Gly Leu Ala Gln Cys Leu Ala Leu Ile				
	170	175	180	
cct ggc gtg tct cgc tcc ggc ggc acc atc tct gct ggt ttg ttc ctt				691
Pro Gly Val Ser Arg Ser Gly Gly Thr Ile Ser Ala Gly Leu Phe Leu				
	185	190	195	
ggt ctc aag cgt gaa gta gcc acc aag ttc tcc ttc ctg ctg gca atc				739
Gly Leu Lys Arg Glu Val Ala Thr Lys Phe Ser Phe Leu Leu Ala Ile				
	200	205	210	
cct gca gtg ctt ggc tcc ggt ttg tac tcc ctg cct gac gct ttt gcg				787
Pro Ala Val Leu Gly Ser Gly Leu Tyr Ser Leu Pro Asp Ala Phe Ala				
	215	220	225	
cca agc tcc gga caa gct gcc tcc ggc cta cag ctc acc gtg ggt acc				835
Pro Ser Ser Gly Gln Ala Ala Ser Gly Leu Gln Leu Thr Val Gly Thr				
	230	235	240	245
ctg gtt gcc ttc gta gtt ggc tac att tcc att gcg tgg ctg atg aag				883
Leu Val Ala Phe Val Val Gly Tyr Ile Ser Ile Ala Trp Leu Met Lys				
	250	255	260	
ttc gtg gca aac cac tcc ttc agc tgg ttt gct gca tac cgt att cct				931
Phe Val Ala Asn His Ser Phe Ser Trp Phe Ala Ala Tyr Arg Ile Pro				
	265	270	275	
gca ggt ctg ctc gtg atg ctg ctg ctc gca ctg ggc atg ctc aac cca				979
Ala Gly Leu Leu Val Met Leu Leu Leu Ala Leu Gly Met Leu Asn Pro				
	280	285	290	
taaaattcct gtacatctta aaa				1002

<210> 126

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

Val Asn Glu Glu Ile Thr Leu Leu Ala Ala Ala Asp Pro Ala Ala
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 Thr Glu Asn Ile Gly Trp Val Gln Thr Ile Val Leu Ser Ile Val Gln
 20 25 30
 Gly Leu Thr Glu Phe Leu Pro Ile Ser Ser Ser Gly His Leu Arg Ile
 35 40 45
 Ile Ser Glu Leu Phe Trp Gly Ala Asp Ala Gly Ala Ser Phe Thr Ala
 50 55 60
 Val Val Gln Leu Gly Thr Glu Ala Ala Val Leu Val Phe Phe Ala Lys
 65 70 75 80
 Glu Ile Trp Gln Ile Ile Thr Gly Trp Phe Ala Gly Val Phe Asn Lys
 85 90 95
 Glu Arg Arg Gly Phe Glu Tyr Arg Met Gly Trp Met Ile Ile Val Ala
 100 105 110
 Thr Ile Pro Val Val Ile Leu Gly Val Leu Gly Lys Asp Leu Ile Arg
 115 120 125
 Glu Ala Leu Arg Asn Met Trp Ile Thr Ala Ser Val Leu Ile Leu Phe
 130 135 140
 Ser Leu Val Phe Ile Leu Ala Glu Lys Met Gly Lys Lys Glu Arg Asp
 145 150 155 160
 Tyr Asp Lys Leu Thr Met Lys Asp Ala Ile Ile Met Gly Leu Ala Gln
 165 170 175
 Cys Leu Ala Leu Ile Pro Gly Val Ser Arg Ser Gly Gly Thr Ile Ser
 180 185 190
 Ala Gly Leu Phe Leu Gly Leu Lys Arg Glu Val Ala Thr Lys Phe Ser
 195 200 205
 Phe Leu Leu Ala Ile Pro Ala Val Leu Gly Ser Gly Leu Tyr Ser Leu
 210 215 220
 Pro Asp Ala Phe Ala Pro Ser Ser Gly Gln Ala Ala Ser Gly Leu Gln
 225 230 235 240
 Leu Thr Val Gly Thr Leu Val Ala Phe Val Val Gly Tyr Ile Ser Ile
 245 250 255
 Ala Trp Leu Met Lys Phe Val Ala Asn His Ser Phe Ser Trp Phe Ala
 260 265 270
 Ala Tyr Arg Ile Pro Ala Gly Leu Leu Val Met Leu Leu Leu Ala Leu
 275 280 285
 Gly Met Leu Asn Pro

290

<210> 127
 <211> 975
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(952)
 <223> RXA00900

<400> 127

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tagtgatcgc acgcctggcg caggggcttg gcggcggtgc gtg cgt ggt att gcg 115
                               Val Arg Gly Ile Ala
                               1           5

cgc gcg atc gtg cca gac ctt gaa cgc gga caa aag gct gcg cac gcc 163
Arg Ala Ile Val Pro Asp Leu Glu Arg Gly Gln Lys Ala Ala His Ala
                10                15                20

ttt gca ctg ctg atg att att cag gga att gct ccc gtg gta gct ccg 211
Phe Ala Leu Leu Met Ile Ile Gln Gly Ile Ala Pro Val Val Ala Pro
                25                30                35

ctc att ggt ggt gtg ctg gtc ggg cct ttt ggc tgg cgg gga att ttc 259
Leu Ile Gly Gly Val Leu Val Gly Pro Phe Gly Trp Arg Gly Ile Phe
                40                45                50

tgg gca ctt gca ctg gtg aat ttt gcg cag ctg ctt gtt gct ttg ctg 307
Trp Ala Leu Ala Leu Val Asn Phe Ala Gln Leu Leu Val Ala Leu Leu
                55                60                65

cag att aag gag tcg aag cca gtt gaa gag cgt acc gca gca gga ctt 355
Gln Ile Lys Glu Ser Lys Pro Val Glu Glu Arg Thr Ala Ala Gly Leu
                70                75                80                85

ggc gga atg ctg tcc aac tat gtc ttt gtg ctg aag aat cct caa ttt 403
Gly Gly Met Leu Ser Asn Tyr Val Phe Val Leu Lys Asn Pro Gln Phe
                90                95                100

ttg gca tat gta ttc aca ttg ggg ctg tct ttt ggg gcg atg ttc tcc 451
Leu Ala Tyr Val Phe Thr Leu Gly Leu Ser Phe Gly Ala Met Phe Ser
                105                110                115

tac att tcg gcg tcg ccg ttc gtg ctg cag aat caa atg ggc att ccg 499
Tyr Ile Ser Ala Ser Pro Phe Val Leu Gln Asn Gln Met Gly Ile Pro
                120                125                130

gta ctg ctg tat tcc att att ttc gga gtg aat gct ttt ggt ttg att 547
Val Leu Leu Tyr Ser Ile Ile Phe Gly Val Asn Ala Phe Gly Leu Ile
                135                140                145

gtg ggc gga atg gtc aat agg cga ctt ctg cag cgg att cat cca cac 595

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Val Gly Gly Met Val Asn Arg Arg Leu Leu Gln Arg Ile His Pro His	
150 155 160 165	
cgc atc atg caa act gtg ctg gcc agt ttt act gtg ctg tgt gcg ctt	643
Arg Ile Met Gln Thr Val Leu Ala Ser Phe Thr Val Leu Cys Ala L u	
170 175 180	
ttg ctg att gaa gtg ctg ttt att aat tgg ata ccg ctg ttc ctg ttg	691
Leu Leu Ile Glu Val Leu Phe Ile Asn Trp Ile Pro Leu Phe Leu Leu	
185 190 195	
ctg ctg ttt ctt atc gtt tcc cat att ccg atg gtt atg gct aac gcg	739
Leu Leu Phe Leu Ile Val Ser His Ile Pro Met Val Met Ala Asn Ala	
200 205 210	
aca gct ctg gga act gaa gtg gtg cga agc agg gcg gga tcg ggt tct	787
Thr Ala Leu Gly Thr Glu Val Val Arg Ser Arg Ala Gly Ser Gly Ser	
215 220 225	
gca att ttg ggt ttc gtg caa ttc acg atg ggt gct ttg gtg agt tca	835
Ala Ile Leu Gly Phe Val Gln Phe Thr Met Gly Ala Leu Val Ser Ser	
230 235 240 245	
ctg gtc gga tta ggc tct gat aag gct ttg act atg gga atc gca atg	883
Leu Val Gly Leu Gly Ser Asp Lys Ala Leu Thr Met Gly Ile Ala Met	
250 255 260	
act gct tgt gca ctg ctg gcg tgt ggg tgt gcg tac ctg gca ggt cga	931
Thr Ala Cys Ala Leu Leu Ala Cys Gly Cys Ala Tyr Leu Ala Gly Arg	
265 270 275	
aaa ggt att cca gaa atg aag tagctctagg tggcgtttta agg	975
Lys Gly Ile Pro Glu Met Lys	
280	

<210> 128

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

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Lys Ala Ala His Ala Phe Ala Leu Leu Met Ile Ile Gln Gly Ile Ala	
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Pro Val Val Ala Pro Leu Ile Gly Gly Val Leu Val Gly Pro Phe Gly	
35 40 45	
Trp Arg Gly Ile Phe Trp Ala Leu Ala Leu Val Asn Phe Ala Gln Leu	
50 55 60	
Leu Val Ala Leu Leu Gln Ile Lys Glu Ser Lys Pro Val Glu Glu Arg	
65 70 75 80	

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<210> 129
<211> 537
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(514)  
<223> RXN00901
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<400> 129
ttttaagtat tgggtgctatc ttccggtgct gatggtacct gaatgaaaat ttctaattaa 60

aaataccccc aaatcttcga tatagataca cgagacagtg atg cag aaa aaa caa 115
                Met Gln Lys Lys Gln
                1         5

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cag ctg agc acc gcc ctg att atg gga ttg gca tta ttg tca gcc agc 163
 Gln Leu Ser Thr Ala Leu Ile Met Gly Leu Ala Leu Leu Ser Ala Ser
 10 15 20

tcc gcg cta gcg act gat atg tat ttg ccg gca atg cct ggt att gcg 211
 Ser Ala Leu Ala Thr Asp Met Tyr Leu Pro Ala Met Pro Gly Ile Ala
 25 30 35

gaa gat ttg ggg aca act gca ccg atg gtg cag tta act ctt tct tcc 259
 Glu Asp Leu Gly Thr Thr Ala Pro Met Val Gln Leu Thr Leu Ser Ser
 40 45 50

ttt atg gct gga atg gcg att ggc caa ttg atc att ggt cct ttg tcg 307
 Phe Met Ala Gly Met Ala Ile Gly Gln Leu Ile Ile Gly Pro Leu Ser
 55 60 65

gat caa ttg gga agg aaa ggc ctg ctc gtt gca ggt gcg gtg gct gcg 355
 Asp Gln Leu Gly Arg Lys Gly Leu Leu Val Ala Gly Ala Val Ala Ala
 70 75 80 85

ctg gtc gct agt gtg gtg tgc gcg ctg gcg ccg tcg ata agc gta tta 403
 Leu Val Ala Ser Val Val Cys Ala Leu Ala Pro Ser Ile Ser Val Leu
 90 95 100

gtg atc gca cgc ctg gtg cag ggg ctt ggc ggc ggt gcg tgc gtg gta 451
 Val Ile Ala Arg Leu Val Gln Gly Leu Gly Gly Gly Ala Cys Val Val
 105 110 115

ttg cgc gcg cga tgc tgc cag acc ttg aac gcg gac aaa agg ctg cgc 499
 Leu Arg Ala Arg Ser Cys Gln Thr Leu Asn Ala Asp Lys Arg Leu Arg
 120 125 130

acg cct ttg cac tgc tgatgattat tcagggaatt gct 537
 Thr Pro Leu His Cys
 135

<210> 130

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

Met Gln Lys Lys Gln Gln Leu Ser Thr Ala Leu Ile Met Gly Leu Ala
 1 5 10 15

Leu Leu Ser Ala Ser Ser Ala Leu Ala Thr Asp Met Tyr Leu Pro Ala
 20 25 30

Met Pro Gly Ile Ala Glu Asp Leu Gly Thr Thr Ala Pro Met Val Gln
 35 40 45

Leu Thr Leu Ser Ser Phe Met Ala Gly Met Ala Ile Gly Gln Leu Ile
 50 55 60

Ile Gly Pro Leu Ser Asp Gln Leu Gly Arg Lys Gly Leu Leu Val Ala
 65 70 75 80

Gly	Ala	Val	Ala	Ala	Leu	Val	Ala	Ser	Val	Val	Cys	Ala	Leu	Ala	Pro
				85					90					95	
Ser	Ile	Ser	Val	Leu	Val	Ile	Ala	Arg	Leu	Val	Gln	Gly	Leu	Gly	Gly
			100					105					110		
Gly	Ala	Cys	Val	Val	Leu	Arg	Ala	Arg	Ser	Cys	Gln	Thr	Leu	Asn	Ala
		115					120					125			
Asp	Lys	Arg	Leu	Arg	Thr	Pro	Leu	His	Cys						
	130					135									

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<210> 131
<211> 501
<212> DNA
<213> Corynebacterium glutamicum
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<220> .
<221> CDS
<222> (101)..(478)
<223> FRXA00901
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<400> 131
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agtgatgcag aaaaaacaac agctgagcac cgccctgatt atg gga ttg gca tta 115
Met Gly Leu Ala Leu
1 5

ttg	tca	gcc	agc	tcc	gcg	cta	gcg	act	gat	atg	tat	ttg	ccg	gca	atg	163
Leu	Ser	Ala	Ser	Ser	Ala	Leu	Ala	Thr	Asp	Met	Tyr	Leu	Pro	Ala	Met	
				10				15						20		

cct ggt att gcg gaa gat ttg ggg aca act gca ccg atg gtg cag tta 211
Pro Gly Ile Ala Glu Asp Leu Gly Thr Thr Ala Pro Met Val Gln Leu
25 30 35

act ctt tct tcc ttt atg gct gga atg gcg att ggc caa ttg atc att 259
Thr Leu Ser Ser Phe Met Ala Gly Met Ala Ile Gly Gln Leu Ile Ile
40 45 50

ggt cct ttg tcg gat caa ttg gga agg aaa ggc ctg ctc gtt gca ggt 307
Gly Pro Leu Ser Asp Gln Leu Gly Arg Lys Gly Leu Leu Val Ala Gly
55 60 65

gcg gtg gct gcg ctg gtc gct agt gtg gtg tgc gcg ctg gcg ccg tcg 355
Ala Val Ala Ala Leu Val Ala Ser Val Val Cys Ala Leu Ala Pro Ser
70 75 80 85

ata agc gta tta gtg atc gca cgc ctg gtg cag ggg ctt ggc ggc ggt 403
Ile Ser Val Leu Val Ile Ala Arg Leu Val Gln Gly Leu Gly Gly Gly
90 95 100

gcg tgc gtg gta ttg cgc gcg cga tgc tgc cag acc ttg aac gcg gac 451
Ala Cys Val Val Leu Arg Ala Arg Ser Cys Gln Thr Leu Asn Ala Asp

105 110 115
 aaa agg ctg cgc acg cct ttg cac tgc tgatgattat tcaggggaatt 498
 Lys Arg Leu Arg Thr Pro Leu His Cys
 120 125

gct 501

<210> 132
 <211> 126
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 132
 Met Gly Leu Ala Leu Leu Ser Ala Ser Ser Ala Leu Ala Thr Asp Met
 1 5 10 15
 Tyr Leu Pro Ala Met Pro Gly Ile Ala Glu Asp Leu Gly Thr Thr Ala
 20 25 30
 Pro Met Val Gln Leu Thr Leu Ser Ser Phe Met Ala Gly Met Ala Ile
 35 40 45
 Gly Gln Leu Ile Ile Gly Pro Leu Ser Asp Gln Leu Gly Arg Lys Gly
 50 55 60
 Leu Leu Val Ala Gly Ala Val Ala Ala Leu Val Ala Ser Val Val Cys
 65 70 75 80
 Ala Leu Ala Pro Ser Ile Ser Val Leu Val Ile Ala Arg Leu Val Gln
 85 90 95
 Gly Leu Gly Gly Gly Ala Cys Val Val Leu Arg Ala Arg Ser Cys Gln
 100 105 110
 Thr Leu Asn Ala Asp Lys Arg Leu Arg Thr Pro Leu His Cys
 115 120 125

<210> 133
 <211> 1299
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1276)
 <223> RXA00289

<400> 133
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 accccattaa acagcccgat tcaagaaagg cttcgcagcc atg agc acc acc acc 115
 Met Ser Thr Thr Thr
 1 5

gcg ccc gaa gca cgg ttt cct gtc gtc cct ttg acc gcc atg agt ttc Ala Pro Glu Ala Arg Phe Pro Val Val Pro Leu Thr Ala Met Ser Phe 10 15 20	163
gcg gca ttt gtt tat gtc acg ttc gag atg ttt gca gtt ggc ctc atc Ala Ala Phe Val Tyr Val Thr Phe Glu Met Phe Ala Val Gly Leu Ile 25 30 35	211
aag ccg atg gcc agc gat ctt gga gtg tca gaa tcc agc atc ggc ctg Lys Pro Met Ala Ser Asp Leu Gly Val Ser Glu Ser Ser Ile Gly Leu 40 45 50	259
ttg atg act gtg tat gcg act gtc gtt gcc gtg gtg acg atc cct gcc Leu Met Thr Val Tyr Ala Thr Val Val Ala Val Val Thr Ile Pro Ala 55 60 65	307
atg ttg tgg gtt tct cga ttt aac aag cgc aca gtt ttc ctg att act Met Leu Trp Val Ser Arg Phe Asn Lys Arg Thr Val Phe Leu Ile Thr 70 75 80 85	355
ctg gca ttt ttg gcc acg ggc att gtt gtt cag gca ctg acc gtt aat Leu Ala Phe Leu Ala Thr Gly Ile Val Val Gln Ala Leu Thr Val Asn 90 95 100	403
tat gga atg cta gcc atc ggc cgc act atc gca gca ttg act cac ggg Tyr Gly Met Leu Ala Ile Gly Arg Thr Ile Ala Ala Leu Thr His Gly 105 110 115	451
gtg ttt tgg gca ctt gtt ggg cca atg gca gcg cgt atg tcc cca ggt Val Phe Trp Ala Leu Val Gly Pro Met Ala Ala Arg Met Ser Pro Gly 120 125 130	499
cac act ggt cgt gca gta ggc gtt gtg tcg att gga tca acc atg gcg His Thr Gly Arg Ala Val Gly Val Val Ser Ile Gly Ser Thr Met Ala 135 140 145	547
ctg gtc gtt ggt tct ccg ctg gca aca tgg atc ggt gaa ctc atc gga Leu Val Val Gly Ser Pro Leu Ala Thr Trp Ile Gly Glu Leu Ile Gly 150 155 160 165	595
tgg cgt cct gcc acc tgg att ctt ggt gcg ctg acc att gcg gcc gtg Trp Arg Pro Ala Thr Trp Ile Leu Gly Ala Leu Thr Ile Ala Ala Val 170 175 180	643
gct gta ctc att cca acc gtt cca tca ctg cca cca ctt cca gac acg Ala Val Leu Ile Pro Thr Val Pro Ser Leu Pro Pro Leu Pro Asp Thr 185 190 195	691
gaa tca gag tcc aaa gaa aag aaa tcc ctt cca tgg ggt ctc att tcc Glu Ser Glu Ser Lys Glu Lys Lys Ser Leu Pro Trp Gly Leu Ile Ser 200 205 210	739
ctg gtc att ttc ctt ctc ctt gcc gtc acc ggt gtt ttt gct gcc tac Leu Val Ile Phe Leu Leu Leu Ala Val Thr Gly Val Phe Ala Ala Tyr 215 220 225	787
acc tac ctt ggc ctc atc atc gct gaa aca gca ggg gac agc ttc gtg	835

Thr	Tyr	Leu	Gly	Leu	Ile	Ile	Ala	Glu	Thr	Ala	Gly	Asp	Ser	Phe	Val	
230					235					240					245	
tcc	att	ggc	ttg	ttc	gcc	ttc	ggt	gca	ctc	gga	ctc	att	ggc	gtg	aca	883
Ser	Ile	Gly	Leu	Phe	Ala	Ph	Gly	Ala	Leu	Gly	Leu	Ile	Gly	Val	Thr	
				250					255					260		
gtg	gca	acc	cga	act	gtg	gat	caa	cgc	atg	ctg	cgt	gga	agt	gtt	cac	931
Val	Ala	Thr	Arg	Thr	Val	Asp	Gln	Arg	Met	Leu	Arg	Gly	Ser	Val	His	
			265					270					275			
acc	acc	act	ttg	ttt	gtc	att	gct	gca	att	ctc	gga	cag	atc	gca	ttc	979
Thr	Thr	Thr	Leu	Phe	Val	Ile	Ala	Ala	Ile	Leu	Gly	Gln	Ile	Ala	Phe	
			280				285					290				
gga	tta	gag	ggc	aca	cta	gcc	gta	gta	gct	atc	ttc	ctt	gca	gtc	acc	1027
Gly	Leu	Glu	Gly	Thr	Leu	Ala	Val	Val	Ala	Ile	Phe	Leu	Ala	Val	Thr	
	295					300					305					
gtg	ttt	ggt	gga	gca	tac	ggc	gct	ctc	cca	acc	ctg	gga	acc	acc	atc	1075
Val	Phe	Gly	Gly	Ala	Tyr	Gly	Ala	Leu	Pro	Thr	Leu	Gly	Thr	Thr	Ile	
310					315				320						325	
ttc	ctc	cat	gcg	ggt	cgc	gac	cac	cca	gat	act	gca	tcc	tcc	att	tat	1123
Phe	Leu	His	Ala	Gly	Arg	Asp	His	Pro	Asp	Thr	Ala	Ser	Ser	Ile	Tyr	
				330					335					340		
gtg	gtc	act	tac	caa	gtg	ggt	atc	gcg	tct	ggc	gcg	gca	ctt	ggc	gcg	1171
Val	Val	Thr	Tyr	Gln	Val	Gly	Ile	Ala	Ser	Gly	Ala	Ala	Leu	Gly	Ala	
			345					350					355			
atg	gct	gtg	gat	gcc	gat	tgg	gtt	gct	ggc	act	ttg	tgg	atc	atg	gct	1219
Met	Ala	Val	Asp	Ala	Asp	Trp	Val	Ala	Gly	Thr	Leu	Trp	Ile	Met	Ala	
			360				365					370				
gga	ctg	tca	ttg	gct	tcc	acg	ttg	gcc	ttg	gcg	ctg	tgg	tcc	cgc	ccg	1267
Gly	Leu	Ser	Leu	Ala	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Trp	Ser	Arg	Pro	
	375					380					385					
cta	ctg	aag	tagcagccca	aattcagccc	act											1299
Leu	Leu	Lys														
390																

<210> 134

<211> 392

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

Met	Ser	Thr	Thr	Thr	Ala	Pro	Glu	Ala	Arg	Phe	Pro	Val	Val	Pro	Leu	
1					5				10					15		

Thr	Ala	Met	Ser	Phe	Ala	Ala	Phe	Val	Tyr	Val	Thr	Phe	Glu	Met	Phe	
			20					25					30			

Ala	Val	Gly	Leu	Ile	Lys	Pro	Met	Ala	Ser	Asp	Leu	Gly	Val	Ser	Glu	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

35	40	45
Ser Ser Ile Gly Leu Leu Met Thr Val Tyr Ala Thr Val Val Ala Val 50 55 60		
Val Thr Ile Pro Ala Met Leu Trp Val Ser Arg Phe Asn Lys Arg Thr 65 70 75 80		
Val Phe Leu Ile Thr Leu Ala Phe Leu Ala Thr Gly Ile Val Val Gln 85 90 95		
Ala Leu Thr Val Asn Tyr Gly Met Leu Ala Ile Gly Arg Thr Ile Ala 100 105 110		
Ala Leu Thr His Gly Val Phe Trp Ala Leu Val Gly Pro Met Ala Ala 115 120 125		
Arg Met Ser Pro Gly His Thr Gly Arg Ala Val Gly Val Val Ser Ile 130 135 140		
Gly Ser Thr Met Ala Leu Val Val Gly Ser Pro Leu Ala Thr Trp Ile 145 150 155 160		
Gly Glu Leu Ile Gly Trp Arg Pro Ala Thr Trp Ile Leu Gly Ala Leu 165 170 175		
Thr Ile Ala Ala Val Ala Val Leu Ile Pro Thr Val Pro Ser Leu Pro 180 185 190		
Pro Leu Pro Asp Thr Glu Ser Glu Ser Lys Glu Lys Lys Ser Leu Pro 195 200 205		
Trp Gly Leu Ile Ser Leu Val Ile Phe Leu Leu Leu Ala Val Thr Gly 210 215 220		
Val Phe Ala Ala Tyr Thr Tyr Leu Gly Leu Ile Ile Ala Glu Thr Ala 225 230 235 240		
Gly Asp Ser Phe Val Ser Ile Gly Leu Phe Ala Phe Gly Ala Leu Gly 245 250 255		
Leu Ile Gly Val Thr Val Ala Thr Arg Thr Val Asp Gln Arg Met Leu 260 265 270		
Arg Gly Ser Val His Thr Thr Thr Leu Phe Val Ile Ala Ala Ile Leu 275 280 285		
Gly Gln Ile Ala Phe Gly Leu Glu Gly Thr Leu Ala Val Val Ala Ile 290 295 300		
Phe Leu Ala Val Thr Val Phe Gly Gly Ala Tyr Gly Ala Leu Pro Thr 305 310 315 320		
Leu Gly Thr Thr Ile Phe Leu His Ala Gly Arg Asp His Pro Asp Thr 325 330 335		
Ala Ser Ser Ile Tyr Val Val Thr Tyr Gln Val Gly Ile Ala Ser Gly		

340	345	350	
Ala Ala Leu Gly Ala Met Ala Val Asp Ala Asp Trp Val Ala Gly Thr			
355	360	365	
Leu Trp Ile Met Ala Gly Leu Ser Leu Ala Ser Thr Leu Ala Leu Ala			
370	375	380	
Leu Trp Ser Arg Pro Leu Leu Lys			
385	390		
<210> 135			
<211> 420			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(397)			
<223> RXN01984			
<400> 135			
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caatagtgcc ggtgagggag ctgtccgata ttgtgcttac	atg cac gaa tct gga	115	
	Met His Glu Ser Gly		
	1 5		
aaa aat cct gtc aag gtt gtc gac tcg cag gca cca caa gga cgc ggt		163	
Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala Pro Gln Gly Arg Gly			
10 15 20			
ggg cat atc ggc gga cat atc aaa cgc cgc ccg att cct agg caa acg		211	
Gly His Ile Gly Gly His Ile Lys Arg Arg Pro Ile Pro Arg Gln Thr			
25 30 35			
gaa att tcc gag gtt cgt cga tat atc gtc atg act gcc ctc gca ctc		259	
Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met Thr Ala Leu Ala Leu			
40 45 50			
ggg ggc ttc gcc atc ggt gtg acg gaa ttt gtc tcc atg ggt ctg ctc		307	
Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val Ser Met Gly Leu Leu			
55 60 65			
agc gcg atc gcc tcc gac ttt gag atc tcc gaa gac caa gcc gga cac		355	
Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu Asp Gln Ala Gly His			
70 75 80 85			
atc atc acc atc tac gcc ctc gcg tgg ttg tgg gtg ccc cgc		397	
Ile Ile Thr Ile Tyr Ala Leu Ala Trp Leu Trp Val Pro Arg			
90 95			
tgatcacagc gtttaccggc aaa		420	

<210> 136

<211> 99
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 136

M t His Glu Ser Gly Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala
 1 5 10 15

Pro Gln Gly Arg Gly Gly His Ile Gly Gly His Ile Lys Arg Arg Pro
 20 25 30

Ile Pro Arg Gln Thr Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met
 35 40 45

Thr Ala Leu Ala Leu Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val
 50 55 60

Ser Met Gly Leu Leu Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu
 65 70 75 80

Asp Gln Ala Gly His Ile Ile Thr Ile Tyr Ala Leu Ala Trp Leu Trp
 85 90 95

Val Pro Arg

<210> 137
 <211> 379
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(379)

<223> FRXA01984

<400> 137

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caatagtgcc ggtgaggag ctgtccgata ttgtgcttac atg cac gaa tct gga 115
 Met His Glu Ser Gly
 1 5

aaa aat cct gtc aag gtt gtc gac tcg cag gca cca caa gga cgc ggt 163
 Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala Pro Gln Gly Arg Gly
 10 15 20

ggg cat atc ggc gga cat atc aaa cgc cgc ccg att cct agg caa acg 211
 Gly His Ile Gly Gly His Ile Lys Arg Arg Pro Ile Pro Arg Gln Thr
 25 30 35

gaa att tcc gag gtt cgt cga tat atc gtc atg act gcc ctc gca ctc 259
 Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met Thr Ala Leu Ala Leu
 40 45 50

ggg ggc ttc gcc atc ggt gtg acg gaa ttt gtc tcc atg ggt ctg ctc 307

Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val Ser Met Gly Leu Leu
 55 60 65
 agc gcg atc gcc tcc gac ttt gag atc tcc gaa gac caa gcc gga cac 355
 Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu Asp Gln Ala Gly His
 70 75 80 85
 atc atc acc atc tac gcc ctc gcg 379
 Ile Ile Thr Ile Tyr Ala Leu Ala
 90

<210> 138
 <211> 93
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 138
 Met His Glu Ser Gly Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala
 1 5 10 15
 Pro Gln Gly Arg Gly Gly His Ile Gly Gly His Ile Lys Arg Arg Pro
 20 25 30
 Ile Pro Arg Gln Thr Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met
 35 40 45
 Thr Ala Leu Ala Leu Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val
 50 55 60
 Ser Met Gly Leu Leu Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu
 65 70 75 80
 Asp Gln Ala Gly His Ile Ile Thr Ile Tyr Ala Leu Ala
 85 90

<210> 139
 <211> 735
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(712)
 <223> RXA00109

<400> 139
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 cggcgaaaag gaagtttcgc ccatctatga gaggttgaat gtg gct tca gag aag 115
 Val Ala Ser Glu Lys
 1 5
 aat cta aaa ttg cgt acc ttg gcg gca gct gct ggg gtg ttg ggc gtt 163
 Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Gly Val Leu Gly Val
 10 15 20

ggc gcg atg tcg atg ctc gtg gct ccg cag gct gct gcc cat gat gtg 211
 Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala Ala Ala His Asp Val
 25 30 35

gtg gtg gat tct aat cct gaa aat ggc agt gtc gtt gat gag ttc ccg 259
 Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val Val Asp Glu Phe Pro
 40 45 50

gag acc att gag ttg gag ttt tcc ggt att cct cag gat ctg ttc aca 307
 Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro Gln Asp Leu Phe Thr
 55 60 65

aca gtt gca ttg agc aat gcg gat tcc gga gag gtg tta act tct gga 355
 Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu Val Leu Thr Ser Gly
 70 75 80 85

act cct cag ctt gag ggg cag cac ttg agc tat gaa gtg cca tct gat 403
 Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr Glu Val Pro Ser Asp
 90 95 100

gtg cag acg gga gct ggt aac tac att ttg ggt ttc cag atc act tct 451
 Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly Phe Gln Ile Thr Ser
 105 110 115

tct gat ggt cac gct act aaa ggt tca atc tct ttt gag gtg aca ggc 499
 Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser Phe Glu Val Thr Gly
 120 125 130

tct gct gaa acg aca aca gag aca aca gca gag acg aca act gag tca 547
 Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu Thr Thr Thr Glu Ser
 135 140 145

gca gca acc act gac acc tca gag acc acc gaa gca gag aca act gaa 595
 Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu Ala Glu Thr Thr Glu
 150 155 160 165

act gct gat gaa act tct gga att cct gcg ccg tgg aat tgg gtt ttg 643
 Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro Trp Asn Trp Val Leu
 170 175 180

agc atc gtg gcg gtg ctt gtt gtt gca agt gcc atc gtc atg atg att 691
 Ser Ile Val Ala Val Leu Val Val Ala Ser Ala Ile Val Met Met Ile
 185 190 195

gca aag aat cgt aac cag aaa taagagggtt tattcaccat gaa 735
 Ala Lys Asn Arg Asn Gln Lys
 200

<210> 140

<211> 204

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 140

Val Ala Ser Glu Lys Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Ala

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Gly Val Leu Gly Val Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala	20	25	30
Ala Ala His Asp Val Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val	35	40	45
Val Asp Glu Phe Pro Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro	50	55	60
Gln Asp Leu Phe Thr Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu	65	70	75
Val Leu Thr Ser Gly Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr	85	90	95
Glu Val Pro Ser Asp Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly	100	105	110
Phe Gln Ile Thr Ser Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser	115	120	125
Phe Glu Val Thr Gly Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu	130	135	140
Thr Thr Thr Glu Ser Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu	145	150	155
Ala Glu Thr Thr Glu Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro	165	170	175
Trp Asn Trp Val Leu Ser Ile Val Ala Val Leu Val Val Ala Ser Ala	180	185	190
Ile Val Met Met Ile Ala Lys Asn Arg Asn Gln Lys	195	200	

<210> 141

<211> 735

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(712)

<223> RXA00109

<400> 141

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cggcgaaaag gaagtttcgc ccatctatga gaggttgaat gtg gct tca gag aag 115
 Val Ala Ser Glu Lys
 1 5

aat cta aaa ttg cgt acc ttg gcg gca gct gct ggg gtg ttg ggc gtt 163

Asn	Leu	Lys	Leu	Arg	Thr	Leu	Ala	Ala	Ala	Ala	Gly	Val	Leu	Gly	Val		
				10					15					20			
ggc	gcg	atg	tcg	atg	ctc	gtg	gct	ccg	cag	gct	gct	gcc	cat	gat	gtg	211	
Gly	Ala	Met	Ser	Met	Leu	Val	Ala	Pro	Gln	Ala	Ala	Ala	His	Asp	Val		
			25					30					35				
gtg	gtg	gat	tct	aat	cct	gaa	aat	ggc	agt	gtc	gtt	gat	gag	ttc	ccg	259	
Val	Val	Asp	Ser	Asn	Pro	Glu	Asn	Gly	Ser	Val	Val	Asp	Glu	Phe	Pro		
		40					45					50					
gag	acc	att	gag	ttg	gag	ttt	tcc	ggc	att	cct	cag	gat	ctg	ttc	aca	307	
Glu	Thr	Ile	Glu	Leu	Glu	Phe	Ser	Gly	Ile	Pro	Gln	Asp	Leu	Phe	Thr		
	55					60					65						
aca	gtt	gca	ttg	agc	aat	gcg	gat	tcc	gga	gag	gtg	tta	act	tct	gga	355	
Thr	Val	Ala	Leu	Ser	Asn	Ala	Asp	Ser	Gly	Glu	Val	Leu	Thr	Ser	Gly		
	70				75				80						85		
act	cct	cag	ctt	gag	ggg	cag	cac	ttg	agc	tat	gaa	gtg	cca	tct	gat	403	
Thr	Pro	Gln	Leu	Glu	Gly	Gln	His	Leu	Ser	Tyr	Glu	Val	Pro	Ser	Asp		
			90					95						100			
gtg	cag	acg	gga	gct	ggc	aac	tac	att	ttg	ggc	ttc	cag	atc	act	tct	451	
Val	Gln	Thr	Gly	Ala	Gly	Asn	Tyr	Ile	Leu	Gly	Phe	Gln	Ile	Thr	Ser		
			105					110					115				
tct	gat	ggc	cac	gct	act	aaa	ggc	tca	atc	tct	ttt	gag	gtg	aca	ggc	499	
Ser	Asp	Gly	His	Ala	Thr	Lys	Gly	Ser	Ile	Ser	Phe	Glu	Val	Thr	Gly		
		120					125					130					
tct	gct	gaa	acg	aca	aca	gag	aca	aca	gca	gag	acg	aca	act	gag	tca	547	
Ser	Ala	Glu	Thr	Thr	Thr	Glu	Thr	Thr	Ala	Glu	Thr	Thr	Thr	Glu	Ser		
		135				140					145						
gca	gca	acc	act	gac	acc	tca	gag	acc	acc	gaa	gca	gag	aca	act	gaa	595	
Ala	Ala	Thr	Thr	Asp	Thr	Ser	Glu	Thr	Thr	Glu	Ala	Glu	Thr	Thr	Glu		
		150			155					160					165		
act	gct	gat	gaa	act	tct	gga	att	cct	gcg	ccg	tgg	aat	tgg	gtt	ttg	643	
Thr	Ala	Asp	Glu	Thr	Ser	Gly	Ile	Pro	Ala	Pro	Trp	Asn	Trp	Val	Leu		
			170					175						180			
agc	atc	gtg	gcg	gtg	ctt	gtt	gtt	gca	agt	gcc	atc	gtc	atg	atg	att	691	
Ser	Ile	Val	Ala	Val	Leu	Val	Val	Ala	Ser	Ala	Ile	Val	Met	Met	Ile		
			185					190					195				
gca	aag	aat	cgt	aac	cag	aaa	taagagggtt	tattcaccat	gaa							735	
Ala	Lys	Asn	Arg	Asn	Gln	Lys											
			200														

<210> 142

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 142

Val Ala Ser Glu Lys Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Ala
 1 5 10 15

Gly Val Leu Gly Val Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala
 20 25 30

Ala Ala His Asp Val Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val
 35 40 45

Val Asp Glu Phe Pro Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro
 50 55 60

Gln Asp Leu Phe Thr Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu
 65 70 75 80

Val Leu Thr Ser Gly Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr
 85 90 95

Glu Val Pro Ser Asp Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly
 100 105 110

Phe Gln Ile Thr Ser Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser
 115 120 125

Phe Glu Val Thr Gly Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu
 130 135 140

Thr Thr Thr Glu Ser Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu
 145 150 155 160

Ala Glu Thr Thr Glu Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro
 165 170 175

Trp Asn Trp Val Leu Ser Ile Val Ala Val Leu Val Val Ala Ser Ala
 180 185 190

Ile Val Met Met Ile Ala Lys Asn Arg Asn Gln Lys
 195 200

<210> 143

<211> 864

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(841)

<223> RXA00996

<400> 143

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acctctatct tgcacctgat ctggcgtaga ctcataagtt atg agc acc gta acg 115
 Met Ser Thr Val Thr
 1 5

gca gtg cag gtc aac ggc cta aaa gtt tcc ata tcg tcc ggt ttt tca	163
Ala Val Gln Val Asn Gly Leu Lys Val Ser Ile Ser Ser Gly Phe Ser	
10 15 20	
cgc aag aaa aca aaa acg atc ttg cat gat ctc gat ttc acc gta gag	211
Arg Lys Lys Thr Lys Thr Ile Leu His Asp Leu Asp Phe Thr Val Glu	
25 30 35	
acc gga aag atc acg gga ttg ctg ggg cca tcg ggc agc ggc aag aca	259
Thr Gly Lys Ile Thr Gly Leu Leu Gly Pro Ser Gly Ser Gly Lys Thr	
40 45 50	
act ttg atg cgc gcg att gtg gga gtg caa aac ttc gac ggc acc ctt	307
Thr Leu Met Arg Ala Ile Val Gly Val Gln Asn Phe Asp Gly Thr Leu	
55 60 65	
gag gtg ttt gat cag ccc gca ggt gct gcc tct ctg cgc ggg aaa atc	355
Glu Val Phe Asp Gln Pro Ala Gly Ala Ala Ser Leu Arg Gly Lys Ile	
70 75 80 85	
ggc tat gtc acc caa aac gcc agc gta tat cac gat ctg tcg gtg ata	403
Gly Tyr Val Thr Gln Asn Ala Ser Val Tyr His Asp Leu Ser Val Ile	
90 95 100	
gaa aac ctc aag tat ttc ggg gct ctg gct aaa gga acc tcc act cca	451
Glu Asn Leu Lys Tyr Phe Gly Ala Leu Ala Lys Gly Thr Ser Thr Pro	
105 110 115	
cgc acc ccg gaa aag att ctg gag gtc tta gac atc gca gat ctt gct	499
Arg Thr Pro Glu Lys Ile Leu Glu Val Leu Asp Ile Ala Asp Leu Ala	
120 125 130	
caa cgc caa gta tca aca cta tct ggt ggg cag cgc ggc cga gtc tcc	547
Gln Arg Gln Val Ser Thr Leu Ser Gly Gly Gln Arg Gly Arg Val Ser	
135 140 145	
ctt gga tgt gcg ctt att gcc tca cca gaa ctc ttg gtg atg gat gag	595
Leu Gly Cys Ala Leu Ile Ala Ser Pro Glu Leu Leu Val Met Asp Glu	
150 155 160 165	
cca acc gtg ggt ttg gat ccc att acc cgg caa gca ctg tgg gaa gag	643
Pro Thr Val Gly Leu Asp Pro Ile Thr Arg Gln Ala Leu Trp Glu Glu	
170 175 180	
ttc acc acc atc gca aaa gca ggt gct gga gtg gtt atc tcc agt cac	691
Phe Thr Thr Ile Ala Lys Ala Gly Ala Gly Val Val Ile Ser Ser His	
185 190 195	
gtg ttg gag gaa gcc gcg cgg tgc gac aac ctc att ttg ttg cgt gat	739
Val Leu Glu Glu Ala Ala Arg Cys Asp Asn Leu Ile Leu Leu Arg Asp	
200 205 210	
ggt cgg atc atc tgg agg gga aca ccc aca cgc ctt cta gaa gat aca	787
Gly Arg Ile Ile Trp Arg Gly Thr Pro Thr Arg Leu Leu Glu Asp Thr	
215 220 225	

ggc aaa agc tca tac gaa gat gct ttc ttg gct gcc att gac ggg gta 835
 Gly Lys Ser Ser Tyr Glu Asp Ala Phe Leu Ala Ala Ile Asp Gly Val
 230 235 240 245

agg tca tgaaccctca ctatctgctt gcc 864
 Arg Ser

<210> 144

<211> 247

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Met Ser Thr Val Thr Ala Val Gln Val Asn Gly Leu Lys Val Ser Ile
 1 5 10 15

Ser Ser Gly Phe Ser Arg Lys Lys Thr Lys Thr Ile Leu His Asp Leu
 20 25 30

Asp Phe Thr Val Glu Thr Gly Lys Ile Thr Gly Leu Leu Gly Pro Ser
 35 40 45

Gly Ser Gly Lys Thr Thr Leu Met Arg Ala Ile Val Gly Val Gln Asn
 50 55 60

Phe Asp Gly Thr Leu Glu Val Phe Asp Gln Pro Ala Gly Ala Ala Ser
 65 70 75 80

Leu Arg Gly Lys Ile Gly Tyr Val Thr Gln Asn Ala Ser Val Tyr His
 85 90 95

Asp Leu Ser Val Ile Glu Asn Leu Lys Tyr Phe Gly Ala Leu Ala Lys
 100 105 110

Gly Thr Ser Thr Pro Arg Thr Pro Glu Lys Ile Leu Glu Val Leu Asp
 115 120 125

Ile Ala Asp Leu Ala Gln Arg Gln Val Ser Thr Leu Ser Gly Gly Gln
 130 135 140

Arg Gly Arg Val Ser Leu Gly Cys Ala Leu Ile Ala Ser Pro Glu Leu
 145 150 155 160

Leu Val Met Asp Glu Pro Thr Val Gly Leu Asp Pro Ile Thr Arg Gln
 165 170 175

Ala Leu Trp Glu Glu Phe Thr Thr Ile Ala Lys Ala Gly Ala Gly Val
 180 185 190

Val Ile Ser Ser His Val Leu Glu Glu Ala Ala Arg Cys Asp Asn Leu
 195 200 205

Ile Leu Leu Arg Asp Gly Arg Ile Ile Trp Arg Gly Thr Pro Thr Arg
 210 215 220

Leu Leu Glu Asp Thr Gly Lys Ser Ser Tyr Glu Asp Ala Phe Leu Ala
 225 230 235 240

Ala Ile Asp Gly Val Arg Ser
 245

<210> 145

<211> 2463

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2440)

<223> RXN00829

<400> 145

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caagcgcgaa caggcctatg caaacggtac gatatgacac atg caa aaa gct gat 115
 Met Gln Lys Ala Asp
 1 5

tcc cat gat tgg att tcg gtc cac ggt gcg aat gaa aac aac ctc aaa 163
 Ser His Asp Trp Ile Ser Val His Gly Ala Asn Glu Asn Asn Leu Lys
 10 15 20

aat gtg tcg gtg cgc atc cct aaa agg cgt ctc acc gtg ttc acg ggt 211
 Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu Thr Val Phe Thr Gly
 25 30 35

gtg tcg gga tct ggc aag tcc tcg ctg gtg ttc ggc aca att gct gcg 259
 Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe Gly Thr Ile Ala Ala
 40 45 50

gaa tca cgc cgg ttg atc aac gaa acc tat agc act ttt gtg caa ggt 307
 Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser Thr Phe Val Gln Gly
 55 60 65

ttc atg ccg tcg atg gca agg ccc gat gtt gac cat ttg gaa ggc atc 355
 Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp His Leu Glu Gly Ile
 70 75 80 85

acc acg gcg atc atc gtc gat cag gag cag atg ggc gca aac cca cgg 403
 Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met Gly Ala Asn Pro Arg
 90 95 100

tct acg gtg ggt acc gca act gat gcc acc gcg atg ttg cgc att ttg 451
 Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala Met Leu Arg Ile Leu
 105 110 115

ttt tcc cga atc gcg gaa cct aac gcg ggt ggc ccg gga gct tat tcc 499
 Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly Pro Gly Ala Tyr Ser
 120 125 130

ttc aac gtc ccc tct gtt tcc gca tcc ggc gcc atc acg gtg gaa aag 547

Phe	Asn	Val	Pro	Ser	Val	Ser	Ala	Ser	Gly	Ala	Ile	Thr	Val	Glu	Lys	
135						140					145					
ggc gga aac acc aag cgg gag aaa gct acc ttc aaa cgc acg ggt ggc	595															
Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe Lys Arg Thr Gly Gly																
150 155 160 165																
atg tgc cca gcg tgc gag ggc atg ggc agg gcc tca gac atc gac ctc	643															
Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala Ser Asp Ile Asp Leu																
170 175 180																
aaa gag ctt ttc gac gcc tcc ctc tcc ctc aac gac ggc gcc ctg acc	691															
Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn Asp Gly Ala Leu Thr																
185 190 195																
atc ccc ggt tac acc cca ggt gga tgg agt tat cgg atg tat tca gaa	739															
Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr Arg Met Tyr Ser Glu																
200 205 210																
tcg ggc ctt ttt gat gct gcc aag ccg att aag gat ttc acc gag gaa	787															
Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys Asp Phe Thr Glu Glu																
215 220 225																
gaa cgc cac aac ttc ctt tat ctt gag ccc acc aag atg aag atc gct	835															
Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr Lys Met Lys Ile Ala																
230 235 240 245																
ggc atc aac atg acc tat gag ggt ctt atc ccc cgc att cag aaa tcc	883															
Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro Arg Ile Gln Lys Ser																
250 255 260																
atg ttg tct aag gat cgc gaa ggc atg cag aag cat att cgt gcg ttc	931															
Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys His Ile Arg Ala Phe																
265 270 275																
gtg gat cga gcg gtt acc ttc att cct tgc cct gcg tgt ggt gga act	979															
Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro Ala Cys Gly Gly Thr																
280 285 290																
cga tta gcg cca cat gcc ttg gag tcc aag atc aat ggc aaa aac atc	1027															
Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile Asn Gly Lys Asn Ile																
295 300 305																
gct gag ttg tgc gcg atg gag gtc cgt gat ttg gcc aag tgg atc aaa	1075															
Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu Ala Lys Trp Ile Lys																
310 315 320 325																
acg gtg gaa gcc ccc tcg gtt gct ccc ctg ctc acc gca ctg act gaa	1123															
Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu Thr Ala Leu Thr Glu																
330 335 340																
acc ctg gat aac ttc gtg gag atc ggt ttg ggc tat atc caa ctc gat	1171															
Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly Tyr Ile Gln Leu Asp																
345 350 355																
cgc ccc gct ggc acg ttg tct ggt ggt gag gca cag cgc acc aag atg	1219															
Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala Gln Arg Thr Lys Met																

360	365	370	
atc cgc cat ttg ggc tct gca ttg act gac gtc acc tat gtt ttt gat Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val Thr Tyr Val Phe Asp 375 380 385			1267
gaa ccc acc gcc ggt ttg cac gcc tac gac att gaa cgc atg aac aag Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile Glu Arg Met Asn Lys 390 395 400 405			1315
ttg ctg ctc gat ctt cgc gat aaa ggc aat acc gtt tta gtc gtg gag Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr Val Leu Val Val Glu 410 415 420			1363
cac aag ccg gaa acc atc gcc att gca gat cat gtg gtg gac ctt ggg His Lys Pro Glu Thr Ile Ala Ile Ala Asp His Val Val Asp Leu Gly 425 430 435			1411
cca ggt gca ggc gcg ggt gga ggt gaa att cgg ttt gag ggg agc gtc Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg Phe Glu Gly Ser Val 440 445 450			1459
gac aag ctt aaa gac agc gac acc gtg act ggc ctc cat ttt aat gac Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly Leu His Phe Asn Asp 455 460 465			1507
cgg gcg tca ttg aag gaa tcc gtg cgt gcg ccg cat ggc gcc ctg gag Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro His Gly Ala Leu Glu 470 475 480 485			1555
atc cgc ggg gcc gat cga aat aat ttg aac aat gtg gat gtc gat att Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn Val Asp Val Asp Ile 490 495 500			1603
ccg ctc ggc gtg ttc acg gcg att tcc ggc gtt gca ggt tcg ggt aag Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val Ala Gly Ser Gly Lys 505 510 515			1651
tcc tcg ttg att cat gag att ccg cgt gat gag tcg gtt gtg ttt gtc Ser Ser Leu Ile His Glu Ile Pro Arg Asp Glu Ser Val Val Phe Val 520 525 530			1699
gat caa acc gca atc cac ggt tct aat cgt tcc aat cct gcg aca tat Asp Gln Thr Ala Ile His Gly Ser Asn Arg Ser Asn Pro Ala Thr Tyr 535 540 545			1747
aca ggc atg ctg gat tcg att cgc aag gct ttt gcc aag gcc aat gat Thr Gly Met Leu Asp Ser Ile Arg Lys Ala Phe Ala Lys Ala Asn Asp 550 555 560 565			1795
gtg aaa ccg gcg ctg ttc tcc ccc aat tct gaa ggc gcg tgc cca aac Val Lys Pro Ala Leu Phe Ser Pro Asn Ser Glu Gly Ala Cys Pro Asn 570 575 580			1843
tgt aag ggc gcc ggc tcg gtc tat gtc gat ttg ggc atg atg gct ggg Cys Lys Gly Ala Gly Ser Val Tyr Val Asp Leu Gly Met Met Ala Gly 585 590 595			1891

gta tct tcg ccg tgt gag gtg tgc gag ggc aag cgt ttt gat gag tcc 1939
 Val Ser Ser Pro Cys Glu Val Cys Glu Gly Lys Arg Phe Asp Glu Ser
 600 605 610

gtg ttg gac tac cac ttt ggt ggc aag gac atc gca gac gtg ttg ggg 1987
 Val Leu Asp Tyr His Phe Gly Gly Lys Asp Ile Ala Asp Val Leu Gly
 615 620 625

ctg tcg gct gcc aat gcg tat gag ttt ttc gcg gcg aaa gat tca aag 2035
 Leu Ser Ala Ala Asn Ala Tyr Glu Phe Phe Ala Ala Lys Asp Ser Lys
 630 635 640 645

att ttg cct gcg gca aag atc gca aag agg ctt gtc gac gtc ggc ctc 2083
 Ile Leu Pro Ala Ala Lys Ile Ala Lys Arg Leu Val Asp Val Gly Leu
 650 655 660

ggc tac atc acc ctc ggc cag ccg ctc acc acg ttg tcc ggc ggt gaa 2131
 Gly Tyr Ile Thr Leu Gly Gln Pro Leu Thr Thr Leu Ser Gly Gly Glu
 665 670 675

cgc cag cgt ttg aag ctc gcc acc cac atg gca gac aag gcc acc acc 2179
 Arg Gln Arg Leu Lys Leu Ala Thr His Met Ala Asp Lys Ala Thr Thr
 680 685 690

ttt att ttg gat gag ccc acc aca ggc ctg cac ctc gct gat gtg aaa 2227
 Phe Ile Leu Asp Glu Pro Thr Thr Gly Leu His Leu Ala Asp Val Lys
 695 700 705

acc ttg ctg gat ctt ttt gat caa ctg gtt gat gac ggc aag tct gtc 2275
 Thr Leu Leu Asp Leu Phe Asp Gln Leu Val Asp Asp Gly Lys Ser Val
 710 715 720 725

atc gtc atc gaa cac cac ctc ggc gtg ctc gct cac gct gac cac atc 2323
 Ile Val Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile
 730 735 740

att gat gtc ggc cct ggt gca ggt tct gat ggt ggc tcg att gta ttc 2371
 Ile Asp Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe
 745 750 755

gag ggc agc ccc gcg gaa ctc atc aaa act gat act cca aca gga cgc 2419
 Glu Gly Ser Pro Ala Glu Leu Ile Lys Thr Asp Thr Pro Thr Gly Arg
 760 765 770

cac ctt aaa gct tat gta gat tagttttctta tggaaaaccc tgg 2463
 His Leu Lys Ala Tyr Val Asp
 775 780

<210> 146

<211> 780

<212> PRT

<213> Corynebacterium glutamicum

<400> 146

Met Gln Lys Ala Asp Ser His Asp Trp Ile Ser Val His Gly Ala Asn

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Glu Asn Asn Leu Lys Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu	20	25	30
Thr Val Phe Thr Gly Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe	35	40	45
Gly Thr Ile Ala Ala Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser	50	55	60
Thr Phe Val Gln Gly Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp	65	70	75
His Leu Glu Gly Ile Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met	85	90	95
Gly Ala Asn Pro Arg Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala	100	105	110
Met Leu Arg Ile Leu Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly	115	120	125
Pro Gly Ala Tyr Ser Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala	130	135	140
Ile Thr Val Glu Lys Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe	145	150	155
Lys Arg Thr Gly Gly Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala	165	170	175
Ser Asp Ile Asp Leu Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn	180	185	190
Asp Gly Ala Leu Thr Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr	195	200	205
Arg Met Tyr Ser Glu Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys	210	215	220
Asp Phe Thr Glu Glu Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr	225	230	235
Lys Met Lys Ile Ala Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro	245	250	255
Arg Ile Gln Lys Ser Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys	260	265	270
His Ile Arg Ala Phe Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro	275	280	285
Ala Cys Gly Gly Thr Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile	290	295	300
Asn Gly Lys Asn Ile Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu			

305	310	315	320
Ala Lys Trp Ile Lys Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu	325	330	335
Thr Ala Leu Thr Glu Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly	340	345	350
Tyr Ile Gln Leu Asp Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala	355	360	365
Gln Arg Thr Lys Met Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val	370	375	380
Thr Tyr Val Phe Asp Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile	385	390	395
Glu Arg Met Asn Lys Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr	405	410	415
Val Leu Val Val Glu His Lys Pro Glu Thr Ile Ala Ile Ala Asp His	420	425	430
Val Val Asp Leu Gly Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg	435	440	445
Phe Glu Gly Ser Val Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly	450	455	460
Leu His Phe Asn Asp Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro	465	470	475
His Gly Ala Leu Glu Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn	485	490	495
Val Asp Val Asp Ile Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val	500	505	510
Ala Gly Ser Gly Lys Ser Ser Leu Ile His Glu Ile Pro Arg Asp Glu	515	520	525
Ser Val Val Phe Val Asp Gln Thr Ala Ile His Gly Ser Asn Arg Ser	530	535	540
Asn Pro Ala Thr Tyr Thr Gly Met Leu Asp Ser Ile Arg Lys Ala Phe	545	550	555
Ala Lys Ala Asn Asp Val Lys Pro Ala Leu Phe Ser Pro Asn Ser Glu	565	570	575
Gly Ala Cys Pro Asn Cys Lys Gly Ala Gly Ser Val Tyr Val Asp Leu	580	585	590
Gly Met Met Ala Gly Val Ser Ser Pro Cys Glu Val Cys Glu Gly Lys	595	600	605
Arg Phe Asp Glu Ser Val Leu Asp Tyr His Phe Gly Gly Lys Asp Ile			

610

615

620

Ala Asp Val Leu Gly Leu Ser Ala Ala Asn Ala Tyr Glu Phe Phe Ala
625 630 635 640

Ala Lys Asp Ser Lys Ile Leu Pro Ala Ala Lys Ile Ala Lys Arg Leu
645 650 655

Val Asp Val Gly Leu Gly Tyr Ile Thr Leu Gly Gln Pro Leu Thr Thr
660 665 670

Leu Ser Gly Gly Glu Arg Gln Arg Leu Lys Leu Ala Thr His Met Ala
675 680 685

Asp Lys Ala Thr Thr Phe Ile Leu Asp Glu Pro Thr Thr Gly Leu His
690 695 700

Leu Ala Asp Val Lys Thr Leu Leu Asp Leu Phe Asp Gln Leu Val Asp
705 710 715 720

Asp Gly Lys Ser Val Ile Val Ile Glu His His Leu Gly Val Leu Ala
725 730 735

His Ala Asp His Ile Ile Asp Val Gly Pro Gly Ala Gly Ser Asp Gly
740 745 750

Gly Ser Ile Val Phe Glu Gly Ser Pro Ala Glu Leu Ile Lys Thr Asp
755 760 765

Thr Pro Thr Gly Arg His Leu Lys Ala Tyr Val Asp
770 775 780

<210> 147

<211> 278

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(255)

<223> FRXA00829

<400> 147

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1 5 10 15

ctg gat ctt ttt gat caa ctg gtt gat gac ggc aag tct gtc atc gtc 96
Leu Asp Leu Phe Asp Gln Leu Val Asp Asp Gly Lys Ser Val Ile Val
20 25 30

atc gaa cac cac ctc ggc gtg ctc gct cac gct gac cac atc att gat 144
Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile Ile Asp
35 40 45

gtc ggc cct ggt gca ggt tct gat ggt ggc tcg att gta ttc gag ggc 192

Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe Glu Gly
 50 55 60

agc ccc gcg gaa ctc atc aaa act gat act cca aca gga cgc cac ctt 240
 Ser Pro Ala Glu Leu Ile Lys Thr Asp Thr Pro Thr Gly Arg His Leu
 65 70 75 80

aaa gct tat gta gat tagtttctta tggaaaaccc tgg 278
 Lys Ala Tyr Val Asp
 85

<210> 148

<211> 85

<212> PRT

<213> Corynebacterium glutamicum

<400> 148

Leu Asp Glu Pro Thr Thr Gly Leu His Leu Ala Asp Val Lys Thr Leu
 1 5 10 15

Leu Asp Leu Phe Asp Gln Leu Val Asp Asp Gly Lys Ser Val Ile Val
 20 25 30

Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile Ile Asp
 35 40 45

Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe Glu Gly
 50 55 60

Ser Pro Ala Glu Leu Ile Lys Thr Asp Thr Pro Thr Gly Arg His Leu
 65 70 75 80

Lys Ala Tyr Val Asp
 85

<210> 149

<211> 1663

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1663)

<223> FRXA00834

<400> 149

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caagcgcgaa caggcctatg caaacggtac gatatgacac atg caa aaa gct gat 115
 Met Gln Lys Ala Asp
 1 5

tcc cat gat tgg att tcg gtc cac ggt gcg aat gaa aac aac ctc aaa 163
 Ser His Asp Trp Ile Ser Val His Gly Ala Asn Glu Asn Asn Leu Lys
 10 15 20

aat gtg tcg gtg cgc atc cct aaa agg cgt ctc acc gtg ttc acg ggt	211
Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu Thr Val Phe Thr Gly	
25 30 35	
gtg tcg gga tct ggc aag tcc tcg ctg gtg ttc ggc aca att gct gcg	259
Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe Gly Thr Ile Ala Ala	
40 45 50	
gaa tca cgc cgg ttg atc aac gaa acc tat agc act ttt gtg caa ggt	307
Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser Thr Phe Val Gln Gly	
55 60 65	
ttc atg ccg tcg atg gca agg ccc gat gtt gac cat ttg gaa ggc atc	355
Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp His Leu Glu Gly Ile	
70 75 80 85	
acc acg gcg atc atc gtc gat cag gag cag atg ggc gca aac cca cgg	403
Thr Thr Ala Ile Ile Val Asp Gln Glu Met Gly Ala Asn Pro Arg	
90 95 100	
tct acg gtg ggt acc gca act gat gcc acc gcg atg ttg cgc att ttg	451
Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala Met Leu Arg Ile Leu	
105 110 115	
ttt tcc cga atc gcg gaa cct aac gcg ggt ggc ccg gga gct tat tcc	499
Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly Pro Gly Ala Tyr Ser	
120 125 130	
ttc aac gtc ccc tct gtt tcc gca tcc ggc gcc atc acg gtg gaa aag	547
Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala Ile Thr Val Glu Lys	
135 140 145	
ggc gga aac acc aag cgg gag aaa gct acc ttc aaa cgc acg ggt ggc	595
Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe Lys Arg Thr Gly Gly	
150 155 160 165	
atg tgc cca gcg tgc gag ggc atg ggc agg gcc tca gac atc gac ctc	643
Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala Ser Asp Ile Asp Leu	
170 175 180	
aaa gag ctt ttc gac gcc tcc ctc tcc ctc aac gac ggc gcc ctg acc	691
Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn Asp Gly Ala Leu Thr	
185 190 195	
atc ccc ggt tac acc cca ggt gga tgg agt tat cgg atg tat tca gaa	739
Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr Arg Met Tyr Ser Glu	
200 205 210	
tcg ggc ctt ttt gat gct gcc aag ccg att aag gat ttc acc gag gaa	787
Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys Asp Phe Thr Glu Glu	
215 220 225	
gaa cgc cac aac ttc ctt tat ctt gag ccc acc aag atg aag atc gct	835
Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr Lys Met Lys Ile Ala	
230 235 240 245	

ggc atc aac atg acc tat gag ggt ctt atc ccc cgc att cag aaa tcc Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro Arg Ile Gln Lys Ser 250 255 260	883
atg ttg tct aag gat cgc gaa ggc atg cag aag cat att cgt gcg ttc Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys His Ile Arg Ala Phe 265 270 275	931
gtg gat cga gcg gtt acc ttc att cct tgc cct gcg tgt ggt gga act Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro Ala Cys Gly Gly Thr 280 285 290	979
cga tta gcg cca cat gcc ttg gag tcc aag atc aat ggc aaa aac atc Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile Asn Gly Lys Asn Ile 295 300 305	1027
gct gag ttg tgc gcg atg gag gtc cgt gat ttg gcc aag tgg atc aaa Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu Ala Lys Trp Ile Lys 310 315 320 325	1075
acg gtg gaa gcc ccc tgc gtt gct ccc ctg ctc acc gca ctg act gaa Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu Thr Ala Leu Thr Glu 330 335 340	1123
acc ctg gat aac ttc gtg gag atc ggt ttg ggc tat atc caa ctc gat Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly Tyr Ile Gln Leu Asp 345 350 355	1171
cgc ccc gct ggc acg ttg tct ggt ggt gag gca cag cgc acc aag atg Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala Gln Arg Thr Lys Met 360 365 370	1219
atc cgc cat ttg ggc tct gca ttg act gac gtc acc tat gtt ttt gat Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val Thr Tyr Val Phe Asp 375 380 385	1267
gaa ccc acc gcc ggt ttg cac gcc tac gac att gaa cgc atg aac aag Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile Glu Arg Met Asn Lys 390 395 400 405	1315
ttg ctg ctc gat ctt cgc gat aaa ggc aat acc gtt tta gtc gtg gag Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr Val Leu Val Val Glu 410 415 420	1363
cac aag ccg gaa acc atc gcc att gca gat cat gtg gtg gac ctt ggg His Lys Pro Glu Thr Ile Ala Ile Ala Asp His Val Val Asp Leu Gly 425 430 435	1411
cca ggt gca ggc gcg ggt gga ggt gaa att cgg ttt gag ggg agc gtc Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg Phe Glu Gly Ser Val 440 445 450	1459
gac aag ctt aaa gac agc gac acc gtg act ggc ctc cat ttt aat gac Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly Leu His Phe Asn Asp 455 460 465	1507
cgg gcg tca ttg aag gaa tcc gtg cgt gcg ccg cat ggc gcc ctg gag	1555

Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro His Gly Ala Leu Glu
 470 475 480 485

atc cgc ggg gcc gat cga aat aat ttg aac aat gtg gat gtc gat att 1603
 Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn Val Asp Val Asp Ile
 490 495 500

cgc ctc ggc gtg ttc acg gcg att tcc ggc gtt gca ggt tcg ggt aag 1651
 Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val Ala Gly Ser Gly Lys
 505 510 515

tcc tcg ttg att 1663
 Ser Ser Leu Ile
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<210> 150

<211> 521

<212> PRT

<213> Corynebacterium glutamicum

<400> 150

Met Gln Lys Ala Asp Ser His Asp Trp Ile Ser Val His Gly Ala Asn
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Glu Asn Asn Leu Lys Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu
 20 25 30

Thr Val Phe Thr Gly Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe
 35 40 45

Gly Thr Ile Ala Ala Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser
 50 55 60

Thr Phe Val Gln Gly Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp
 65 70 75 80

His Leu Glu Gly Ile Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met
 85 90 95

Gly Ala Asn Pro Arg Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala
 100 105 110

Met Leu Arg Ile Leu Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly
 115 120 125

Pro Gly Ala Tyr Ser Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala
 130 135 140

Ile Thr Val Glu Lys Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe
 145 150 155 160

Lys Arg Thr Gly Gly Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala
 165 170 175

Ser Asp Ile Asp Leu Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn
 180 185 190

Asp Gly Ala Leu Thr Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr
 195 200 205
 Arg Met Tyr Ser Glu Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys
 210 215 220
 Asp Phe Thr Glu Glu Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr
 225 230 235 240
 Lys Met Lys Ile Ala Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro
 245 250 255
 Arg Ile Gln Lys Ser Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys
 260 265 270
 His Ile Arg Ala Phe Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro
 275 280 285
 Ala Cys Gly Gly Thr Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile
 290 295 300
 Asn Gly Lys Asn Ile Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu
 305 310 315 320
 Ala Lys Trp Ile Lys Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu
 325 330 335
 Thr Ala Leu Thr Glu Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly
 340 345 350
 Tyr Ile Gln Leu Asp Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala
 355 360 365
 Gln Arg Thr Lys Met Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val
 370 375 380
 Thr Tyr Val Phe Asp Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile
 385 390 395 400
 Glu Arg Met Asn Lys Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr
 405 410 415
 Val Leu Val Val Glu His Lys Pro Glu Thr Ile Ala Ile Ala Asp His
 420 425 430
 Val Val Asp Leu Gly Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg
 435 440 445
 Phe Glu Gly Ser Val Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly
 450 455 460
 Leu His Phe Asn Asp Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro
 465 470 475 480
 His Gly Ala Leu Glu Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn
 485 490 495

Val Asp Val Asp Ile Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val
 500 505 510

Ala Gly Ser Gly Lys Ser Ser Leu Ile
 515 520

<210> 151

<211> 864

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(841)

<223> RXA00995

<400> 151

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 Met Asn Pro His Tyr
 1 5

ctg ctt gcc acg gtc aaa cga gtc ctg ctg cag ctg aaa gcc gat aaa 163
 Leu Leu Ala Thr Val Lys Arg Val Leu Leu Gln Leu Lys Ala Asp Lys
 10 15 20

cgt tcc atc gcg ctg att ctt cta gca ccc gtg gcg ttg atg tcg ctg 211
 Arg Ser Ile Ala Leu Ile Leu Leu Ala Pro Val Ala Leu Met Ser Leu
 25 30 35

ttt tat tac atg tat tcc tcc aca ccg gca ggc acc cag ctg ttt aag 259
 Phe Tyr Tyr Met Tyr Ser Ser Thr Pro Ala Gly Thr Gln Leu Phe Lys
 40 45 50

acc att tcc acg gtc atg atc gca gtg ttc ccc ttg atg ctc atg ttt 307
 Thr Ile Ser Thr Val Met Ile Ala Val Phe Pro Leu Met Leu Met Phe
 55 60 65

ttg atg acg tcg gtg acg atg caa aga gaa cgc aac gct gga acg ctc 355
 Leu Met Thr Ser Val Thr Met Gln Arg Glu Arg Asn Ala Gly Thr Leu
 70 75 80 85

gag cgc ttg tgg acc acg aac att cac cgc gtt gat ttg atc ggt ggc 403
 Glu Arg Leu Trp Thr Thr Asn Ile His Arg Val Asp Leu Ile Gly Gly
 90 95 100

tac ggg gtg gcc ttc ggc atc atg gcg gtg gcg caa tct ttg ctc atg 451
 Tyr Gly Val Ala Phe Gly Ile Met Ala Val Ala Gln Ser Leu Leu Met
 105 110 115

gtg ctc acc ctt cgg tat ctc ctg ggt gtg gaa acc gaa tcg gag tgg 499
 Val Leu Thr Leu Arg Tyr Leu Leu Gly Val Glu Thr Glu Ser Glu Trp
 120 125 130

tgg att tct acg ctc att gct gcg atc acc ggt ctt atc gga gtg tct 547
 Trp Ile Ser Thr Leu Ile Ala Ala Ile Thr Gly Leu Ile Gly Val Ser
 135 140 145

 ctt ggc ctg ttg agc tct gcg ttt gcc agc act gag ttc caa gct atc 595
 Leu Gly Leu Leu Ser Ser Ala Phe Ala Ser Thr Glu Phe Gln Ala Ile
 150 155 160 165

 caa acg ctg ccg ttg ctt att ttg ccc cag ttc cta ttg tgc ggt ttg 643
 Gln Thr Leu Pro Leu Leu Ile Leu Pro Gln Phe Leu Leu Cys Gly Leu
 170 175-- 180

 ctg atc cca cgg gat gat ctg ccg gat gtg ttg cgc tgg gtt tct aat 691
 Leu Ile Pro Arg Asp Asp Leu Pro Asp Val Leu Arg Trp Val Ser Asn
 185 190 195

 gtg ttg ccg ctg tcc tat gca gtt gat gca gcg ctt gag gcc tca cgg 739
 Val Leu Pro Leu Ser Tyr Ala Val Asp Ala Ala Leu Glu Ala Ser Arg
 200 205 210

 acg gga atc gga cag caa gta gtg gtc aac att gcc atc tgc gcc gcg 787
 Thr Gly Ile Gly Gln Gln Val Val Val Asn Ile Ala Ile Cys Ala Ala
 215 220 225

 ttt gcc gtg agc ttc ctg ctg gtg gcg gcg cta tcg atg ccg aga atg 835
 Phe Ala Val Ser Phe Leu Leu Val Ala Ala Leu Ser Met Pro Arg Met
 230 235 240 245

 acc cgc tagattactc ttccagcgag gtg 864
 Thr Arg

<210> 152

<211> 247

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

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 Leu Lys Ala Asp Lys Arg Ser Ile Ala Leu Ile Leu Leu Ala Pro Val
 20 25 30

 Ala Leu Met Ser Leu Phe Tyr Tyr Met Tyr Ser Ser Thr Pro Ala Gly
 35 40 45

 Thr Gln Leu Phe Lys Thr Ile Ser Thr Val Met Ile Ala Val Phe Pro
 50 55 60

 Leu Met Leu Met Phe Leu Met Thr Ser Val Thr Met Gln Arg Glu Arg
 65 70 75 80

 Asn Ala Gly Thr Leu Glu Arg Leu Trp Thr Thr Asn Ile His Arg Val
 85 90 95

Asp Leu Ile Gly Gly Tyr Gly Val Ala Phe Gly Ile Met Ala Val Ala
 100 105 110
 Gln Ser Leu Leu Met Val Leu Thr Leu Arg Tyr Leu Leu Gly Val Glu
 115 120 125
 Thr Glu Ser Glu Trp Trp Ile Ser Thr Leu Ile Ala Ala Ile Thr Gly
 130 135 140
 Leu Ile Gly Val Ser Leu Gly Leu Leu Ser Ser Ala Phe Ala Ser Thr
 145 150 155 160
 Glu Phe Gln Ala Ile Gln Thr Leu Pro Leu Leu Ile Leu Pro Gln Phe
 165 170 175
 Leu Leu Cys Gly Leu Leu Ile Pro Arg Asp Asp Leu Pro Asp Val Leu
 180 185 190
 Arg Trp Val Ser Asn Val Leu Pro Leu Ser Tyr Ala Val Asp Ala Ala
 195 200 205
 Leu Glu Ala Ser Arg Thr Gly Ile Gly Gln Gln Val Val Val Asn Ile
 210 215 220
 Ala Ile Cys Ala Ala Phe Ala Val Ser Phe Leu Leu Val Ala Ala Leu
 225 230 235 240
 Ser Met Pro Arg Met Thr Arg
 245

<210> 153
 <211> 1353
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1330)
 <223> RXN00803

<400> 153
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 Met Gly Val Ser Ala
 1 5
 ctt aac atg tct gac atg gtg gcg aac aaa cgg gca cag cgt aaa gtc 163
 Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg Ala Gln Arg Lys Val
 10 15 20
 tgg cta gcg gta gct tta tcg gtc ttt acg gtc gcg tgg ggt ggc aat 211
 Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val Ala Trp Gly Gly Asn
 25 30 35
 gaa ttc act ccc ttg ctg gtg ttt tac cga ggt gaa ggg ttc ttt agc 259

Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly Glu Gly Phe Phe Ser	
40 45 50	
aac ctg ttc atc gac ctt ttg ctg gtg ttt tat gcc atc gga gta gcg	307
Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr Ala Ile Gly Val Ala	
55 60 65	
gta ggt ttg ctg gca gct ggt cct tta tct gac cgc tat ggc cga cgt	355
Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp Arg Tyr Gly Arg Arg	
70 75 80 85	
gcc gtc atg ttg cct gcg cca ttg atc gcg atc ttg ggt tcc gcg ttg	403
Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile Leu Gly Ser Ala Leu	
90 95 100	
att gcc tcg ggt gaa gaa acc gcc atc ctg att gcc att ggt cga gtg	451
Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile Ala Ile Gly Arg Val	
105 110 115	
ctg tcg gga att tcg gtg ggc atg gtg atg aca gcg gga ggt tcc tgg	499
Leu Ser Gly Ile Ser Val Gly Met Val Met Thr Ala Gly Gly Ser Trp	
120 125 130	
att aag gag ctt tca tcg tcg cgg ttt gag cca ggg gtg aaa acc agt	547
Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro Gly Val Lys Thr Ser	
135 140 145	
gct ggt gca aaa cgc gca tcg atg tct ttg acc ggt ggt ttt gcg ctc	595
Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr Gly Gly Phe Ala Leu	
150 155 160 165	
ggc cca gcg ctt gct ggt gtg atg gca cag tgg ctg cca cta cct gga	643
Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp Leu Pro Leu Pro Gly	
170 175 180	
cag ttg gca tat gtt ttg cac att att ctc act ctg att ttg ttc ccg	691
Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr Leu Ile Leu Phe Pro	
185 190 195	
ttg ctt att aca gcg ccg gaa act cgt caa tca gcg cac ctg aaa act	739
Leu Leu Ile Thr Ala Pro Glu Thr Arg Gln Ser Ala His Leu Lys Thr	
200 205 210	
aag gga tca ttc tgg tca gat gtg ctt gtg cca tct gca cta gac aag	787
Lys Gly Ser Phe Trp Ser Asp Val Leu Val Pro Ser Ala Leu Asp Lys	
215 220 225	
cga ttc ttg ttt gtg gtt gct cca att gga ccg tgg gtt ttc ggt gcg	835
Arg Phe Leu Phe Val Val Ala Pro Ile Gly Pro Trp Val Phe Gly Ala	
230 235 240 245	
gcc ttc act gcc tac gca gtt ttg ccg tcg cag ctg cgt gac atg gtt	883
Ala Phe Thr Ala Tyr Ala Val Leu Pro Ser Gln Leu Arg Asp Met Val	
250 255 260	
tct gca ccc gtt gcg tat tct gcg ctg atc gct ttg gtt acc tta ggt	931
Ser Ala Pro Val Ala Tyr Ser Ala Leu Ile Ala Leu Val Thr Leu Gly	

265	270	275	
tct gga ttt ggt atc caa caa ttc ggt cct caa atc atg ggc acc tct Ser Gly Phe Gly Ile Gln Gln Phe Gly Pro Gln Ile Met Gly Thr Ser 280 285 290			979
aaa act cgc ggg ccg att ttg gcc atg ttc gtc aca gtc atc ggc atg Lys Thr Arg Gly Pro Ile Leu Ala Met Phe Val Thr Val Ile Gly Met 295 300 305			1027
atc ggc gcg gtg atc gtg gtg atg aac cct cat cca tgg tgg gcg cta Ile Gly Ala Val Ile Val Val Met Asn Pro His Pro Trp Trp Ala Leu 310 315 320 325			1075
gtt ggc tgc atg gcc ctg ggc ctg tct tat ggc ctg tgt atg ttc atg Val Gly Cys Met Ala Leu Gly Leu Ser Tyr Gly Leu Cys Met Phe Met 330 335 340			1123
ggg ttg gcg gaa act caa aac att gct cca cct att gat atg gca ggc Gly Leu Ala Glu Thr Gln Asn Ile Ala Pro Pro Ile Asp Met Ala Gly 345 350 355			1171
ctg acg ggt att ttc tac tgc ctg acg tac gta ggt atg gtc ttt cca Leu Thr Gly Ile Phe Tyr Cys Leu Thr Tyr Val Gly Met Val Phe Pro 360 365 370			1219
gcc ttg atg acc tgg ttg aat caa tgg ctg agt tac ccg ttc atg ctg Ala Leu Met Thr Trp Leu Asn Gln Trp Leu Ser Tyr Pro Phe Met Leu 375 380 385			1267
ggc ttt ggt gcg gtg atg gca act att tgt ctg atc att gtg agt ttt Gly Phe Gly Ala Val Met Ala Thr Ile Cys Leu Ile Ile Val Ser Phe 390 395 400 405			1315
agt gca cgc cga ttc tgagaaacaa ctaaagtgag cca Ser Ala Arg Arg Phe 410			1353

<210> 154

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

Met Gly Val Ser Ala Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg 1 5 10 15
Ala Gln Arg Lys Val Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val 20 25 30
Ala Trp Gly Gly Asn Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly 35 40 45
Glu Gly Phe Phe Ser Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr 50 55 60

Ala Ile Gly Val Ala Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp
 65 70 75 80
 Arg Tyr Gly Arg Arg Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile
 85 90 95
 Leu Gly Ser Ala Leu Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile
 100 105 110
 Ala Ile Gly Arg Val Leu Ser Gly Ile Ser Val Gly Met Val Met Thr
 115 120 125
 Ala Gly Gly Ser Trp Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro
 130 135 140
 Gly Val Lys Thr Ser Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr
 145 150 155 160
 Gly Gly Phe Ala Leu Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp
 165 170 175
 Leu Pro Leu Pro Gly Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr
 180 185 190
 Leu Ile Leu Phe Pro Leu Leu Ile Thr Ala Pro Glu Thr Arg Gln Ser
 195 200 205
 Ala His Leu Lys Thr Lys Gly Ser Phe Trp Ser Asp Val Leu Val Pro
 210 215 220
 Ser Ala Leu Asp Lys Arg Phe Leu Phe Val Val Ala Pro Ile Gly Pro
 225 230 235 240
 Trp Val Phe Gly Ala Ala Phe Thr Ala Tyr Ala Val Leu Pro Ser Gln
 245 250 255
 Leu Arg Asp Met Val Ser Ala Pro Val Ala Tyr Ser Ala Leu Ile Ala
 260 265 270
 Leu Val Thr Leu Gly Ser Gly Phe Gly Ile Gln Gln Phe Gly Pro Gln
 275 280 285
 Ile Met Gly Thr Ser Lys Thr Arg Gly Pro Ile Leu Ala Met Phe Val
 290 295 300
 Thr Val Ile Gly Met Ile Gly Ala Val Ile Val Val Met Asn Pro His
 305 310 315 320
 Pro Trp Trp Ala Leu Val Gly Cys Met Ala Leu Gly Leu Ser Tyr Gly
 325 330 335
 Leu Cys Met Phe Met Gly Leu Ala Glu Thr Gln Asn Ile Ala Pro Pro
 340 345 350
 Ile Asp Met Ala Gly Leu Thr Gly Ile Phe Tyr Cys Leu Thr Tyr Val
 355 360 365

Gly Met Val Phe Pro Ala Leu Met Thr Trp Leu Asn Gln Trp Leu Ser
 370 375 380

Tyr Pro Phe Met Leu Gly Phe Gly Ala Val Met Ala Thr Ile Cys Leu
 385 390 395 400

Ile Ile Val Ser Phe Ser Ala Arg Arg Phe
 405 410

<210> 155

<211> 703

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> FRXA00803

<400> 155

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 Met Gly Val Ser Ala
 1 5

ctt aac atg tct gac atg gtg gcg aac aaa cgg gca cag cgt aaa gtc 163
 Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg Ala Gln Arg Lys Val
 10 15 20

tgg cta gcg gta gct tta tcg gtc ttt acg gtc gcg tgg ggt ggc aat 211
 Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val Ala Trp Gly Gly Asn
 25 30 35

gaa ttc act ccc ttg ctg gtg ttt tac cga ggt gaa ggg ttc ttt agc 259
 Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly Glu Gly Phe Phe Ser
 40 45 50

aac ctg ttc atc gac ctt ttg ctg gtg ttt tat gcc atc gga gta gcg 307
 Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr Ala Ile Gly Val Ala
 55 60 65

gta ggt ttg ctg gca gct ggt cct tta tct gac cgc tat ggc cga cgt 355
 Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp Arg Tyr Gly Arg Arg
 70 75 80 85

gcc gtc atg ttg cct gcg cca ttg atc gcg atc ttg ggt tcc gcg ttg 403
 Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile Leu Gly Ser Ala Leu
 90 95 100

att gcc tcg ggt gaa gaa acc gcc atc ctg att gcc att ggt cga gtg 451
 Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile Ala Ile Gly Arg Val
 105 110 115

ctg tcg gga att tcg gtg ggc atg gtg atg aca gcg gga ggt tcc tgg 499
 Leu Ser Gly Ile Ser Val Gly Met Val Met Thr Ala Gly Gly Ser Trp

120	125	130	
att aag gag ctt tca tcg tcg cgg ttt gag cca ggg gtg aaa acc agt			547
Il Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro Gly Val Lys Thr Ser			
135	140	145	
gct ggt gca aaa cgc gca tcg atg tct ttg acc ggt ggt ttt gcg ctc			595
Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr Gly Gly Phe Ala Leu			
150	155	160	165
ggc cca gcg ctt gct ggt gtg atg gca cag tgg ctg cca caa cct gga			643
Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp Leu Pro Gln Pro Gly			
	170	175	180
cag ttg gca tat gtt ttg cac att att ctc act ctg att ttg ttc ccg			691
Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr Leu Ile Leu Phe Pro			
	185	190	195
ttg ctt att aca			703
Leu Leu Ile Thr			
200			

<210> 156

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

Met Gly Val Ser Ala Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg			
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	20	25	30
Ala Trp Gly Gly Asn Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly			
	35	40	45
Glu Gly Phe Phe Ser Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr			
	50	55	60
Ala Ile Gly Val Ala Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp			
	65	70	75
Arg Tyr Gly Arg Arg Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile			
	85	90	95
Leu Gly Ser Ala Leu Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile			
	100	105	110
Ala Ile Gly Arg Val Leu Ser Gly Ile Ser Val Gly Met Val Met Thr			
	115	120	125
Ala Gly Gly Ser Trp Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro			
	130	135	140
Gly Val Lys Thr Ser Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr			

208

tac cgc ttg gta atc acc gca gca cca ttc atg ttc act ttg ctc ttc 499
 Tyr Arg Leu Val Ile Thr Ala Ala Pro Phe Met Phe Thr Leu Leu Phe
 120 125 130

caa gtg gcg ttt ggg tgg tct gca aca tta gcg ggt gcc atg gtg gtc 547
 Gln Val Ala Phe Gly Trp Ser Ala Thr Leu Ala Gly Ala Met Val Val
 135 140 145

gca cta ttc gca ggc aac gtg gca atc aaa cct ttc acc acg ccg atc 595
 Ala Leu Phe Ala Gly Asn Val Ala Ile Lys Pro Phe Thr Thr Pro Ile
 150 155 160 165

att aaa cgc tgg aat ttc aaa cca gta ctg gtc ttt tct aac gct gct 643
 Ile Lys Arg Trp Asn Phe Lys Pro Val Leu Val Phe Ser Asn Ala Ala
 170 175 180

ggc gcc ttg gta ttg gca act ttt ttg ttc gtt cgt gca gat acc cca 691
 Gly Ala Leu Val Leu Ala Thr Phe Leu Phe Val Arg Ala Asp Thr Pro
 185 190 195

ctg gtt ctc atc gtg ctg ctg ctc ttt gtt tcg ggc gca tta agg tcc 739
 Leu Val Leu Ile Val Leu Leu Leu Phe Val Ser Gly Ala Leu Arg Ser
 200 205 210

ctc ggt ttc agc gcc tac aac acc ttg cag ttt gtc gat atc tca cca 787
 Leu Gly Phe Ser Ala Tyr Asn Thr Leu Gln Phe Val Asp Ile Ser Pro
 215 220 225

gaa caa acc agc aac gcc aac gtg tta tca gca acc ctg cac caa cta 835
 Glu Gln Thr Ser Asn Ala Asn Val Leu Ser Ala Thr Leu His Gln Leu
 230 235 240 245

ggc atg tct ttg ggt att gcg gta gca gtc atc gcc atg tcc ctt gca 883
 Gly Met Ser Leu Gly Ile Ala Val Ala Val Ile Ala Met Ser Leu Ala
 250 255 260

ccc acc gcc aac tgg gca ttc cca ctg gca gca gcg ttg ttc ctc att 931
 Pro Thr Ala Asn Trp Ala Phe Pro Leu Ala Ala Ala Leu Phe Leu Ile
 265 270 275

cct cta atc ggc gca cta tct ttg cct cgc gac ggc ggt gcc cga gcc 979
 Pro Leu Ile Gly Ala Leu Ser Leu Pro Arg Asp Gly Gly Ala Arg Ala
 280 285 290

ttt tcc tcc tct tagaaaccca cttctgaaag gta 1014
 Phe Ser Ser Ser
 295

<210> 158

<211> 297

<212> PRT

<213> Corynebacterium glutamicum

<400> 158

Leu Gln Asp Thr Ile Gly Cys Arg Trp Ile Phe Leu Leu Asn Val Pro
 1 5 10 15

Leu Gly Ile Ile Ala Ile Met Ala Gly Leu Phe Ile Gln Pro Lys Asn
 20 25 30
 Thr Ala Val Asn Val Lys Arg Phe Asp Arg Pro Gly Phe Leu Gly Ala
 35 40 45
 Met Leu Val Met Val Ala Gln Ala Val Ile Ala Glu Leu Ile Cys Ser
 50 55 60
 Arg Ser Pro Ala Ala Leu Thr Ile Cys Ala Cys Leu Val Leu Ser Ala
 65 70 75 80
 Ala Val Val Cys Gly Phe Val Val Arg Trp Leu Arg Val Pro Gly Arg
 85 90 95
 Leu Phe Asp Leu Ser Ile Met Arg Ile Pro Gly Phe Arg Val Gly Asn
 100 105 110
 Ser Ser Gly Ser Ile Tyr Arg Leu Val Ile Thr Ala Ala Pro Phe Met
 115 120 125
 Phe Thr Leu Leu Phe Gln Val Ala Phe Gly Trp Ser Ala Thr Leu Ala
 130 135 140
 Gly Ala Met Val Val Ala Leu Phe Ala Gly Asn Val Ala Ile Lys Pro
 145 150 155 160
 Phe Thr Thr Pro Ile Ile Lys Arg Trp Asn Phe Lys Pro Val Leu Val
 165 170 175
 Phe Ser Asn Ala Ala Gly Ala Leu Val Leu Ala Thr Phe Leu Phe Val
 180 185 190
 Arg Ala Asp Thr Pro Leu Val Leu Ile Val Leu Leu Leu Phe Val Ser
 195 200 205
 Gly Ala Leu Arg Ser Leu Gly Phe Ser Ala Tyr Asn Thr Leu Gln Phe
 210 215 220
 Val Asp Ile Ser Pro Glu Gln Thr Ser Asn Ala Asn Val Leu Ser Ala
 225 230 235 240
 Thr Leu His Gln Leu Gly Met Ser Leu Gly Ile Ala Val Ala Val Ile
 245 250 255
 Ala Met Ser Leu Ala Pro Thr Ala Asn Trp Ala Phe Pro Leu Ala Ala
 260 265 270
 Ala Leu Phe Leu Ile Pro Leu Ile Gly Ala Leu Ser Leu Pro Arg Asp
 275 280 285
 Gly Gly Ala Arg Ala Phe Ser Ser Ser
 290 295

<210> 159

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<211> 324
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(301)  
<223> RXA01408
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<400> 159
cgcatagagt tatctcgaaa ctaccaagac ggtttctttt ctttagatct aaggaggaga 60

gaccgtcttt caccctttca tctgattgga catcgacgcc atg cgc aat gat cgg 115
Met Arg Asn Asp Arg
1 5

tcc ttt agc gtt ccc att gcg cta ctt gcc gcg gga gca ctg ttt cta 163
Ser Phe Ser Val Pro Ile Ala Leu Leu Ala Ala Gly Ala Leu Phe Leu
10 15 20

gaa atc ctc gac ggc acc atc ctg aca acc gca gtg cca gct att gct 211
Glu Ile Leu Asp Gly Thr Ile Leu Thr Thr Ala Val Pro Ala Ile Ala
25 30 35

cgt gac ttc ggt att gac gcc gtg gat gtc agc att gca ctg gtt gct 259
Arg Asp Phe Gly Ile Asp Ala Val Asp Val Ser Ile Ala Leu Val Ala
40 45 50

tac ttg gca gcc gca gca gct ggc att ccg ctg cag ggt ggc 301
Tyr Leu Ala Ala Ala Ala Ala Ala Gly Ile Pro Leu Gln Gly Gly
55 60 65

taqcqgacgc atttggtgtg cgc 324

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<210> 160
<211> 67
<212> PRT
<213> Corynebacterium glutamicum
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<400> 160
Met  Arg  Asn  Asp  Arg  Ser  Phe  Ser  Val  Pro  Ile  Ala  Leu  Leu  Ala  Ala
  1              5              10              15

Gly  Ala  Leu  Phe  Leu  Glu  Ile  Leu  Asp  Gly  Thr  Ile  Leu  Thr  Thr  Ala
          20              25              30

Val  Pro  Ala  Ile  Ala  Arg  Asp  Phe  Gly  Ile  Asp  Ala  Val  Asp  Val  Ser
          35              40              45

Ile  Ala  Leu  Val  Ala  Tyr  Leu  Ala  Ala  Ala  Ala  Ala  Gly  Ile  Pro  Leu
  50              55              60

Gln  Gly  Gly
  65

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<210> 161
 <211> 1275
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1252)
 <223> RXN01922

<400> 161

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acactccttt ggtcacctgg tttggttgag ggaaacagac cgcccaagaa cccaagaaat 60
cccaagaaaa catgctgctt atgaattaaa gtgagcaccc atg aga tca gga aac 115
                                         Met Arg Ser Gly Asn
                                         1 5

gcc aat cgc gtc ttc ata ggt gtt acc atc ctg ctg ttt act gca gga 163
Ala Asn Arg Val Phe Ile Gly Val Thr Ile Leu Leu Phe Thr Ala Gly
                        10 15 20

tgg gca gcc aat cat ttc gcg tca gtg ttg gtg ttg atc cgt gaa caa 211
Trp Ala Ala Asn His Phe Ala Ser Val Leu Val Leu Ile Arg Glu Gln
                        25 30 35

tta gac gta tca agc gtg ctg gtc aac ggc gct ttt ggt att tat gca 259
Leu Asp Val Ser Ser Val Leu Val Asn Gly Ala Phe Gly Ile Tyr Ala
                        40 45 50

ctg gga ctt ctt cca agt ttg ctc gca ggc ggt gtg ctt gcc gac cgt 307
Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly Gly Val Leu Ala Asp Arg
                        55 60 65

ttt ggt gcc cgc atg gtg gta ctc acc gga ggt gta ctt tct gcg ctt 355
Phe Gly Ala Arg Met Val Val Leu Thr Gly Gly Val Leu Ser Ala Leu
                        70 75 80 85

gga aac ctt tct ctt tta gcg ttt cat gat ggt cct tcc ctc ctg gta 403
Gly Asn Leu Ser Leu Leu Ala Phe His Asp Gly Pro Ser Leu Leu Val
                        90 95 100

gga cga ttc atc gtt ggt ctg ggc gtt gga tta gtc gtc agc gcg ggc 451
Gly Arg Phe Ile Val Gly Leu Gly Val Gly Leu Val Val Ser Ala Gly
                        105 110 115

acc gca tgg gcg ggc aga ttg cgc gga gca agc ggc gtg aca ttg gcc 499
Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala Ser Gly Val Thr Leu Ala
                        120 125 130

ggc att att ctg acc gcc ggt ttc atg atg ggg ccg att gtg aca agt 547
Gly Ile Ile Leu Thr Ala Gly Phe Met Met Gly Pro Ile Val Thr Ser
                        135 140 145

ggg ttg ggg atg gcg tcg aca agc att att acg ccc ttt gcc ata agc 595
Gly Leu Gly Met Ala Ser Thr Ser Ile Ile Thr Pro Phe Ala Ile Ser
150 155 160 165

```


gtt gcc ctc tcg ctg atc gcg gtg gtt gtg gga ttt gcg ctt ggc gat	643
Val Ala Leu Ser Leu Ile Ala Val Val Val Gly Phe Ala Leu Gly Asp	
170 175 180	
gcc cgc agc acc ccg agc gca ctt ggc gca tcc agc gga atc aaa cac	691
Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala Ser Ser Gly Ile Lys His	
185 190 195	
gaa cga agc atg aaa aag gcc ctc gcg gtg tcc ttg ccg atg gca att	739
Glu Arg Ser Met Lys Lys Ala Leu Ala Val Ser Leu Pro Met Ala Ile	
200 205 210	
tgg gtg ttc agc tgc atc acc acc tcc ctg atc gtg atg tcc gcg cgc	787
Trp Val Phe Ser Cys Ile Thr Thr Ser Leu Ile Val Met Ser Ala Arg	
215 220 225	
atc gac tcc acc ttc ggc aac gcc att ctt ctc ccc gga atc ggc gcg	835
Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu Leu Pro Gly Ile Gly Ala	
230 235 240 245	
gcg atc gcc ttc agc gca ggc ctg atc gca caa ttt tta ggt agg aaa	883
Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala Gln Phe Leu Gly Arg Lys	
250 255 260	
ttc gcg tgg ggt cgt ggc tcc gga atc gtg ggc gcg ctg tgt gcc ctc	931
Phe Ala Trp Gly Arg Gly Ser Gly Ile Val Gly Ala Leu Cys Ala Leu	
265 270 275	
gcg ggt ttt gcg ctg gca gct ttt ggt ggc gac tcc att cca gtg tgg	979
Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly Asp Ser Ile Pro Val Trp	
280 285 290	
ctt ttc gtt atc gcc tcg atc ctg ttc ggc acc gca tat ggc ctc tgc	1027
Leu Phe Val Ile Ala Ser Ile Leu Phe Gly Thr Ala Tyr Gly Leu Cys	
295 300 305	
ctg cgc gaa ggc ctc ctc agc atc gaa act tac acg cca ctc aac cga	1075
Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr Tyr Thr Pro Leu Asn Arg	
310 315 320 325	
cgt ggc acc ggc atc ggc atc tat tat gtg ttc acg tat ttg gga ttc	1123
Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val Phe Thr Tyr Leu Gly Phe	
330 335 340	
ggg ctg cca gtg ctt ctc gac gcc ctc ctc ccg cac ctt ggc gcc tcc	1171
Gly Leu Pro Val Leu Leu Asp Ala Leu Leu Pro His Leu Gly Ala Ser	
345 350 355	
att ccg ctg tac gcg ctg gcg gcg ctc gcc ctt ggc tcc gca gta atc	1219
Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala Leu Gly Ser Ala Val Ile	
360 365 370	
cgc ggc gta caa atc aag cgc ggg tat gtg gtt tagatttcta cctacgacct	1272
Arg Gly Val Gln Ile Lys Arg Gly Tyr Val Val	
375 380	
gaa	1275

<210> 162

<211> 384

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

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Met Arg Ser Gly Asn Ala Asn Arg Val Phe Ile Gly Val Thr Ile Leu
 1           5           10           15

Leu Phe Thr Ala Gly Trp Ala Ala Asn His Phe Ala Ser Val Leu Val
          20           25           30

Leu Ile Arg Glu Gln Leu Asp Val Ser Ser Val Leu Val Asn Gly Ala
          35           40           45

Phe Gly Ile Tyr Ala Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly Gly
          50           55           60

Val Leu Ala Asp Arg Phe Gly Ala Arg Met Val Val Leu Thr Gly Gly
          65           70           75           80

Val Leu Ser Ala Leu Gly Asn Leu Ser Leu Leu Ala Phe His Asp Gly
          85           90           95

Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly Leu
          100           105           110

Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala Ser
          115           120           125

Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met Gly
          130           135           140

Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile Thr
          145           150           155           160

Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val Gly
          165           170           175

Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala Ser
          180           185           190

Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val Ser
          195           200           205

Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu Ile
          210           215           220

Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu Leu
          225           230           235           240

Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala Gln
          245           250           255

Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val Gly

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260				265				270							
Ala	Leu	Cys	Ala	Leu	Ala	Gly	Phe	Ala	Leu	Ala	Ala	Phe	Gly	Gly	Asp
		275					280					285			
Ser	Ile	Pro	Val	Trp	Leu	Phe	Val	Ile	Ala	Ser	Ile	Leu	Phe	Gly	Thr
	290					295					300				
Ala	Tyr	Gly	Leu	Cys	Leu	Arg	Glu	Gly	Leu	Leu	Ser	Ile	Glu	Thr	Tyr
305					310					315					320
Thr	Pro	Leu	Asn	Arg	Arg	Gly	Thr	Gly	Ile	Gly	Ile	Tyr	Tyr	Val	Phe
				325					330					335	
Thr	Tyr	Leu	Gly	Phe	Gly	Leu	Pro	Val	Leu	Leu	Asp	Ala	Leu	Leu	Pro
			340					345					350		
His	Leu	Gly	Ala	Ser	Ile	Pro	Leu	Tyr	Ala	Leu	Ala	Ala	Leu	Ala	Leu
		355					360					365			
Gly	Ser	Ala	Val	Ile	Arg	Gly	Val	Gln	Ile	Lys	Arg	Gly	Tyr	Val	Val
	370					375					380				

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<210> 163
<211> 1130
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (1)..(1107)
<223> FRXA01922
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<400> 163																
ctg	ctg	ttt	act	gca	gga	tgg	gca	gcc	aat	cat	ttc	gcg	tca	gtg	ttg	48
Leu	Leu	Phe	Thr	Ala	Gly	Trp	Ala	Ala	Asn	His	Phe	Ala	Ser	Val	Leu	
1				5					10					15		
gtg	ttg	atc	cgt	gaa	caa	tta	gac	gta	tca	agc	gtg	ctg	gtc	aac	ggc	96
Val	Leu	Ile	Arg	Glu	Gln	Leu	Asp	Val	Ser	Ser	Val	Leu	Val	Asn	Gly	
			20					25					30			
gct	ttt	ggg	att	tat	gca	ctg	gga	ctt	ctt	cca	agt	ttg	ctc	gca	ggc	144
Ala	Phe	Gly	Ile	Tyr	Ala	Leu	Gly	Leu	Leu	Pro	Ser	Leu	Leu	Ala	Gly	
		35					40					45				
ggg	gtg	ctt	gcc	gac	cgt	ttt	ggg	gcc	cgc	atg	gtg	gta	ctc	acc	gga	192
Gly	Val	Leu	Ala	Asp	Arg	Phe	Gly	Ala	Arg	Met	Val	Val	Leu	Thr	Gly	
	50					55					60					
ggg	gta	ctt	tct	gcg	ctt	gga	aac	ctt	tct	ctt	tta	gcg	ttt	cat	gat	240
Gly	Val	Leu	Ser	Ala	Leu	Gly	Asn	Leu	Ser	Leu	Leu	Ala	Phe	His	Asp	
65					70					75					80	

ggt cct tcc ctc ctg gta gga cga ttc atc gtt ggt ctg ggc gtt gga Gly Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly	288
85 90 95	
tta gtc gtc agc gcg ggc acc gca tgg gcg ggc aga ttg cgc gga gca Leu Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala	336
100 105 110	
agc ggc gtg aca ttg gcc ggc att att ctg acc gcc ggt ttc atg atg Ser Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met	384
115 120 125	
ggg ccg att gtg aca agt ggg ttg ggg atg gcg tcg aca agc att att Gly Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile	432
130 135 140	
acg ccc ttt gcc ata agc gtt gcc ctc tcg ctg atc gcg gtg gtt gtg Thr Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val	480
145 150 155 160	
gga ttt gcg ctt ggc gat gcc cgc agc acc ccg agc gca ctt ggc gca Gly Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala	528
165 170 175	
tcc agc gga atc aaa cac gaa cga agc atg aaa aag gcc ctc gcg gtg Ser Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val	576
180 185 190	
tcc ttg ccg atg gca att tgg gtg ttc agc tgc atc acc acc tcc ctg Ser Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu	624
195 200 205	
atc gtg atg tcc gcg cgc atc gac tcc acc ttc ggc aac gcc att ctt Ile Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu	672
210 215 220	
ctc ccc gga atc ggc gcg gcg atc gcc ttc agc gca ggc ctg atc gca Leu Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala	720
225 230 235 240	
caa ttt tta ggt agg aaa ttc gcg tgg ggt cgt ggc tcc gga atc gtg Gln Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val	768
245 250 255	
ggc gcg ctg tgt gcc ctc gcg ggt ttt gcg ctg gca gct ttt ggt ggc Gly Ala Leu Cys Ala Leu Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly	816
260 265 270	
gac tcc att cca gtg tgg ctt ttc gtt atc gcc tcg atc ctg ttc ggc Asp Ser Ile Pro Val Trp Leu Phe Val Ile Ala Ser Ile Leu Phe Gly	864
275 280 285	
acc gca tat ggc ctc tgc ctg cgc gaa ggc ctc ctc agc atc gaa act Thr Ala Tyr Gly Leu Cys Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr	912
290 295 300	

tac acg cca ctc aac cga cgt ggc acc ggc atc ggc atc tat tat gtg 960
 Tyr Thr Pro Leu Asn Arg Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val
 305 310 315 320

 ttc acg tat ttg gga ttc ggg ctg cca gtg ctt ctc gac gcc ctc ctc 1008
 Phe Thr Tyr Leu Gly Phe Gly Leu Pro Val Leu Leu Asp Ala Leu Leu
 325 330 335

 ccg cac ctt ggc gcc tcc att ccg ctg tac gcg ctg gcg gcg ctc gcc 1056
 Pro His Leu Gly Ala Ser Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala
 340 345 350

 ctt ggc tcc gca gta atc cgc ggc gta caa atc aag cgc ggg tat gtg 1104
 Leu Gly Ser Ala Val Ile Arg Gly Val Gln Ile Lys Arg Gly Tyr Val
 355 360 365

 gtt tagatttcta cctacgacct gaa 1130
 Val

<210> 164

<211> 369

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 164

Leu Leu Phe Thr Ala Gly Trp Ala Ala Asn His Phe Ala Ser Val Leu
 1 5 10 15

 Val Leu Ile Arg Glu Gln Leu Asp Val Ser Ser Val Leu Val Asn Gly
 20 25 30

 Ala Phe Gly Ile Tyr Ala Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly
 35 40 45

 Gly Val Leu Ala Asp Arg Phe Gly Ala Arg Met Val Val Leu Thr Gly
 50 55 60

 Gly Val Leu Ser Ala Leu Gly Asn Leu Ser Leu Leu Ala Phe His Asp
 65 70 75 80

 Gly Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly
 85 90 95

 Leu Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala
 100 105 110

 Ser Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met
 115 120 125

 Gly Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile
 130 135 140

 Thr Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val
 145 150 155 160

Gly Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro S r Ala Leu Gly Ala
 165 170 175
 Ser Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val
 180 185 190
 Ser Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu
 195 200 205
 Ile Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu
 210 215 220
 Leu Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala
 225 230 235 240
 Gln Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val
 245 250 255
 Gly Ala Leu Cys Ala Leu Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly
 260 265 270
 Asp Ser Ile Pro Val Trp Leu Phe Val Ile Ala Ser Ile Leu Phe Gly
 275 280 285
 Thr Ala Tyr Gly Leu Cys Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr
 290 295 300
 Tyr Thr Pro Leu Asn Arg Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val
 305 310 315 320
 Phe Thr Tyr Leu Gly Phe Gly Leu Pro Val Leu Leu Asp Ala Leu Leu
 325 330 335
 Pro His Leu Gly Ala Ser Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala
 340 345 350
 Leu Gly Ser Ala Val Ile Arg Gly Val Gln Ile Lys Arg Gly Tyr Val
 355 360 365
 Val

<210> 165
 <211> 362
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(339)
 <223> RXA02060

<400> 165
 gaa ttt gcc cgc att ttg aag cca aag gga cag gtc atc gtg ctt acc 48
 Glu Phe Ala Arg Ile Leu Lys Pro Lys Gly Gln Val Ile Val Leu Thr
 1 5 10 15

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<400> 166
Glu Phe Ala Arg Ile Leu Lys Pro Lys Gly Gln Val Ile Val Leu Thr
  1             5             10             15
Ala Asp Thr Gly His Leu Ala Glu Leu Arg Glu Pro Leu Gly Ile Ile
      20             25             30
Asp Val Glu Ala Gly Lys Val Asp Arg Met Ile Glu Gln Ala Ala Gly
      35             40             45
His Leu Lys Pro Val Gly Glu Arg Asp Leu Val Glu Phe Glu Met Leu
      50             55             60
Leu Asp Gln Lys Ser Ile Ala Ser Gln Ile Gly Met Ser Pro Ser Ala
      65             70             75             80
Arg His Ile Lys Pro Glu Ala Leu Ala Glu Arg Ile Ala Ala Leu Pro
      85             90             95
Glu Gln Met Lys Val Thr Ala Arg Ala Lys Ile Thr Arg Leu Glu Arg
      100             105             110

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Ile

<210> 167

<211> 1395

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1372)

<223> RXN01936

<400> 167

gcgcggtgac accacagccg ttgtcagcgg cgcttgggtct gtggaggatc gccgagggtta 60

ctaacaaata ggcccaacaa agaggtctaa gctctacctg	gtg agt ttc cga gat	115
	Val Ser Phe Arg Asp	
	1 5	

att ttc gct gac acc aga ccg ctg aaa gaa ccg gcc ttc aaa cgc ctc	163
Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro Ala Phe Lys Arg Leu	
10 15 20	

tgg ctt ggc aat gtt gcc acc gtc att ggt gcc caa tta act gtt gtt	211
Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala Gln Leu Thr Val Val	
25 30 35	

gcc gtt ccg gtg cag att tac caa atg act ggg tcc tcc ggc tat gtg	259
Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly Ser Ser Gly Tyr Val	
40 45 50	

ggc ttg acc ggg ctt ttt ggc ctt att cct ttg gtt att ttt ggc ctt	307
Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu Val Ile Phe Gly Leu	
55 60 65	

tat ggt gga tcc att gcg gat gct ttt gat aaa cgc atc gtg ctg atc	355
Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys Arg Ile Val Leu Ile	
70 75 80 85	

tgc acc acg atc ggc atg tgt gtc acc act gcc ggt ttt tgg gtg ctg	403
Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala Gly Phe Trp Val Leu	
90 95 100	

acc att tta ggc aat gag aat att tgg ctc ctg tta ata aac ttt tct	451
Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu Leu Ile Asn Phe Ser	
105 110 115	

tta cag cag gca ttt ttc gcg gtg aat caa ccc acc cga acg gcg atc	499
Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro Thr Arg Thr Ala Ile	
120 125 130	

ctt cga agt att ttg ccg att gat caa tta gcg tcg gca aca tca ctg	547
Leu Arg Ser Ile Leu Pro Ile Asp Gln Leu Ala Ser Ala Thr Ser Leu	
135 140 145	

aat atg ctg ctc atg cag acc ggc gca atc gtt ggc ccg ctg atc gca Asn Met Leu Leu Met Gln Thr Gly Ala Ile Val Gly Pro Leu Ile Ala 150 155 160 165	595
ggc ggc ttg att ccg ctg atc ggt ttc ggg tgg ctg tat ttc ctt gat Gly Ala Leu Ile Pro Leu Ile Gly Phe Gly Trp Leu Tyr Phe Leu Asp 170 175 180	643
gtt gtc tcc atc atc ccc aca ctg tgg gct gta tgg tca ctg cct tcg Val Val Ser Ile Ile Pro Thr Leu Trp Ala Val Trp Ser Leu Pro Ser 185 190 195	691
atc aag cca tcc ggc aag gtg atg aag gct ggt ttc gcc agt gtg gtg Ile Lys Pro Ser Gly Lys Val Met Lys Ala Gly Phe Ala Ser Val Val 200 205 210	739
gat ggc ctg aag tat ttg gct ggc caa ccc gtg ttg ttg atg gtg atg Asp Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val Leu Leu Met Val Met 215 220 225	787
gtg ctg gat ctt atc gcc atg att ttc ggc atg cca cgt gcg ctt tac Val Leu Asp Leu Ile Ala Met Ile Phe Gly Met Pro Arg Ala Leu Tyr 230 235 240 245	835
ccc gag atc gca gaa gtg aac ttc ggt ggg ggt gac gcc ggt gca acg Pro Glu Ile Ala Glu Val Asn Phe Gly Gly Gly Asp Ala Gly Ala Thr 250 255 260	883
atg ctg gcg ttc atg tac tca tcc atg gct gtt ggc gca gtt ctt ggc Met Leu Ala Phe Met Tyr Ser Ser Met Ala Val Gly Ala Val Leu Gly 265 270 275	931
ggc gtg ctg tct ggt tgg gtg gcc cgg att agc cgc cag ggt gtt gca Gly Val Leu Ser Gly Trp Val Ala Arg Ile Ser Arg Gln Gly Val Ala 280 285 290	979
gtt tat tgg tgc atc atc gcc tgg ggc gca gcc gtt gct ttg ggt ggt Val Tyr Trp Cys Ile Ile Ala Trp Gly Ala Ala Val Ala Leu Gly Gly 295 300 305	1027
gtg gca att gtt gtc agc ccc ggc gcg gtg act gcg tgg gcg tgg atg Val Ala Ile Val Val Ser Pro Gly Ala Val Thr Ala Trp Ala Trp Met 310 315 320 325	1075
ttc atc atc atg atg gtc att ggt ggc atg gct gac atg ttc agc tcg Phe Ile Ile Met Met Val Ile Gly Gly Met Ala Asp Met Phe Ser Ser 330 335 340	1123
gca gtt cga aac gct att ttg cag cag tct gct gcg gaa cat gtg cag Ala Val Arg Asn Ala Ile Leu Gln Gln Ser Ala Ala Glu His Val Gln 345 350 355	1171
ggc cga atc caa ggt gtg tgg atc atc gtc gtg gtg ggt gga cct cgt Gly Arg Ile Gln Gly Val Trp Ile Ile Val Val Val Gly Gly Pro Arg 360 365 370	1219
tta gct gac gtc ctt cac ggt tgg gcc gct gag ccc ctc ggc gca ggt	1267

Leu Ala Asp Val Leu His Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly
 375 380 385
 tgg acg gta tta tgg ggc gga gta gcg gtg gtt gta ctc act gca att 1315
 Trp Thr Val Leu Trp Gly Gly Val Ala Val Val Val Leu Thr Ala Ile
 390 395 400 405
 tgt atg gtg gcg gtg cct aaa ttc tgg aaa tac gag aaa cca aaa att 1363
 Cys Met Val Ala Val Pro Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile
 410 415 420
 acc ggc atc taaataactta tccatgccca ttt 1395
 Thr Gly Ile

<210> 168

<211> 424

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

Val Ser Phe Arg Asp Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro
 1 5 10 15
 Ala Phe Lys Arg Leu Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala
 20 25 30
 Gln Leu Thr Val Val Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly
 35 40 45
 Ser Ser Gly Tyr Val Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu
 50 55 60
 Val Ile Phe Gly Leu Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys
 65 70 75 80
 Arg Ile Val Leu Ile Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala
 85 90 95
 Gly Phe Trp Val Leu Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu
 100 105 110
 Leu Ile Asn Phe Ser Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro
 115 120 125
 Thr Arg Thr Ala Ile Leu Arg Ser Ile Leu Pro Ile Asp Gln Leu Ala
 130 135 140
 Ser Ala Thr Ser Leu Asn Met Leu Leu Met Gln Thr Gly Ala Ile Val
 145 150 155 160
 Gly Pro Leu Ile Ala Gly Ala Leu Ile Pro Leu Ile Gly Phe Gly Trp
 165 170 175
 Leu Tyr Phe Leu Asp Val Val Ser Ile Ile Pro Thr Leu Trp Ala Val
 180 185 190

Trp Ser Leu Pro Ser Ile Lys Pro Ser Gly Lys Val Met Lys Ala Gly
 195 200 205
 Phe Ala Ser Val Val Asp Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val
 210 215 220
 Leu Leu Met Val Met Val Leu Asp Leu Ile Ala Met Ile Phe Gly Met
 225 230 235 240
 Pro Arg Ala Leu Tyr Pro Glu Ile Ala Glu Val Asn Phe Gly Gly Gly
 245 250 255
 Asp Ala Gly Ala Thr Met Leu Ala Phe Met Tyr Ser Ser Met Ala Val
 260 265 270
 Gly Ala Val Leu Gly Gly Val Leu Ser Gly Trp Val Ala Arg Ile Ser
 275 280 285
 Arg Gln Gly Val Ala Val Tyr Trp Cys Ile Ile Ala Trp Gly Ala Ala
 290 295 300
 Val Ala Leu Gly Gly Val Ala Ile Val Val Ser Pro Gly Ala Val Thr
 305 310 315 320
 Ala Trp Ala Trp Met Phe Ile Ile Met Met Val Ile Gly Gly Met Ala
 325 330 335
 Asp Met Phe Ser Ser Ala Val Arg Asn Ala Ile Leu Gln Gln Ser Ala
 340 345 350
 Ala Glu His Val Gln Gly Arg Ile Gln Gly Val Trp Ile Ile Val Val
 355 360 365
 Val Gly Gly Pro Arg Leu Ala Asp Val Leu His Gly Trp Ala Ala Glu
 370 375 380
 Pro Leu Gly Ala Gly Trp Thr Val Leu Trp Gly Gly Val Ala Val Val
 385 390 395 400
 Val Leu Thr Ala Ile Cys Met Val Ala Val Pro Lys Phe Trp Lys Tyr
 405 410 415
 Glu Lys Pro Lys Ile Thr Gly Ile
 420

<210> 169

<211> 945

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(922)

<223> FRXA01936

<400> 169

tttacagcag gcatttttcg cggtgaatca acccaccga acggcgatcc ttcgaagtat 60

tttgccgatt gatcaataag cgtcggcaac atcactgaat atg ctg ctc atg cag 115
Met Leu Leu Met Gln
1 5

acc ggc gca atc gtt ggc ccg ctg atc gca ggt gcg ttg att ccg ctg 163
Thr Gly Ala Ile Val Gly Pro Leu Ile Ala Gly Ala Leu Ile Pro Leu
10 15 20

atc ggt ttc ggg tgg ctg tat ttc ctt gat gtt gtc tcc atc atc ccc 211
Ile Gly Phe Gly Trp Leu Tyr Phe Leu Asp Val Val Ser Ile Ile Pro
25 30 35

aca ctg tgg gct gta tgg tca ctg cct tcg atc aag cca tcc ggc aag 259
Thr Leu Trp Ala Val Trp Ser Leu Pro Ser Ile Lys Pro Ser Gly Lys
40 45 50

gtg atg aag gct ggt ttc gcc agt gtg gtg gat ggc ctg aag tat ttg 307
Val Met Lys Ala Gly Phe Ala Ser Val Val Asp Gly Leu Lys Tyr Leu
55 60 65

gct ggc caa ccc gtg ttg ttg atg gtg atg gtg ctg gat ctt atc gcc 355
Ala Gly Gln Pro Val Leu Leu Met Val Met Val Leu Asp Leu Ile Ala
70 75 80 85

atg att ttc ggc atg cca cgt gcg ctt tac ccc gag atc gca gaa gtg 403
Met Ile Phe Gly Met Pro Arg Ala Leu Tyr Pro Glu Ile Ala Glu Val
90 95 100

aac ttc ggt ggg ggt gac gcc ggt gca acg atg ctg gcg ttc atg tac 451
Asn Phe Gly Gly Gly Asp Ala Gly Ala Thr Met Leu Ala Phe Met Tyr
105 110 115

tca tcc atg gct gtt ggc gca gtt ctt ggc ggc gtg ctg tct ggt tgg 499
Ser Ser Met Ala Val Gly Ala Val Leu Gly Gly Val Leu Ser Gly Trp
120 125 130

gtg gcc cgg att agc cgc cag ggt gtt gca gtt tat tgg tgc atc atc 547
Val Ala Arg Ile Ser Arg Gln Gly Val Ala Val Tyr Trp Cys Ile Ile
135 140 145

gcc tgg ggc gca gcc gtt gct ttg ggt ggt gtg gca att gtt gtc agc 595
Ala Trp Gly Ala Ala Val Ala Leu Gly Gly Val Ala Ile Val Val Ser
150 155 160 165

ccc ggc gcg gtg act gcg tgg gcg tgg atg ttc atc atc atg atg gtc 643
Pro Gly Ala Val Thr Ala Trp Ala Trp Met Phe Ile Ile Met Met Val
170 175 180

att ggt ggc atg gct gac atg ttc agc tcg gca gtt cga aac gct att 691
Ile Gly Gly Met Ala Asp Met Phe Ser Ser Ala Val Arg Asn Ala Ile
185 190 195

ttg cag cag tct gct gcg gaa cat gtg cag ggc cga atc caa ggt gtg 739
Leu Gln Gln Ser Ala Ala Glu His Val Gln Gly Arg Ile Gln Gly Val

200	205	210	
tgg atc atc gtc gtg gtg ggt gga cct cgt tta gct gac gtc ctt cac			787
Trp Ile Ile Val Val Val Gly Gly Pro Arg Leu Ala Asp Val Leu His			
215	220	225	
ggt tgg gcc gct gag ccc ctc ggc gca ggt tgg acg gta tta tgg ggc			835
Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly Trp Thr Val Leu Trp Gly			
230	235	240	245
gga gta gcg gtg gtt gta ctc act gca att tgt atg gtg gcg gtg cct			883
Gly Val Ala Val Val Val Leu Thr Ala Ile Cys Met Val Ala Val Pro			
250	255	260	
aaa ttc tgg aaa tac gag aaa cca aaa att acc ggc atc taaataactta			932
Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile Thr Gly Ile			
265	270		
tccatgccca ttt			945
<210> 170			
<211> 274			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 170			
Met Leu Leu Met Gln Thr Gly Ala Ile Val Gly Pro Leu Ile Ala Gly			
1	5	10	15
Ala Leu Ile Pro Leu Ile Gly Phe Gly Trp Leu Tyr Phe Leu Asp Val			
20	25	30	
Val Ser Ile Ile Pro Thr Leu Trp Ala Val Trp Ser Leu Pro Ser Ile			
35	40	45	
Lys Pro Ser Gly Lys Val Met Lys Ala Gly Phe Ala Ser Val Val Asp			
50	55	60	
Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val Leu Leu Met Val Met Val			
65	70	75	80
Leu Asp Leu Ile Ala Met Ile Phe Gly Met Pro Arg Ala Leu Tyr Pro			
85	90	95	
Glu Ile Ala Glu Val Asn Phe Gly Gly Gly Asp Ala Gly Ala Thr Met			
100	105	110	
Leu Ala Phe Met Tyr Ser Ser Met Ala Val Gly Ala Val Leu Gly Gly			
115	120	125	
Val Leu Ser Gly Trp Val Ala Arg Ile Ser Arg Gln Gly Val Ala Val			
130	135	140	
Tyr Trp Cys Ile Ile Ala Trp Gly Ala Ala Val Ala Leu Gly Gly Val			
145	150	155	160

Ala Ile Val Val Ser Pro Gly Ala Val Thr Ala Trp Ala Trp Met Phe
 165 170 175

Ile Il Met Met Val Ile Gly Gly Met Ala Asp Met Phe Ser Ser Ala
 180 185 190

Val Arg Asn Ala Ile Leu Gln Gln Ser Ala Ala Glu His Val Gln Gly
 195 200 205

Arg Ile Gln Gly Val Trp Ile Ile Val Val Val Gly Gly Pro Arg Leu
 210 215 220

Ala Asp Val Leu His Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly Trp
 225 230 235 240

Thr Val Leu Trp Gly Gly Val Ala Val Val Val Leu Thr Ala Ile Cys
 245 250 255

Met Val Ala Val Pro Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile Thr
 260 265 270

Gly Ile

<210> 171
 <211> 549
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(526)
 <223> FRXA01937

<400> 171
 gcgcggtgac accacagccg ttgtcagcgg cgcttggtct gtggaggatc gccgaggtta 60

ctaacaata ggcccaacaa agaggtctaa gctctacctg gtg agt ttc cga gat 115
 Val Ser Phe Arg Asp
 1 5

att ttc gct gac acc aga ccg ctg aaa gaa ccg gcc ttc aaa cgc ctc 163
 Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro Ala Phe Lys Arg Leu
 10 15 20

tgg ctt ggc aat gtt gcc acc gtc att ggt gcc caa tta act gtt gtt 211
 Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala Gln Leu Thr Val Val
 25 30 35

gcc gtt ccg gtg cag att tac caa atg act ggg tcc tcc ggc tat gtg 259
 Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly Ser Ser Gly Tyr Val
 40 45 50

ggc ttg acc ggg ctt ttt ggc ctt att cct ttg gtt att ttt ggc ctt 307
 Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu Val Ile Phe Gly Leu
 55 60 65

tat ggt gga tcc att gcg gat gct ttt gat aaa cgc atc gtg ctg atc 355
 Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys Arg Ile Val Leu Ile
 70 75 80 85
 tgc acc acg atc ggc atg tgt gtc acc act gcc ggt ttt tgg gtg ctg 403
 Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala Gly Phe Trp Val Leu
 90 95 100
 acc att tta ggc aat gag aat att tgg ctc ctg tta ata aac ttt tct 451
 Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu Ile Asn Phe Ser
 105 110 115
 tta cag cag gca ttt ttc gcg gtg aat caa ccc acc cga acg gcg atc 499
 Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro Thr Arg Thr Ala Ile
 120 125 130
 ctt cga agt att ttg ccg att gat caa taagcgtcgg caacatcact 546
 Leu Arg Ser Ile Leu Pro Ile Asp Gln
 135 140
 gaa 549

<210> 172

<211> 142

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 172

Val Ser Phe Arg Asp Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro
 1 5 10 15
 Ala Phe Lys Arg Leu Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala
 20 25 30
 Gln Leu Thr Val Val Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly
 35 40 45
 Ser Ser Gly Tyr Val Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu
 50 55 60
 Val Ile Phe Gly Leu Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys
 65 70 75 80
 Arg Ile Val Leu Ile Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala
 85 90 95
 Gly Phe Trp Val Leu Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu
 100 105 110
 Leu Ile Asn Phe Ser Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro
 115 120 125
 Thr Arg Thr Ala Ile Leu Arg Ser Ile Leu Pro Ile Asp Gln
 130 135 140

gcg tca ctg ttt att ttg gtg gcg cga ctc ccc gtt gtt cca cca cca 643
 Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro Val Val Pro Pro Pro
 170 175 180

tca gca tcg aag caa aac gtt agt ggc aag gtg cag tgg gga ccg acc 691
 Ser Ala Ser Lys Gln Asn Val Ser Gly Lys Val Gln Trp Gly Pro Thr
 185 190 195

atc atc cac atg gtt tcc ggc ttt gtg gtg ggc atc ggc atc atc ggc 739
 Ile Ile His Met Val Ser Gly Phe Val Val Gly Ile Gly Ile Ile Gly
 200 205 210

att gga ttc atg aca tcg ctg cac gtt ggc gag caa ttc gga ctt gat 787
 Ile Gly Phe Met Thr Ser Leu His Val Gly Glu Gln Phe Gly Leu Asp
 215 220 225

gct gca gcg cgt ggt ttg gtg gtc atg tgt ggt ggc ctg gct gcg ttc 835
 Ala Ala Ala Arg Gly Leu Val Val Met Cys Gly Gly Leu Ala Ala Phe
 230 235 240 245

ttt gcc tcc cgc aag att ggc gat ttg gca gac aaa ttt ggt gtg cgc 883
 Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp Lys Phe Gly Val Arg
 250 255 260

gcg gtg ctc att gtc agt gct gtc atc ggt acc atc gca ctc gca ctg 931
 Ala Val Leu Ile Val Ser Ala Val Ile Gly Thr Ile Ala Leu Ala Leu
 265 270 275

ctg ccg atc gca ccg tgg atc att gtg gtg gcc gta ctg tgg gcc ttc 979
 Leu Pro Ile Ala Pro Trp Ile Ile Val Val Ala Val Leu Trp Ala Phe
 280 285 290

gca gta gca gca gca caa gga atc caa gca acc gtc aac ttg gct gtc 1027
 Ala Val Ala Ala Ala Gln Gly Ile Gln Ala Thr Val Asn Leu Ala Val
 295 300 305

atc gga agc ccc ggt gga tca tcg ctg ctt tct acc gtg cag gct ttc 1075
 Ile Gly Ser Pro Gly Gly Ser Ser Leu Leu Ser Thr Val Gln Ala Phe
 310 315 320 325

cga ttc ttc gga tca gcg gca gca cca gtg aca ttc ctt cct atc tat 1123
 Arg Phe Phe Gly Ser Ala Ala Ala Pro Val Thr Phe Leu Pro Ile Tyr
 330 335 340

atg ggc atc ggc tcg ggg gcg ttt tgg gtc agc gcg gta gcg ctg ttc 1171
 Met Gly Ile Gly Ser Gly Ala Phe Trp Val Ser Ala Val Ala Leu Phe
 345 350 355

ttc gtt gcc atc gcc cag tgg ctc aac ccg cag ccg gtg gag ccg ggc 1219
 Phe Val Ala Ile Ala Gln Trp Leu Asn Pro Gln Arg Val Glu Arg Gly
 360 365 370

tgagggagac gtcgagaagc gtc 1242

<210> 174

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 174

Met Lys Lys Leu Gln Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly
 1 5 10 15

Pro Phe Thr Gly Gln Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp
 20 25 30

Thr Phe Asp Ile Ser Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr
 35 40 45

Leu Leu Pro Phe Ala Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg
 50 55 60

Lys Ile His Pro His Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu
 65 70 75 80

Pro Leu Ala Leu Leu Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met
 85 90 95

Ala Ala Tyr Ala Thr Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val
 100 105 110

Leu Gln Ile Met Leu Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys
 115 120 125

Ala Leu Gly Thr Tyr Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala
 130 135 140

Pro Leu Ile Ala Gly Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe
 145 150 155 160

Leu Val Thr Ala Ala Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro
 165 170 175

Val Val Pro Pro Pro Ser Ala Ser Lys Gln Asn Val Ser Gly Lys Val
 180 185 190

Gln Trp Gly Pro Thr Ile Ile His Met Val Ser Gly Phe Val Val Gly
 195 200 205

Ile Gly Ile Ile Gly Ile Gly Phe Met Thr Ser Leu His Val Gly Glu
 210 215 220

Gln Phe Gly Leu Asp Ala Ala Ala Arg Gly Leu Val Val Met Cys Gly
 225 230 235 240

Gly Leu Ala Ala Phe Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp
 245 250 255

Lys Phe Gly Val Arg Ala Val Leu Ile Val Ser Ala Val Ile Gly Thr
 260 265 270

Ile Ala Leu Ala Leu Leu Pro Ile Ala Pro Trp Ile Ile Val Val Ala

275	280	285
Val Leu Trp Ala Phe Ala	Val Ala Ala Ala Gln Gly	Ile Gln Ala Thr
290	295	300
Val Asn Leu Ala Val	Ile Gly Ser Pro Gly Gly	Ser Ser Leu Leu Ser
305	310	315
Thr Val Gln Ala Phe Arg	Phe Phe Gly Ser Ala Ala	Ala Pro Val Thr
325	330	335
Phe Leu Pro Ile Tyr Met	Gly Ile Gly Ser Gly Ala	Phe Trp Val Ser
340	345	350
Ala Val Ala Leu Phe Phe	Val Ala Ile Ala Gln Trp	Leu Asn Pro Gln
355	360	365
Arg Val Glu Arg Gly		
370		

<210> 175
 <211> 871
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(871)
 <223> FRXA01010

<400> 175
 gtgccaaagc gtttcctgta aaacgcataa cccgaatac cccctgtttc cagatccaaa 60
 aaaagatctg gcaggggggtt taggcataga ttaggaactt atg aag aaa ctg caa 115
 Met Lys Lys Leu Gln
 1 5
 atg ccg gcc att ttg gtc gga ggc ttt gtg ggg ccg ttt act ggc caa 163
 Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly Pro Phe Thr Gly Gln
 10 15 20
 gct cta tca gtg gtc ttg ccg gaa ttt gca gac acc ttt gat atc agt 211
 Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp Thr Phe Asp Ile Ser
 25 30 35
 gtc agc cag gca gcg ctg acc atg acc gca tac ttg ttg ccc ttt gcc 259
 Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr Leu Leu Pro Phe Ala
 40 45 50
 acc atg atg ttg ttt tcg ggg cgc atc acc aga aag atc cat ccg cat 307
 Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg Lys Ile His Pro His
 55 60 65
 aag gtg gtg cag gcg gct tat att gtc aca ctg cca ctt gcg ctg ttg 355
 Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu Pro Leu Ala Leu Leu
 70 75 80 85

ctc cta gtt aca cca tcg tgg ggg ctg ttt atg gct gcg tat gcc acg 403
 Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met Ala Ala Tyr Ala Thr
 90 95 100

att ggt atc gct aat gca ttt acc act ccg gtg ctg caa att atg ttg 451
 Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val Leu Gln Ile Met Leu
 105 110 115

cgt gag ctt gtt ccg ccg cgt tct ttg ggt aag gca ttg ggc acc tat 499
 Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys Ala Leu Gly Thr Tyr
 120 125 130

gct gcg atg caa tca ctc ggc atg ttg tcg gcg cca ctg atc gca ggt 547
 Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala Pro Leu Ile Ala Gly
 135 140 145

gtg tct tcg gtg gtg tcg tgg agg ttg acc ttc ctg gtc act gca gca 595
 Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe Leu Val Thr Ala Ala
 150 155 160 165

gcg tca ctg ttt att ttg gtg gcg cga ctc ccc gtt gtt cca cca cca 643
 Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro Val Val Pro Pro Pro
 170 175 180

tca gca ttg aag caa aac gtt agt ggc aag gtg cag tgg gga ccg acc 691
 Ser Ala Leu Lys Gln Asn Val Ser Gly Lys Val Gln Trp Gly Pro Thr
 185 190 195

atc atc cac atg gtt tcc ggc ttt gtg gtg ggc atc ggc atc atc ggc 739
 Ile Ile His Met Val Ser Gly Phe Val Val Gly Ile Gly Ile Ile Gly
 200 205 210

att gga ttc atg aca tcg ctg cac gtt ggc gag caa ttc gga ctt aat 787
 Ile Gly Phe Met Thr Ser Leu His Val Gly Glu Gln Phe Gly Leu Asn
 215 220 225

act gca gcg cgt ggt ttg gtg gtc atg tgt ggt ggc cgg gct gcg ttc 835
 Thr Ala Ala Arg Gly Leu Val Val Met Cys Gly Gly Arg Ala Ala Phe
 230 235 240 245

ttt gcc tcc cgc aag ata ggc gat ttg gca gac aaa 871
 Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp Lys
 250 255

<210> 176

<211> 257

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 176

Met Lys Lys Leu Gln Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly
 1 5 10 15

Pro Phe Thr Gly Gln Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp
 20 25 30

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Thr Phe Asp Ile Ser Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr
   35                               40                               45

Leu Leu Pro Phe Ala Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg
   50                               55                               60

Lys Ile His Pro His Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu
   65                               70                               75                               80

Pro Leu Ala Leu Leu Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met
      85                               90                               95

Ala Ala Tyr Ala Thr Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val
      100                               105                               110

Leu Gln Ile Met Leu Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys
      115                               120                               125

Ala Leu Gly Thr Tyr Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala
      130                               135                               140

Pro Leu Ile Ala Gly Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe
      145                               150                               155                               160

Leu Val Thr Ala Ala Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro
      165                               170                               175

Val Val Pro Pro Pro Ser Ala Leu Lys Gln Asn Val Ser Gly Lys Val
      180                               185                               190

Gln Trp Gly Pro Thr Ile Ile His Met Val Ser Gly Phe Val Val Gly
      195                               200                               205

Ile Gly Ile Ile Gly Ile Gly Phe Met Thr Ser Leu His Val Gly Glu
      210                               215                               220

Gln Phe Gly Leu Asn Thr Ala Ala Arg Gly Leu Val Val Met Cys Gly
      225                               230                               235                               240

Gly Arg Ala Ala Phe Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp
      245                               250                               255

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Lys

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<210> 177
<211> 1266
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
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<223> RXN03142

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                               Val Phe Ile Leu Gly
                               1 5
tgg ctc gtc aac ttg acc cag tac ttg agc ttc tac ttc ctg atc aca 163
Trp Leu Val Asn Leu Thr Gln Tyr Leu Ser Phe Tyr Phe Leu Ile Thr
                               10 15 20
gtc atg gcg ctg tat gcg atg gaa agc ttc gcc gtt tca gag gcc gct 211
Val Met Ala Leu Tyr Ala Met Glu Ser Phe Ala Val Ser Glu Ala Ala
                               25 30 35
gtc gga ttt gcg gcc agc tcc ttt gtt atc ggc gca acc gtg gct cgt 259
Val Gly Phe Ala Ala Ser Ser Phe Val Ile Gly Ala Thr Val Ala Arg
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gtg ttc gcg gga tgg acg tcc gac cgt ttt ggt aaa aaa cag atc ctg 307
Val Phe Ala Gly Trp Thr Ser Asp Arg Phe Gly Lys Lys Gln Ile Leu
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ctc atc ttt gtc ggc ttg gaa gcg gta gca tca cta ttc tat att cca 355
Leu Ile Phe Val Gly Leu Glu Ala Val Ala Ser Leu Phe Tyr Ile Pro
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gct gcc tca cta cca gcg ctg gtt gct gtg cgt ttt gtt cac ggt ttt 403
Ala Ala Ser Leu Pro Ala Leu Val Ala Val Arg Phe Val His Gly Phe
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Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala Leu Val Gln Ser Val
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Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly Tyr Phe Ala Leu Gly
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Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile Ala Leu Phe Val Ile
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gat gac ttc aac tac aac acc ctg ttc tgg att acc act gcg acc agt 595
Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr Ser
150 155 160 165
gtt ttc ggc ctg atc ctc acc gtt ttg atc cgc aag ccg gag ttc att 643
Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe Ile
                               170 175 180
aag aat gcg gaa cac ggc aga gta aag cca gtc tgg tct atc aag act 691
Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys Thr
185 190 195
gtt gtg cac cca tcg gtc atg ctc att gga ttc ttc atg ctc gct gtc 739
Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala Val

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200	205	210	
gga ctg gct tac gca ggc gtg atc acc ttc ctc aac ggc ttc gcg caa Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala Gln 215 220 225			787
gac act ggc ctc acc gcc gga gcg ggt ctt ttc ttt atc gct tat gcg Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala 230 235 240 245			835
gtt gcg atg ctg gtc atg cgt ttc ttc ctt gga cgc att cag gac aaa Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp Lys 250 255 260			883
cat ggt gac aac ccg gtt att tac ttc ggt ttg atc agc ttc gcc ctc His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala Leu 265 270 275			931
gcg ctg ggg ctt atg gct ttg gcg act gaa gac tgg cac att gtt ctc Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val Leu 280 285 290			979
gct ggc gca ctc acc ggt ttg ggc tat ggc acc atc atg ccg gcc gca Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr Ile Met Pro Ala Ala 295 300 305			1027
caa gcc att gct gtc gat tca gtt cca agc act cag gtt ggt tcc ggt Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr Gln Val Gly Ser Gly 310 315 320 325			1075
att tct acg ctt ttc ctg ttc acc gac atc ggc att ggc tta ggc cca Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly Ile Gly Leu Gly Pro 330 335 340			1123
atc ctg ctg ggt gga ttg gtt gca gcg acc gga tac aac gtc atg tac Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met Tyr 345 350 355			1171
gca gct ttg gcc gca gtg att gtt gtg gcg ggc gtg ctc tac ctg gtt Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly Val Leu Tyr Leu Val 360 365 370			1219
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<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

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20					25					30					
Val	Ser	Glu	Ala	Ala	Val	Gly	Phe	Ala	Ala	Ser	Ser	Phe	Val	Ile	Gly
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Ala	Thr	Val	Ala	Arg	Val	Phe	Ala	Gly	Trp	Thr	Ser	Asp	Arg	Phe	Gly
		50					55					60			
Lys	Lys	Gln	Ile	Leu	Leu	Ile	Phe	Val	Gly	Leu	Glu	Ala	Val	Ala	Ser
		65					70					75			80
Leu	Phe	Tyr	Ile	Pro	Ala	Ala	Ser	Leu	Pro	Ala	Leu	Val	Ala	Val	Arg
				85					90						95
Phe	Val	His	Gly	Phe	Ser	Tyr	Ser	Leu	Ala	Ser	Thr	Ala	Val	Met	Ala
			100						105					110	
Leu	Val	Gln	Ser	Val	Ile	Pro	Ala	Ser	Arg	Arg	Ala	Glu	Gly	Thr	Gly
		115							120					125	
Tyr	Phe	Ala	Leu	Gly	Ser	Thr	Leu	Ala	Thr	Ala	Phe	Gly	Pro	Ala	Ile
		130							135					140	
Ala	Leu	Phe	Val	Ile	Asp	Asp	Phe	Asn	Tyr	Asn	Thr	Leu	Phe	Trp	Ile
				145					150					155	160
Thr	Thr	Ala	Thr	Ser	Val	Phe	Gly	Leu	Ile	Leu	Thr	Val	Leu	Ile	Arg
				165					170					175	
Lys	Pro	Glu	Phe	Ile	Lys	Asn	Ala	Glu	His	Gly	Arg	Val	Lys	Pro	Val
			180						185					190	
Trp	Ser	Ile	Lys	Thr	Val	Val	His	Pro	Ser	Val	Met	Leu	Ile	Gly	Phe
			195						200					205	
Phe	Met	Leu	Ala	Val	Gly	Leu	Ala	Tyr	Ala	Gly	Val	Ile	Thr	Phe	Leu
			210						215					220	
Asn	Gly	Phe	Ala	Gln	Asp	Thr	Gly	Leu	Thr	Ala	Gly	Ala	Gly	Leu	Phe
				225					230					235	240
Phe	Ile	Ala	Tyr	Ala	Val	Ala	Met	Leu	Val	Met	Arg	Phe	Phe	Leu	Gly
				245					250					255	
Arg	Ile	Gln	Asp	Lys	His	Gly	Asp	Asn	Pro	Val	Ile	Tyr	Phe	Gly	Leu
			260						265					270	
Ile	Ser	Phe	Ala	Leu	Ala	Leu	Gly	Leu	Met	Ala	Leu	Ala	Thr	Glu	Asp
			275						280					285	
Trp	His	Ile	Val	Leu	Ala	Gly	Ala	Leu	Thr	Gly	Leu	Gly	Tyr	Gly	Thr
				290					295					300	
Ile	Met	Pro	Ala	Ala	Gln	Ala	Ile	Ala	Val	Asp	Ser	Val	Pro	Ser	Thr
				305					310					315	320
Gln	Val	Gly	Ser	Gly	Ile	Ser	Thr	Leu	Phe	Leu	Phe	Thr	Asp	Ile	Gly

325 330 335
 Ile Gly Leu Gly Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly
 340 345 350
 Tyr Asn Val Met Tyr Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly
 355 360 365
 Val Leu Tyr Leu Val Ala Leu Gly Arg Lys Ala Ser His
 370 375 380

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 <222> (1)..(891)
 <223> FRXA01150

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 ttt tct tat tct ctt gct tcc acc gct gtg atg gca ctt gtg cag tcc 96
 Phe Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala Leu Val Gln-Ser
 20 25 30
 gtg att cct gca agc cgt agg gca gag ggc acc ggc tac ttc gcg ctc 144
 Val Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly Tyr Phe Ala Leu
 35 40 45
 gga tcc aca ctg gct aca gct ttc ggc cca gca att gcg ctg ttt gtt 192
 Gly Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile Ala Leu Phe Val
 50 55 60
 atc gat gac ttc aac tac aac acc ctg ttc tgg att acc act gcg acc 240
 Ile Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr
 65 70 75 80
 agt gtt ttc ggc ctg atc ctc acc gtt ttg atc cgc aag ccg gag ttc 288
 Ser Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe
 85 90 95
 att aag aat gcg gaa cac ggc aga gta aag cca gtc tgg tct atc aag 336
 Ile Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys
 100 105 110
 act gtt gtg cac cca tcg gtc atg ctc att gga ttc ttc atg ctc gct 384
 Thr Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala
 115 120 125
 gtc gga ctg gct tac gca ggc gtg atc acc ttc ctc aac ggc ttc gcg 432
 Val Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala

130	135	140	
caa gac act ggc ctc acc gcc gga gcg ggt ctt ttc ttt atc gct tat			480
Gln Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr			
145	150	155	160
gcg gtt gcg atg ctg gtc atg cgt ttc ttc ctt gga cgc att cag gac			528
Ala Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp			
	165	170	175
aaa cat ggt gac aac ccg gtt att tac ttc ggt ttg atc agc ttc gcc			576
Lys His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala			
	180	185	190
ctc gcg ctg ggg ctt atg gct ttg gcg act gaa gac tgg cac att gtt			624
Leu Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val			
	195	200	205
ctc gct ggc gca ctc acc ggt ttg ggc tat ggc acc atc atg ccg gcc			672
Leu Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr Ile Met Pro Ala			
	210	215	220
gca caa gcc att gct gtc gat tca gtt cca agc act cag gtt ggt tcc			720
Ala Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr Gln Val Gly Ser			
	225	230	240
ggt att tct acg ctt ttc ctg ttc acc gac atc ggc att ggc tta ggc			768
Gly Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly Ile Gly Leu Gly			
	245	250	255
cca atc ctg ctg ggt gga ttg gtt gca gcg acc gga tac aac gtc atg			816
Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met			
	260	265	270
tac gca gct ttg gcc gca gtg att gtt gtg gcg ggc gtg ctc tac ctg			864
Tyr Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly Val Leu Tyr Leu			
	275	280	285
gtt gct ttg ggt agg aaa gct agc cac taagtttagag cattttattg			911
Val Ala Leu Gly Arg Lys Ala Ser His			
	290	295	
agc			914
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Val Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly Tyr Phe Ala Leu
 35 40 45
 Gly Ser Thr Leu Ala Thr Ala Ph Gly Pro Ala Ile Ala Leu Phe Val
 50 55 60
 Ile Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr
 65 70 75 80
 Ser Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe
 85 90 95
 Ile Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys
 100 105 110
 Thr Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala
 115 120 125
 Val Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala
 130 135 140
 Gln Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr
 145 150 155 160
 Ala Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp
 165 170 175
 Lys His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala
 180 185 190
 Leu Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val
 195 200 205
 Leu Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr Ile Met Pro Ala
 210 215 220
 Ala Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr Gln Val Gly Ser
 225 230 235 240
 Gly Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly Ile Gly Leu Gly
 245 250 255
 Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met
 260 265 270
 Tyr Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly Val Leu Tyr Leu
 275 280 285
 Val Ala Leu Gly Arg Lys Ala Ser His
 290 295

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<211> 1341

<212> DNA

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<220>

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<222> (101)..(1318)

<223> RXN02964

<400> 181

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                               Val Ser Val Ala Glu
                               1 5

gaa ggg aaa ctt ttt aca cca acg ttt gtc atg gga tgg ttt gcc aac 163
Glu Gly Lys Leu Phe Thr Pro Thr Phe Val Met Gly Trp Phe Ala Asn
                               10 15 20

ctt ttc cag ttc ctg gtg ttc tac ttc ctc atc acc acc atg gct ttg 211
Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile Thr Thr Met Ala Leu
                               25 30 35

tac gcc atc aag gaa ttt caa gcc tct gaa gta gaa gct ggc ttc gca 259
Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val Glu Ala Gly Phe Ala
                               40 45 50

tcc agc tca att gtt atc ggc gca gtc ttt tcc agg ttt ttc tcc ggc 307
Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser Arg Phe Phe Ser Gly
                               55 60 65

tat att att gac cgt ttt ggt cga cgc aag att gtg ctc atc tca gtc 355
Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile Val Leu Ile Ser Val
                               70 75 80 85

cta gtc act acc att gcg tgt gcc ttg tac ctt ccc atc gaa tca ttg 403
Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu Pro Ile Glu Ser Leu
                               90 95 100

cca ttg cta tac gca aac agg ttc ctc cac ggt gtt gga tac gct ttt 451
Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly Val Gly Tyr Ala Phe
                               105 110 115

gct gcc acc gcg atc atg gca atg gtc cag gag ctc att cca gcg tca 499
Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu Leu Ile Pro Ala Ser
                               120 125 130

cga cgt tcc gaa ggt act ggt tac ctg gca ttg ggc act acc gtt tct 547
Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu Gly Thr Thr Val Ser
                               135 140 145

gca gca ctt gga cca gcc cta gca ctt ttt gtc cta gga aca ttt gat 595
Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val Leu Gly Thr Phe Asp
                               150 155 160 165

tac gac atg ctg ttt atc gtg gtc ttg gca acc tcg gtc atc tct ttg 643
Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr Ser Val Ile Ser Leu
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atc gcc gtc gtg ttc atg tac ttt aag acc agc gac cct gag cct tct 691

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Ile	Ala	Val	Val	Phe	Met	Tyr	Phe	Lys	Thr	Ser	Asp	Pro	Glu	Pro	Ser		
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ggg	gaa	cca	gcc	aag	ttc	agc	ttc	aaa	tct	att	atg	aac	cca	aag	atc	739	
Gly	Glu	Pro	Ala	Lys	Phe	Ser	Phe	Lys	Ser	Ile	Met	Asn	Pro	Lys	Ile		
		200					205					210					
atc	ccc	atc	ggc	atc	ttt	atc	ttg	ctt	att	tgc	ttt	gct	tac	tct	ggc	787	
Ile	Pro	Ile	Gly	Ile	Phe	Ile	Leu	Leu	Ile	Cys	Phe	Ala	Tyr	Ser	Gly		
	215					220					225						
gtc	att	gcc	tac	atc	aac	gca	ttt	gct	gaa	gaa	cgc	gat	ctg	att	acg	835	
Val	Ile	Ala	Tyr	Ile	Asn	Ala	Phe	Ala	Glu	Glu	Arg	Asp	Leu	Ile	Thr		
230					235				240						245		
ggt	gct	gga	ttg	ttc	ttc	att	gcc	tac	gca	gta	tca	atg	ttt	gtg	atg	883	
Gly	Ala	Gly	Leu	Phe	Phe	Ile	Ala	Tyr	Ala	Val	Ser	Met	Phe	Val	Met		
			250						255					260			
cgc	agc	ttc	ctt	ggc	aaa	ctg	cag	gac	cgt	cgc	gga	gac	aac	gtc	gtt	931	
Arg	Ser	Phe	Leu	Gly	Lys	Leu	Gln	Asp	Arg	Arg	Gly	Asp	Asn	Val	Val		
		265						270					275				
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Ile	Tyr	Phe	Gly	Leu	Phe	Phe	Phe	Val	Ile	Ser	Leu	Thr	Ile	Leu	Ser		
	280						285					290					
ttt	gcc	act	tcc	aac	tgg	cac	gtt	gtg	ttg	tcc	gga	gtc	att	gca	ggt	1027	
Phe	Ala	Thr	Ser	Asn	Trp	His	Val	Val	Leu	Ser	Gly	Val	Ile	Ala	Gly		
	295					300					305						
ctg	gga	tac	ggc	act	ttg	atg	cca	gca	gtg	cag	tcc	atc	gct	gtt	ggt	1075	
Leu	Gly	Tyr	Gly	Thr	Leu	Met	Pro	Ala	Val	Gln	Ser	Ile	Ala	Val	Gly		
310					315					320					325		
gta	gta	gac	aaa	acc	gaa	ttc	ggt	acg	gcc	ttc	tcc	act	ttg	ttc	ctg	1123	
Val	Val	Asp	Lys	Thr	Glu	Phe	Gly	Thr	Ala	Phe	Ser	Thr	Leu	Phe	Leu		
			330						335					340			
ttt	gtg	gac	tta	ggt	ttt	ggc	ttt	gga	cct	att	atc	ctg	gga	gca	gtt	1171	
Phe	Val	Asp	Leu	Gly	Phe	Gly	Phe	Gly	Pro	Ile	Ile	Leu	Gly	Ala	Val		
		345						350					355				
tct	gcg	gca	att	ggt	ttc	gga	cct	atg	tat	gca	gca	ctg	gca	ggt	gtg	1219	
Ser	Ala	Ala	Ile	Gly	Phe	Gly	Pro	Met	Tyr	Ala	Ala	Leu	Ala	Gly	Val		
	360					365						370					
ggt	gtg	att	gcc	gga	atc	ttc	tac	ctg	ttc	aca	cac	gct	cgc	acc	gat	1267	
Gly	Val	Ile	Ala	Gly	Ile	Phe	Tyr	Leu	Phe	Thr	His	Ala	Arg	Thr	Asp		
	375					380					385						
cga	gct	aag	aat	ggc	ttt	gtt	aaa	cac	cca	gag	cct	gtc	gct	tta	gtt	1315	
Arg	Ala	Lys	Asn	Gly	Phe	Val	Lys	His	Pro	Glu	Pro	Val	Ala	Leu	Val		
390					395					400				405			
agc	tagttcttttc	agctttccct	ccc													1341	
Ser																	

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<211> 406

<212> PRT

<213> Corynebacterium glutamicum

<400> 182

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Thr Thr Met Ala Leu Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val
 35 40 45

Glu Ala Gly Phe Ala Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser
 50 55 60

Arg Phe Phe Ser Gly Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile
 65 70 75 80

Val Leu Ile Ser Val Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu
 85 90 95

Pro Ile Glu Ser Leu Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly
 100 105 110

Val Gly Tyr Ala Phe Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu
 115 120 125

Leu Ile Pro Ala Ser Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu
 130 135 140

Gly Thr Thr Val Ser Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val
 145 150 155 160

Leu Gly Thr Phe Asp Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr
 165 170 175

Ser Val Ile Ser Leu Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser
 180 185 190

Asp Pro Glu Pro Ser Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile
 195 200 205

Met Asn Pro Lys Ile Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys
 210 215 220

Phe Ala Tyr Ser Gly Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu
 225 230 235 240

Arg Asp Leu Ile Thr Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val
 245 250 255

Ser Met Phe Val Met Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg
 260 265 270
 Gly Asp Asn Val Val Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser
 275 280 285
 Leu Thr Ile Leu Ser Phe Ala Thr Ser Asn Trp His Val Val Leu Ser
 290 295 300
 Gly Val Ile Ala Gly Leu Gly Tyr Gly Thr Leu Met Pro Ala Val Gln
 305 310 315 320
 Ser Ile Ala Val Gly Val Val Asp Lys Thr Glu Phe Gly Thr Ala Phe
 325 330 335
 Ser Thr Leu Phe Leu Phe Val Asp Leu Gly Phe Gly Phe Gly Pro Ile
 340 345 350
 Ile Leu Gly Ala Val Ser Ala Ala Ile Gly Phe Gly Pro Met Tyr Ala
 355 360 365
 Ala Leu Ala Gly Val Gly Val Ile Ala Gly Ile Phe Tyr Leu Phe Thr
 370 375 380
 His Ala Arg Thr Asp Arg Ala Lys Asn Gly Phe Val Lys His Pro Glu
 385 390 395 400
 Pro Val Ala Leu Val Ser
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<210> 183

<211> 1006

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1006)

<223> FRXA02116

<400> 183

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 Val Ser Val Ala Glu
 1 5

 gaa ggg aaa ctt ttt aca cca acg ttt gtc atg gga tgg ttt gcc aac 163
 Glu Gly Lys Leu Phe Thr Pro Thr Phe Val Met Gly Trp Phe Ala Asn
 10 15 20

 ctt ttc cag ttc ctg gtg ttc tac ttc ctc atc acc acc atg gct ttg 211
 Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile Thr Thr Met Ala Leu
 25 30 35

tac gcc atc aag gaa ttt caa gcc tct gaa gta gaa gct ggc ttc gca 259

Tyr	Ala	Ile	Lys	Glu	Phe	Gln	Ala	Ser	Glu	Val	Glu	Ala	Gly	Phe	Ala		
	40						45					50					
tcc	agc	tca	att	gtt	atc	ggc	gca	gtc	ttt	tcc	agg	ttt	ttc	tcc	ggc	307	
Ser	Ser	Ser	Il	Val	Ile	Gly	Ala	Val	Phe	Ser	Arg	Phe	Phe	S	r	Gly	
	55					60					65						
tat	att	att	gac	cgt	ttt	ggc	cga	cgc	aag	att	gtg	ctc	atc	tca	gtc	355	
Tyr	Ile	Ile	Asp	Arg	Phe	Gly	Arg	Arg	Lys	Ile	Val	Leu	Ile	Ser	Val		
	70				75					80					85		
cta	gtc	act	acc	att	gcg	tgt	gcc	ttg	tac	ctt	ccc	atc	gaa	tca	ttg	403	
Leu	Val	Thr	Thr	Ile	Ala	Cys	Ala	Leu	Tyr	Leu	Pro	Ile	Glu	Ser	Leu		
				90					95					100			
cca	ttg	cta	tac	gca	aac	agg	ttc	ctc	cac	ggc	gtt	gga	tac	gct	ttt	451	
Pro	Leu	Leu	Tyr	Ala	Asn	Arg	Phe	Leu	His	Gly	Val	Gly	Tyr	Ala	Phe		
			105					110					115				
gct	gcc	acc	gcg	atc	atg	gca	atg	gtc	cag	gag	ctc	att	cca	gcg	tca	499	
Ala	Ala	Thr	Ala	Ile	Met	Ala	Met	Val	Gln	Glu	Leu	Ile	Pro	Ala	Ser		
		120					125					130					
cga	cgt	tcc	gaa	ggc	act	ggc	tac	ctg	gca	ttg	ggc	act	acc	gtt	tct	547	
Arg	Arg	Ser	Glu	Gly	Thr	Gly	Tyr	Leu	Ala	Leu	Gly	Thr	Thr	Val	Ser		
	135					140					145						
gca	gca	ctt	gga	cca	gcc	cta	gca	ctt	ttt	gtc	cta	gga	aca	ttt	gat	595	
Ala	Ala	Leu	Gly	Pro	Ala	Leu	Ala	Leu	Phe	Val	Leu	Gly	Thr	Phe	Asp		
	150				155					160					165		
tac	gac	atg	ctg	ttt	atc	gtg	gtc	ttg	gca	acc	tcg	gtc	atc	tct	ttg	643	
Tyr	Asp	Met	Leu	Phe	Ile	Val	Val	Leu	Ala	Thr	Ser	Val	Ile	Ser	Leu		
				170					175					180			
atc	gcc	gtc	gtg	ttc	atg	tac	ttt	aag	acc	agc	gac	cct	gag	cct	tct	691	
Ile	Ala	Val	Val	Phe	Met	Tyr	Phe	Lys	Thr	Ser	Asp	Pro	Glu	Pro	Ser		
			185					190					195				
ggg	gaa	cca	gcc	aag	ttc	agc	ttc	aaa	tct	att	atg	aac	cca	aag	atc	739	
Gly	Glu	Pro	Ala	Lys	Phe	Ser	Phe	Lys	Ser	Ile	Met	Asn	Pro	Lys	Ile		
		200					205					210					
atc	ccc	atc	ggc	atc	ttt	atc	ttg	ctt	att	tgc	ttt	gct	tac	tct	ggc	787	
Ile	Pro	Ile	Gly	Ile	Phe	Ile	Leu	Leu	Ile	Cys	Phe	Ala	Tyr	Ser	Gly		
	215					220					225						
gtc	att	gcc	tac	atc	aac	gca	ttt	gct	gaa	gaa	cgc	gat	ctg	att	acg	835	
Val	Ile	Ala	Tyr	Ile	Asn	Ala	Phe	Ala	Glu	Glu	Arg	Asp	Leu	Ile	Thr		
	230				235					240					245		
ggc	gct	gga	ttg	ttc	ttc	att	gcc	tac	gca	gta	tca	atg	ttt	gtg	atg	883	
Gly	Ala	Gly	Leu	Phe	Phe	Ile	Ala	Tyr	Ala	Val	Ser	Met	Phe	Val	Met		
			250						255					260			
cgc	agc	ttc	ctt	ggc	aaa	ctg	cag	gac	cgt	cgc	gga	gac	aac	gtc	gtt	931	
Arg	Ser	Phe	Leu	Gly	Lys	Leu	Gln	Asp	Arg	Arg	Gly	Asp	Asn	Val	Val		

265 270 275
 att tac ttt gga ttg ttc ttc ttc gtt att tcc ttg acg att ttg tcc 979
 Ile Tyr Phe Gly Leu Phe Phe Phe Val Il Ser Leu Thr Ile Leu Ser
 280 285 290
 ttt gcc act tcc aac tgg cac gtt gtg 1006
 Phe Ala Thr Ser Asn Trp His Val Val
 295 300

<210> 184
 <211> 302
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 184
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 Thr Thr Met Ala Leu Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val
 35 40 45
 Glu Ala Gly Phe Ala Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser
 50 55 60
 Arg Phe Phe Ser Gly Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile
 65 70 75 80
 Val Leu Ile Ser Val Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu
 85 90 95
 Pro Ile Glu Ser Leu Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly
 100 105 110
 Val Gly Tyr Ala Phe Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu
 115 120 125
 Leu Ile Pro Ala Ser Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu
 130 135 140
 Gly Thr Thr Val Ser Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val
 145 150 155 160
 Leu Gly Thr Phe Asp Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr
 165 170 175
 Ser Val Ile Ser Leu Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser
 180 185 190
 Asp Pro Glu Pro Ser Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile
 195 200 205
 Met Asn Pro Lys Ile Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys

210

215

220

Phe Ala Tyr Ser Gly Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu
 225 230 235 240

Arg Asp Leu Ile Thr Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val
 245 250 255

Ser Met Phe Val Met Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg
 260 265 270

Gly Asp Asn Val Val Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser
 275 280 285

Leu Thr Ile Leu Ser Phe Ala Thr Ser Asn Trp His Val Val
 290 295 300

<210> 185

<211> 568

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(568)

<223> RXA00858

<400> 185

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tcttaaattg tctaaccaag aaccggaggt tctttttgtc atg gaa gta aac tta 115
 Met Glu Val Asn Leu
 1 5

gcc aca tgg cta atc act atc gca gtg att gct ggc ttc ttc att ttc 163
 Ala Thr Trp Leu Ile Thr Ile Ala Val Ile Ala Gly Phe Phe Ile Phe
 10 15 20

gat ttc tat tcc cac gtc cgc acc cca cac gag ccc act atc aaa gaa 211
 Asp Phe Tyr Ser His Val Arg Thr Pro His Glu Pro Thr Ile Lys Glu
 25 30 35

tcc gca tgg tgg agc ctc ttc tac gta gcc ctc gcc tgt gtt ttc ggc 259
 Ser Ala Trp Trp Ser Leu Phe Tyr Val Ala Leu Ala Cys Val Phe Gly
 40 45 50

gtg ttc ctc tgg ttt gct tgg ggc gag cca ggt aac cca cac cag cac 307
 Val Phe Leu Trp Phe Ala Trp Gly Glu Pro Gly Asn Pro His Gln His
 55 60 65

ggc att gag ttc ttc acc ggt tac gtg aca gag aag gcg ttg agt gtt 355
 Gly Ile Glu Phe Phe Thr Gly Tyr Val Thr Glu Lys Ala Leu Ser Val
 70 75 80 85

gat aac ctc ttc atc ttc gcg ctg atc atg ggt tct ttc aag att cct 403
 Asp Asn Leu Phe Ile Phe Ala Leu Ile Met Gly Ser Phe Lys Ile Pro

	90	95	100	
cgc aag tac cag cag aag gtt ctg ctc atc ggt atc gcg ctg gca ctg				451
Arg Lys Tyr Gln Gln Lys Val Leu Leu Ile Gly Ile Ala Leu Ala Leu				
	105	110	115	
gtc ttc cgc ctg gca ttc atc ctc gca ggt gct gca gtt atc gaa gcc				499
Val Phe Arg Leu Ala Phe Ile Leu Ala Gly Ala Ala Val Ile Glu Ala				
	120	125	130	
tgg tcc gat gtc ttc tac atc ttc tcc atc tgg ctg atc tac acc gct				547
Trp Ser Asp Val Phe Tyr Ile Phe Ser Ile Trp Leu Ile Tyr Thr Ala				
	135	140	145	
gtg aag gct cct gtg cac gag				568
Val Lys Ala Pro Val His Glu				
	150	155		

<210> 186

<211> 156

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

Met Glu Val Asn Leu Ala Thr Trp Leu Ile Thr Ile Ala Val Ile Ala				
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Gly Phe Phe Ile Phe Asp Phe Tyr Ser His Val Arg Thr Pro His Glu				
	20	25	30	
Pro Thr Ile Lys Glu Ser Ala Trp Trp Ser Leu Phe Tyr Val Ala Leu				
	35	40	45	
Ala Cys Val Phe Gly Val Phe Leu Trp Phe Ala Trp Gly Glu Pro Gly				
	50	55	60	
Asn Pro His Gln His Gly Ile Glu Phe Phe Thr Gly Tyr Val Thr Glu				
	65	70	75	80
Lys Ala Leu Ser Val Asp Asn Leu Phe Ile Phe Ala Leu Ile Met Gly				
	85	90	95	
Ser Phe Lys Ile Pro Arg Lys Tyr Gln Gln Lys Val Leu Leu Ile Gly				
	100	105	110	
Ile Ala Leu Ala Leu Val Phe Arg Leu Ala Phe Ile Leu Ala Gly Ala				
	115	120	125	
Ala Val Ile Glu Ala Trp Ser Asp Val Phe Tyr Ile Phe Ser Ile Trp				
	130	135	140	
Leu Ile Tyr Thr Ala Val Lys Ala Pro Val His Glu				
	145	150	155	

<210> 187

<211> 975
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(952)
 <223> RXA02305

<400> 187

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caaacgatga cttcgatccc gaaaagtgga ggaacatgta atg cca gcc ttt gag 115
                                         Met Pro Ala Phe Glu
                                         1 5

gca atg cca gga atg ccg tat tgg atc gac ctg tcc acc tcg gac att 163
Ala Met Pro Gly Met Pro Tyr Trp Ile Asp Leu Ser Thr Ser Asp Ile
          10          15          20

gca aaa tct gca cac ttc tac gaa aac gtt ctc ggc tgg gaa att gaa 211
Ala Lys Ser Ala His Phe Tyr Glu Asn Val Leu Gly Trp Glu Ile Glu
          25          30          35

gaa gtc aac gat ggc tac cgc atg gct cgt ctg cag gga cta ccc gtg 259
Glu Val Asn Asp Gly Tyr Arg Met Ala Arg Leu Gln Gly Leu Pro Val
          40          45          50

gca ggg ctg atc gat cag cgc ggt gaa tca agc atc ccg gat acc tgg 307
Ala Gly Leu Ile Asp Gln Arg Gly Glu Ser Ser Ile Pro Asp Thr Trp
          55          60          65

att acc tac ttc ctc tcc tac gat ctg gat gcc act gca aag aag atc 355
Ile Thr Tyr Phe Leu Ser Tyr Asp Leu Asp Ala Thr Ala Lys Lys Ile
          70          75          80          85

gca gaa ctg ggt gga cga att ctg gcc gag cca act gac gtg cac ttg 403
Ala Glu Leu Gly Gly Arg Ile Leu Ala Glu Pro Thr Asp Val His Leu
          90          95          100

gga cgc atg atc cta gct gtt gat act gcc ggc gca ctg ttc ggc gtt 451
Gly Arg Met Ile Leu Ala Val Asp Thr Ala Gly Ala Leu Phe Gly Val
          105          110          115

att gag cca ggc agc gag gaa tca ttc gtc gct gct ggt gaa cca ggc 499
Ile Glu Pro Gly Ser Glu Glu Ser Phe Val Ala Ala Gly Glu Pro Gly
          120          125          130

aca tcc gtg tgg cat gaa ctc acc act gtc tcc aaa tat tcc gaa gct 547
Thr Ser Val Trp His Glu Leu Thr Thr Val Ser Lys Tyr Ser Glu Ala
          135          140          145

atc gat ttc tac ggt gag ctg ttc act tgg aca acc tct gaa atg gct 595
Ile Asp Phe Tyr Gly Glu Leu Phe Thr Trp Thr Thr Ser Glu Met Ala
          150          155          160          165

agt gct gaa gac gat agt ttc cgc tac acc acc gca ttg gct gac ggt 643
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Ser Ala Glu Asp Asp Ser Phe Arg Tyr Thr Thr Ala Leu Ala Asp Gly
 170 175 180

tcc gcc ttt gct gga att ttt gat gcc aaa ggc cac ttc cca cct cag 691
 Ser Ala Phe Ala Gly Ile Phe Asp Ala Lys Gly His Phe Pro Pro Gln
 185 190 195

gtt cca agc ttc tgg cag tcc tac ctt ggc gtg ctc aac gcc gat gat 739
 Val Pro Ser Phe Trp Gln Ser Tyr Leu Gly Val Leu Asn Ala Asp Asp
 200 205 210

gct gca gcg aag gcc aag gaa ttt ggt ggc gat gtt att cgt aag cca 787
 Ala Ala Ala Lys Ala Lys Glu Phe Gly Gly Asp Val Ile Arg Lys Pro
 215 220 225

tgg gac tca gaa ttt ggc cgc atg gtt ctc atc tct gat tcc act ggt 835
 Trp Asp Ser Glu Phe Gly Arg Met Val Leu Ile Ser Asp Ser Thr Gly
 230 235 240 245

gcc aca att acc ttg tgt gaa gta gag gaa tac gtc gag gaa gca gca 883
 Ala Thr Ile Thr Leu Cys Glu Val Glu Glu Tyr Val Glu Glu Ala Ala
 250 255 260

gaa ggc gat gat ctc ttc gac atc gat ctc agt gct ttc gaa gag cag 931
 Glu Gly Asp Asp Leu Phe Asp Ile Asp Leu Ser Ala Phe Glu Glu Gln
 265 270 275

ttc cgc aag caa gaa gga cag taatcctaca gcgccatgga gga 975
 Phe Arg Lys Gln Glu Gly Gln
 280

<210> 188

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Met Pro Ala Phe Glu Ala Met Pro Gly Met Pro Tyr Trp Ile Asp Leu
 1 5 10 15

Ser Thr Ser Asp Ile Ala Lys Ser Ala His Phe Tyr Glu Asn Val Leu
 20 25 30

Gly Trp Glu Ile Glu Glu Val Asn Asp Gly Tyr Arg Met Ala Arg Leu
 35 40 45

Gln Gly Leu Pro Val Ala Gly Leu Ile Asp Gln Arg Gly Glu Ser Ser
 50 55 60

Ile Pro Asp Thr Trp Ile Thr Tyr Phe Leu Ser Tyr Asp Leu Asp Ala
 65 70 75 80

Thr Ala Lys Lys Ile Ala Glu Leu Gly Gly Arg Ile Leu Ala Glu Pro
 85 90 95

Thr Asp Val His Leu Gly Arg Met Ile Leu Ala Val Asp Thr Ala Gly

100	105	110
Ala Leu Phe Gly Val Ile Glu Pro Gly Ser Glu Glu Ser Phe Val Ala 115	120	125
Ala Gly Glu Pro Gly Thr Ser Val Trp His Glu Leu Thr Thr Val Ser 130	135	140
Lys Tyr Ser Glu Ala Ile Asp Phe Tyr Gly Glu Leu Phe Thr Trp Thr 145	150	155
Thr Ser Glu Met Ala Ser Ala Glu Asp Asp Ser Phe Arg Tyr Thr Thr 165	170	175
Ala Leu Ala Asp Gly Ser Ala Phe Ala Gly Ile Phe Asp Ala Lys Gly 180	185	190
His Phe Pro Pro Gln Val Pro Ser Phe Trp Gln Ser Tyr Leu Gly Val 195	200	205
Leu Asn Ala Asp Asp Ala Ala Ala Lys Ala Lys Glu Phe Gly Gly Asp 210	215	220
Val Ile Arg Lys Pro Trp Asp Ser Glu Phe Gly Arg Met Val Leu Ile 225	230	235
Ser Asp Ser Thr Gly Ala Thr Ile Thr Leu Cys Glu Val Glu Glu Tyr 245	250	255
Val Glu Glu Ala Ala Glu Gly Asp Asp Leu Phe Asp Ile Asp Leu Ser 260	265	270
Ala Phe Glu Glu Gln Phe Arg Lys Gln Glu Gly Gln 275	280	

<210> 189
 <211> 948
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(925)
 <223> RXA00084

<400> 189
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 tcttgaaga catcgatgcc ttcctcgacg cacagcaata atg tcc aca gct ctc 115
 Met Ser Thr Ala Leu
 1 5
 ccc gat cag ctc aag tgg gaa tac agt gcc ttc ccc gtg cag atc tcg 163
 Pro Asp Gln Leu Lys Trp Glu Tyr Ser Ala Phe Pro Val Gln Ile Ser
 10 15 20

cag aag caa cgg ctt agt ccc ggc ttc atg cgg atc acc gtc act ggt Gln Lys Gln Arg Leu Ser Pro Gly Phe Met Arg Ile Thr Val Thr Gly 25 30 35	211
gac aag ctc cga ttc ttt ggc cag tgg ggt ttg gac caa cgc atc aaa Asp Lys Leu Arg Phe Phe Gly Gln Trp Gly Leu Asp Gln Arg Ile Lys 40 45 50	259
ctg atc att cca agc ccg gct ggg aac atc cca gat ttc gga att ctc Leu Ile Ile Pro Ser Pro Ala Gly Asn Ile Pro Asp Phe Gly Ile Leu 55 60 65	307
gac gaa ccc act ccc cca ccg aca acg tgg ctt cct cgt gct aag tct Asp Glu Pro Thr Pro Pro Pro Thr Thr Trp Leu Pro Arg Ala Lys Ser 70 75 80 85	355
ttt cca gcg gac caa cga ccg atc ttg cgc acc tac acc cca tct gcg Phe Pro Ala Asp Gln Arg Pro Ile Leu Arg Thr Tyr Thr Pro Ser Ala 90 95 100	403
gtc cga ccc gaa cta tgc gaa gta gac att gat atc tat ctt cac aac Val Arg Pro Glu Leu Cys Glu Val Asp Ile Asp Ile Tyr Leu His Asn 105 110 115	451
cct tcg gga cca gta tcc aga tgg gca aag aac tgc agt gtt gac gat Pro Ser Gly Pro Val Ser Arg Trp Ala Lys Asn Cys Ser Val Asp Asp 120 125 130	499
gaa cta atc atc acc ggc cct gac gta cgc gca gga gaa acc ggc tac Glu Leu Ile Ile Thr Gly Pro Asp Val Arg Ala Gly Glu Thr Gly Tyr 135 140 145	547
gga atc acc tat cat ccg act tct gcg atc gat cgc ctc tgt ctc atc Gly Ile Thr Tyr His Pro Thr Ser Ala Ile Asp Arg Leu Cys Leu Ile 150 155 160 165	595
ggc gat tgt gca tca gct ccc gcg atc gca aat atc gtc aat caa tca Gly Asp Cys Ala Ser Ala Pro Ala Ile Ala Asn Ile Val Asn Gln Ser 170 175 180	643
aaa gta cct act acg gtt ttc ctc cac gta gac agc cta gaa gat gat Lys Val Pro Thr Thr Val Phe Leu His Val Asp Ser Leu Glu Asp Asp 185 190 195	691
gta ttg atc gcc gat agc tcc acc aag ctc act ttc gaa gac atc gac Val Leu Ile Ala Asp Ser Ser Thr Lys Leu Thr Phe Glu Asp Ile Asp 200 205 210	739
gct tac aaa gca aag gtc ttc caa tgg gct tca gcc aat gca gca gat Ala Tyr Lys Ala Lys Val Phe Gln Trp Ala Ser Ala Asn Ala Ala Asp 215 220 225	787
cct tca gta cac ttc tgg atc gcc ggt gaa act agc atg gtg cgc ttc Pro Ser Val His Phe Trp Ile Ala Gly Glu Thr Ser Met Val Arg Phe 230 235 240 245	835
att cgc aaa gaa cta atc aac agc tac cga gtt gat tcc tca cga atc	883

Ile Arg Lys Glu Leu Ile Asn Ser Tyr Arg Val Asp Ser Ser Arg Ile
 250 255 260

act ttc ctc ggc tac tgg aaa tac ggc cga cga acc gta gac 925
 Thr Phe Leu Gly Tyr Trp Lys Tyr Gly Arg Arg Thr Val Asp
 265 270 275

tagctttcag attcagaccc cag 948

<210> 190

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

Met Ser Thr Ala Leu Pro Asp Gln Leu Lys Trp Glu Tyr Ser Ala Phe
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Pro Val Gln Ile Ser Gln Lys Gln Arg Leu Ser Pro Gly Phe Met Arg
 20 25 30

Ile Thr Val Thr Gly Asp Lys Leu Arg Phe Phe Gly Gln Trp Gly Leu
 35 40 45

Asp Gln Arg Ile Lys Leu Ile Ile Pro Ser Pro Ala Gly Asn Ile Pro
 50 55 60

Asp Phe Gly Ile Leu Asp Glu Pro Thr Pro Pro Thr Thr Trp Leu
 65 70 75 80

Pro Arg Ala Lys Ser Phe Pro Ala Asp Gln Arg Pro Ile Leu Arg Thr
 85 90 95

Tyr Thr Pro Ser Ala Val Arg Pro Glu Leu Cys Glu Val Asp Ile Asp
 100 105 110

Ile Tyr Leu His Asn Pro Ser Gly Pro Val Ser Arg Trp Ala Lys Asn
 115 120 125

Cys Ser Val Asp Asp Glu Leu Ile Ile Thr Gly Pro Asp Val Arg Ala
 130 135 140

Gly Glu Thr Gly Tyr Gly Ile Thr Tyr His Pro Thr Ser Ala Ile Asp
 145 150 155 160

Arg Leu Cys Leu Ile Gly Asp Cys Ala Ser Ala Pro Ala Ile Ala Asn
 165 170 175

Ile Val Asn Gln Ser Lys Val Pro Thr Thr Val Phe Leu His Val Asp
 180 185 190

Ser Leu Glu Asp Asp Val Leu Ile Ala Asp Ser Ser Thr Lys Leu Thr
 195 200 205

Phe Glu Asp Ile Asp Ala Tyr Lys Ala Lys Val Phe Gln Trp Ala Ser
 210 215 220

Ala Asn Ala Ala Asp Pro Ser Val His Phe Trp Ile Ala Gly Glu Thr
225 230 235 240

Ser Met Val Arg Phe Ile Arg Lys Glu Leu Ile Asn S r Tyr Arg Val
245 250 255

Asp Ser Ser Arg Ile Thr Phe Leu Gly Tyr Trp Lys Tyr Gly Arg Arg
260 265 270

Thr Val Asp
275

<210> 191

<211> 468

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(445)

<223> RXA00843

<400> 191

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tttgaataat catggaacaa accttagtag gctcaacggtt atg aaa gtc acg att 115
Met Lys Val Thr Ile
1 5

ttc cat aat ccg cgt tgt tcc aca tcc aga aat acc ctc gct tac ctc 163
Phe His Asn Pro Arg Cys Ser Thr Ser Arg Asn Thr Leu Ala Tyr Leu
10 15 20

cgc gac aag gac att gag cct gaa att gtt cag tat ctc aaa gac acg 211
Arg Asp Lys Asp Ile Glu Pro Glu Ile Val Gln Tyr Leu Lys Asp Thr
25 30 35

ccc acc gct tcc gag ctc aaa gaa cta ttc aat acg ctg gga att cca 259
Pro Thr Ala Ser Glu Leu Lys Glu Leu Phe Asn Thr Leu Gly Ile Pro
40 45 50

gtc cac gac ggc atc aga acc cgc gaa gct gag tac aca gaa ctg ggc 307
Val His Asp Gly Ile Arg Thr Arg Glu Ala Glu Tyr Thr Glu Leu Gly
55 60 65

ctg tca cca gaa aca cct gaa act gag ctt atc gac gcc atc gtt gcc 355
Leu Ser Pro Glu Thr Pro Glu Thr Glu Leu Ile Asp Ala Ile Val Ala
70 75 80 85

cat ccc agg ctc ctt cag cgt ccg atc gtg gtg acg gcc aaa ggc gcg 403
His Pro Arg Leu Leu Gln Arg Pro Ile Val Val Thr Ala Lys Gly Ala
90 95 100

cgc att gcg cgc ccc aaa atc gac gtc att gac agc atc ttg 445
Arg Ile Ala Arg Pro Lys Ile Asp Val Ile Asp Ser Ile Leu

105

110

115

tgacaacatt ttgtagagca acc

468

<210> 192

<211> 115

<212> PRT

<213> Corynebacterium glutamicum

<400> 192

Met Lys Val Thr Ile Phe His Asn Pro Arg Cys Ser Thr Ser Arg Asn
 1 5 10 15

Thr Leu Ala Tyr Leu Arg Asp Lys Asp Ile Glu Pro Glu Ile Val Gln
 20 25 30

Tyr Leu Lys Asp Thr Pro Thr Ala Ser Glu Leu Lys Glu Leu Phe Asn
 35 40 45

Thr Leu Gly Ile Pro Val His Asp Gly Ile Arg Thr Arg Glu Ala Glu
 50 55 60

Tyr Thr Glu Leu Gly Leu Ser Pro Glu Thr Pro Glu Thr Glu Leu Ile
 65 70 75 80

Asp Ala Ile Val Ala His Pro Arg Leu Leu Gln Arg Pro Ile Val Val
 85 90 95

Thr Ala Lys Gly Ala Arg Ile Ala Arg Pro Lys Ile Asp Val Ile Asp
 100 105 110

Ser Ile Leu
 115

<210> 193

<211> 432

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(409)

<223> RXA01052

<400> 193

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acgaacaacg aagagcttgc ccgagagtat cttgggtcgc atg gac aca aaa tta 115
 Met Asp Thr Lys Leu
 1 5

ggc gct gaa ttg ggt act gaa ttt gat ctc att gtt gtt ggt ttc ggc 163
 Gly Ala Glu Leu Gly Thr Glu Phe Asp Leu Ile Val Val Gly Phe Gly
 10 15 20

aaa gca ggc aag act atc gcg atg aaa cgc tcg gca gcg ggg gat aag 211
 Lys Ala Gly Lys Thr Il Ala Met Lys Arg Ser Ala Ala Gly Asp Lys
 25 30 35

gtc gca ctg atc gag cag agt cca cag atg tat ggc ggt acc tgc atc 259
 Val Ala Leu Ile Glu Gln Ser Pro Gln Met Tyr Gly Gly Thr Cys Ile
 40 45 50

aat gta ggt tgc atc ccc acg aag aag ttg ttg ttt gag act gca acg 307
 Asn Val Gly Cys Ile Pro Thr Lys Lys Leu Leu Phe Glu Thr Ala Thr
 55 60 65

ggc aag gat ttc ccg gat gcg gtt gtg gcg cgt gat cag ttg att ggc 355
 Gly Lys Asp Phe Pro Asp Ala Val Val Ala Arg Asp Gln Leu Ile Gly
 70 75 80 85

aag ctg aat gcc aag aat ctt gcg atg gcc aca gac aag ggt gtc acc 403
 Lys Leu Asn Ala Lys Asn Leu Ala Met Ala Thr Asp Lys Gly Val Thr
 90 95 100

cgt cat tgatggaaaa gctacgttta cag 432
 Arg His

<210> 194

<211> 103

<212> PRT

<213> Corynebacterium glutamicum

<400> 194

Met Asp Thr Lys Leu Gly Ala Glu Leu Gly Thr Glu Phe Asp Leu Ile
 1 5 10 15

Val Val Gly Phe Gly Lys Ala Gly Lys Thr Ile Ala Met Lys Arg Ser
 20 25 30

Ala Ala Gly Asp Lys Val Ala Leu Ile Glu Gln Ser Pro Gln Met Tyr
 35 40 45

Gly Gly Thr Cys Ile Asn Val Gly Cys Ile Pro Thr Lys Lys Leu Leu
 50 55 60

Phe Glu Thr Ala Thr Gly Lys Asp Phe Pro Asp Ala Val Val Ala Arg
 65 70 75 80

Asp Gln Leu Ile Gly Lys Leu Asn Ala Lys Asn Leu Ala Met Ala Thr
 85 90 95

Asp Lys Gly Val Thr Arg His
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<210> 195

<211> 543

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(520)

<223> RXA01053

<400> 195

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agccacgaaa tcacaagtaa cttcaggtag tgacactctt gtg ctg tat gcg cca 115
 Val Leu Tyr Ala Pro
 1 5

acg att gtg atc aac acg ggc tcc acg ccg gtc atc ccc aat gtc cca 163
 Thr Ile Val Ile Asn Thr Gly Ser Thr Pro Val Ile Pro Asn Val Pro
 10 15 20

ggc acc gac aat ccg cat gtt ttt gat tcc act ggc att cag cac att 211
 Gly Thr Asp Asn Pro His Val Phe Asp Ser Thr Gly Ile Gln His Ile
 25 30 35

tcg ccc ctg ccg aag cac ctc gcg atc atc ggc ggt ggc ccc atc ggt 259
 Ser Pro Leu Pro Lys His Leu Ala Ile Ile Gly Gly Gly Pro Ile Gly
 40 45 50

ttg gaa ttt gcc acg ctt ttc agt gga caa ggc tcc aaa gtc acc atc 307
 Leu Glu Phe Ala Thr Leu Phe Ser Gly Gln Gly Ser Lys Val Thr Ile
 55 60 65

atc gac cgt ggt gaa ttg ccg ctg aaa aat ttc gac agg gaa gta gcg 355
 Ile Asp Arg Gly Glu Leu Pro Leu Lys Asn Phe Asp Arg Glu Val Ala
 70 75 80 85

gag ctg gcc aaa acc gac ctg gag gcc cgc gga atc acc ttc ctc aac 403
 Glu Leu Ala Lys Thr Asp Leu Glu Ala Arg Gly Ile Thr Phe Leu Asn
 90 95 100

aac gct gaa ctc acc gga ttc agc ggt gac ctc acc atc gcg ctc aaa 451
 Asn Ala Glu Leu Thr Gly Phe Ser Gly Asp Leu Thr Ile Ala Leu Lys
 105 110 115

gac cac gac ctc ctc gcc gac gcc gca ctt ttt gca tcg gcc gac gcc 499
 Asp His Asp Leu Leu Ala Asp Ala Ala Leu Phe Ala Ser Ala Asp Ala
 120 125 130

cgg cac cga cgg gct cgg cct tgaacaggcg ggcataaaaa cag 543
 Arg His Arg Arg Ala Arg Pro
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<210> 196

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

Val Leu Tyr Ala Pro Thr Ile Val Ile Asn Thr Gly Ser Thr Pro Val

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Gly Ile Gln His	Ile Ser Pro Leu	Pro Lys His Leu	Ala Ile Ile Gly
35	40	45	
Gly Gly Pro Ile	Gly Leu Glu Phe	Ala Thr Leu Phe	Ser Gly Gln Gly
50	55	60	
Ser Lys Val Thr	Ile Ile Asp Arg	Gly Glu Leu Pro	Leu Lys Asn Phe
65	70	75	80
Asp Arg Glu Val	Ala Glu Leu Ala	Lys Thr Asp Leu	Glu Ala Arg Gly
85	90	95	
Ile Thr Phe Leu	Asn Asn Ala Glu	Leu Thr Gly Phe	Ser Gly Asp Leu
100	105	110	
Thr Ile Ala Leu	Lys Asp His Asp	Leu Leu Ala Asp	Ala Ala Leu Phe
115	120	125	
Ala Ser Ala Asp	Ala Arg His Arg	Arg Ala Arg Pro	
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Val Leu Val Asp Ala 5			
1			
cac ctc cgg acc aac atc gac ggc atc ttc gct gta ggt gat gtc aat 163			
His Leu Arg Thr Asn Ile Asp Gly Ile Phe Ala Val Gly Asp Val Asn 20			
10			
ggc ggc ccg cag ttt acc tac gtg tcc tac gat gac cac cgc att gtg 211			
Gly Gly Pro Gln Phe Thr Tyr Val Ser Tyr Asp Asp His Arg Ile Val 35			
25			
ctg gat caa cta gcc gga aca ggt aag aaa tcc att gca cac cga ctg 259			
Leu Asp Gln Leu Ala Gly Thr Gly Lys Lys Ser Ile Ala His Arg Leu 50			
40			
atc ccc acc acc acg ttc atc gaa ccg ccg tta tcc acc atc ggt gac 307			

Ile Pro Thr Thr Thr Phe Ile Glu Pro Pro Leu Ser Thr Ile Gly Asp
55 60 65

aac act gaa ggg gaa aat gtg gtg gtg aaa aag gcc ttg att gca gat 355
Asn Thr Glu Gly Glu Asn Val Val Val Lys Lys Ala Leu Ile Ala Asp
70 75 80 85

atg ccg atc gtt ccc cga cca gag att att aac caa cct cac ggt atg 403
M t Pro Ile Val Pro Arg Pro Glu Ile Ile Asn Gln Pro His Gly Met
90 95 100

gtg aag ttt ttc gtc gac aag caa tct gat gcg ctg ctc ggc gcg acc 451
Val Lys Phe Phe Val Asp Lys Gln Ser Asp Ala Leu Leu Gly Ala Thr
105 110 115

ttg tac tgc gcc gac tcc cag gag ctc atc aac acc gtg gcg ctt gcc 499
Leu Tyr Cys Ala Asp Ser Gln Glu Leu Ile Asn Thr Val Ala Leu Ala
120 125 130

atg cgg cat ggc gtc acc gcc tcc gag ctt ggc gac ggc atc tac acc 547
Met Arg His Gly Val Thr Ala Ser Glu Leu Gly Asp Gly Ile Tyr Thr
135 140 145

cac ccc gcc acc tcg gag atc ttc aac caa tta ttg ggc agt 589
His Pro Ala Thr Ser Glu Ile Phe Asn Gln Leu Leu Gly Ser
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<210> 198

<211> 163

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 198

Val Leu Val Asp Ala His Leu Arg Thr Asn Ile Asp Gly Ile Phe Ala
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Val Gly Asp Val Asn Gly Gly Pro Gln Phe Thr Tyr Val Ser Tyr Asp
20 25 30

Asp His Arg Ile Val Leu Asp Gln Leu Ala Gly Thr Gly Lys Lys Ser
35 40 45

Ile Ala His Arg Leu Ile Pro Thr Thr Thr Phe Ile Glu Pro Pro Leu
50 55 60

Ser Thr Ile Gly Asp Asn Thr Glu Gly Glu Asn Val Val Val Lys Lys
65 70 75 80

Ala Leu Ile Ala Asp Met Pro Ile Val Pro Arg Pro Glu Ile Ile Asn
85 90 95

Gln Pro His Gly Met Val Lys Phe Phe Val Asp Lys Gln Ser Asp Ala
100 105 110

Leu Leu Gly Ala Thr Leu Tyr Cys Ala Asp Ser Gln Glu Leu Ile Asn
 115 120 125

Thr Val Ala Leu Ala Met Arg His Gly Val Thr Ala Ser Glu Leu Gly
 130 135 140

Asp Gly Ile Tyr Thr His Pro Ala Thr Ser Glu Ile Phe Asn Gln Leu
 145 150 155 160

Leu Gly Ser

<210> 199

<211> 561

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(538)

<223> RXN03123

<400> 199

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 Val Gly Asp Ala Leu
 1 5

cga ggc cgg gga aag cct gaa gtc atg cgc tac cca gga att ccg ttc 163
 Arg Gly Arg Gly Lys Pro Glu Val Met Arg Tyr Pro Gly Ile Pro Phe
 10 15 20

gcc atc cca gat cca gcg ccg cgt ggc ttc ctt ttc tta ggc gat ctc 211
 Ala Ile Pro Asp Pro Ala Pro Arg Gly Phe Leu Phe Leu Gly Asp Leu
 25 30 35

acc tct tac cca gcg atc tgc tcg att ctg gag acc ttg gac ggt gaa 259
 Thr Ser Tyr Pro Ala Ile Cys Ser Ile Leu Glu Thr Leu Asp Gly Glu
 40 45 50

atc cct gcg acc gcg tat ctt atc gcc cac gat cca ctt gat tac acc 307
 Ile Pro Ala Thr Ala Tyr Leu Ile Ala His Asp Pro Leu Asp Tyr Thr
 55 60 65

ttc gat ttt ccc cag ggc gag cac atc acc gcg cag tgg att tcc aac 355
 Phe Asp Phe Pro Gln Gly Glu His Ile Thr Ala Gln Trp Ile Ser Asn
 70 75 80 85

gaa caa tcc ttc att gat cac atc gct gac acg gat tac acc gat ttt 403
 Glu Gln Ser Phe Ile Asp His Ile Ala Asp Thr Asp Tyr Thr Asp Phe
 90 95 100

tat acc tgg atc ggc gcg gaa tcc tcc gaa acc cgt gcg gcc aag aag 451
 Tyr Thr Trp Ile Gly Ala Glu Ser Ser Glu Thr Arg Ala Ala Lys Lys
 105 110 115

cat ctg cag acc cac gcc ggc atg ccc aag acg cac atg aac gcg caa 499
 His Leu Gln Thr His Ala Gly Met Pro Lys Thr His Met Asn Ala Gln
 120 125 130

ggt tat tgg aac aag ggc aga gcc atg ggt aaa agc aat taaaagattt 548
 Gly Tyr Trp Asn Lys Gly Arg Ala Met Gly Lys Ser Asn
 135 140 145

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<210> 200

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

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Pro Gly Ile Pro Phe Ala Ile Pro Asp Pro Ala Pro Arg Gly Phe Leu
 20 25 30

Phe Leu Gly Asp Leu Thr Ser Tyr Pro Ala Ile Cys Ser Ile Leu Glu
 35 40 45

Thr Leu Asp Gly Glu Ile Pro Ala Thr Ala Tyr Leu Ile Ala His Asp
 50 55 60

Pro Leu Asp Tyr Thr Phe Asp Phe Pro Gln Gly Glu His Ile Thr Ala
 65 70 75 80

Gln Trp Ile Ser Asn Glu Gln Ser Phe Ile Asp His Ile Ala Asp Thr
 85 90 95

Asp Tyr Thr Asp Phe Tyr Thr Trp Ile Gly Ala Glu Ser Ser Glu Thr
 100 105 110

Arg Ala Ala Lys Lys His Leu Gln Thr His Ala Gly Met Pro Lys Thr
 115 120 125

His Met Asn Ala Gln Gly Tyr Trp Asn Lys Gly Arg Ala Met Gly Lys
 130 135 140

Ser Asn
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<210> 201

<211> 736

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(736)

<223> FRXA00993

<400> 201

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atttacaggg tgttgtgaaa gcataaggga gcaaggaaac atg ggc aag gga ttt 115
 Met Gly Lys Gly Phe
 1 5

acc ggc gct att ttg acc gtc atg ggc gtg aaa tcg cat atc gcc acc 163
 Thr Gly Ala Ile Leu Thr Val Met Gly Val Lys Ser His Ile Ala Thr
 10 15 20

acc acg gga aaa acc gtg atc aat gac cgc atg gtg acc att cat ttt 211
 Thr Thr Gly Lys Thr Val Ile Asn Asp Arg Met Val Thr Ile His Phe
 25 30 35

cat tcc gag acg ctg ctc aac acg gaa ggt gaa gtc ccc ggc gat tgg 259
 His Ser Glu Thr Leu Leu Asn Thr Glu Gly Glu Val Pro Gly Asp Trp
 40 45 50

ctg cgt ctg tgg ttc ccg cac gag agc cga cct gga aag ctc tac caa 307
 Leu Arg Leu Trp Phe Pro His Glu Ser Arg Pro Gly Lys Leu Tyr Gln
 55 60 65

cgc gcc tac acc ttg acc aac gtg gat gcc gat gcc ggt acc ttt gac 355
 Arg Ala Tyr Thr Leu Thr Asn Val Asp Ala Asp Ala Gly Thr Phe Asp
 70 75 80 85

ctg gct ttt gtg ctg cac gag ccg ctg ggg ccc gcc tcg gcg tgg gcg 403
 Leu Ala Phe Val Leu His Glu Pro Leu Gly Pro Ala Ser Ala Trp Ala
 90 95 100

acg cgc tgc gag gcc ggg gaa agc ctg gaa gtc atg cgc tac cca gga 451
 Thr Arg Cys Glu Ala Gly Glu Ser Leu Glu Val Met Arg Tyr Pro Gly
 105 110 115

att ccg ttc gcc atc cca gat cca gcg ccg cgt ggc ttc ctt ttc cta 499
 Ile Pro Phe Ala Ile Pro Asp Pro Ala Pro Arg Gly Phe Leu Phe Leu
 120 125 130

ggc gat ctc acc tct tac cca gcg atc tgc tcg att ctg gag acc ttg 547
 Gly Asp Leu Thr Ser Tyr Pro Ala Ile Cys Ser Ile Leu Glu Thr Leu
 135 140 145

gac ggt gaa atc cct gcg acc gcg tat ctt atc gcc cac gat cca ctt 595
 Asp Gly Glu Ile Pro Ala Thr Ala Tyr Leu Ile Ala His Asp Pro Leu
 150 155 160 165

gat tac acc ttc gat ttt ccc cag ggc gag cac atc acc gcg cag tgg 643
 Asp Tyr Thr Phe Asp Phe Pro Gln Gly Glu His Ile Thr Ala Gln Trp
 170 175 180

att tcc aac gaa caa tcc ttc att gat cac atc gct gac acg gat tac 691
 Ile Ser Asn Glu Gln Ser Phe Ile Asp His Ile Ala Asp Thr Asp Tyr
 185 190 195

acc gat ttt tat acc tgg atc ggc gcg gaa tcc tcc gaa acc cgt
 Thr Asp Phe Tyr Thr Trp Ile Gly Ala Glu Ser Ser Glu Thr Arg
 200 205 210

736

<210> 202
 <211> 212
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 202
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 20 25 30
 Val Thr Ile His Phe His Ser Glu Thr Leu Leu Asn Thr Glu Gly Glu
 35 40 45
 Val Pro Gly Asp Trp Leu Arg Leu Trp Phe Pro His Glu Ser Arg Pro
 50 55 60
 Gly Lys Leu Tyr Gln Arg Ala Tyr Thr Leu Thr Asn Val Asp Ala Asp
 65 70 75 80
 Ala Gly Thr Phe Asp Leu Ala Phe Val Leu His Glu Pro Leu Gly Pro
 85 90 95
 Ala Ser Ala Trp Ala Thr Arg Cys Glu Ala Gly Glu Ser Leu Glu Val
 100 105 110
 Met Arg Tyr Pro Gly Ile Pro Phe Ala Ile Pro Asp Pro Ala Pro Arg
 115 120 125
 Gly Phe Leu Phe Leu Gly Asp Leu Thr Ser Tyr Pro Ala Ile Cys Ser
 130 135 140
 Ile Leu Glu Thr Leu Asp Gly Glu Ile Pro Ala Thr Ala Tyr Leu Ile
 145 150 155 160
 Ala His Asp Pro Leu Asp Tyr Thr Phe Asp Phe Pro Gln Gly Glu His
 165 170 175
 Ile Thr Ala Gln Trp Ile Ser Asn Glu Gln Ser Phe Ile Asp His Ile
 180 185 190
 Ala Asp Thr Asp Tyr Thr Asp Phe Tyr Thr Trp Ile Gly Ala Glu Ser
 195 200 205
 Ser Glu Thr Arg
 210

<210> 203
 <211> 732
 <212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(709)

<223> RXA01051

<400> 203

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                                         Met Ser Thr Ile His
                                         1 5

gcc tcc gga atc cag gct cca caa gtg cca cac ggt tcc cac cat gcc 163
Ala Ser Gly Ile Gln Ala Pro Gln Val Pro His Gly Ser His His Ala
                        10 15 20

ccg cca caa aag gac gaa tca gtg aag aag agc ttc aat gcc tct tct 211
Pro Pro Gln Lys Asp Glu Ser Val Lys Lys Ser Phe Asn Ala Ser Ser
                        25 30 35

tta ctg ttc gcg ttt tcc ttc ggc gtg tac ctg gtg ctg ctt gtg atg 259
Leu Leu Phe Ala Phe Ser Phe Gly Val Tyr Leu Val Leu Leu Val Met
                        40 45 50

atg aca ctt ctt aaa agt cgc ctt tct tta ggc gga ctg tgg aac aca 307
Met Thr Leu Leu Lys Ser Arg Leu Ser Leu Gly Gly Leu Trp Asn Thr
                        55 60 65

gaa gca cac caa tac aga tcc atc gac tta gag ctt ttc aac ggc ttt 355
Glu Ala His Gln Tyr Arg Ser Ile Asp Leu Glu Leu Phe Asn Gly Phe
                        70 75 80 85

gct gat cca cca att tgg tgg ggg cct tgg acc aac act ttt ggc aac 403
Ala Asp Pro Pro Ile Trp Trp Gly Pro Trp Thr Asn Thr Phe Gly Asn
                        90 95 100

atc gca ctg ttc atg cca ttt ggg ttt ttc ctg tac aaa atg ctc cgt 451
Ile Ala Leu Phe Met Pro Phe Gly Phe Phe Leu Tyr Lys Met Leu Arg
                        105 110 115

aga ttc aac cat cga ttc ccc ttc gta gaa acc atc ctg ttt gcc agc 499
Arg Phe Asn His Arg Phe Pro Phe Val Glu Thr Ile Leu Phe Ala Ser
                        120 125 130

gtc acc agc ctc agt atc gaa gtt ctg caa tgg gtg ttt gct att gga 547
Val Thr Ser Leu Ser Ile Glu Val Leu Gln Trp Val Phe Ala Ile Gly
                        135 140 145

tat tca gat gtc gat gac ctg ttg ttt aat acg atc ggc gga ctc att 595
Tyr Ser Asp Val Asp Asp Leu Leu Phe Asn Thr Ile Gly Gly Leu Ile
                        150 155 160 165

gga gca tcc gta gca gcg ctt gtc tcg ctt aaa tcc tcc aag gta gtc 643
Gly Ala Ser Val Ala Ala Leu Val Ser Leu Lys Ser Ser Lys Val Val
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Phe Asn Ala Ser Ser Leu Leu Phe Ala Phe Ser Phe Gly Val Tyr Leu
35 40 45

Val Leu Leu Val Met Met Thr Leu Leu Lys Ser Arg Leu Ser Leu Gly
50 55 60

Gly Leu Trp Asn Thr Glu Ala His Gln Tyr Arg Ser Ile Asp Leu Glu
65 70 75 80

Leu Phe Asn Gly Phe Ala Asp Pro Pro Ile Trp Trp Gly Pro Trp Thr
85 90 95

Asn Thr Phe Gly Asn Ile Ala Leu Phe Met Pro Phe Gly Phe Phe Leu
100 105 110

Tyr Lys Met Leu Arg Arg Phe Asn His Arg Phe Pro Phe Val Glu Thr
115 120 125

Ile Leu Phe Ala Ser Val Thr Ser Leu Ser Ile Glu Val Leu Gln Trp
130 135 140

Val Phe Ala Ile Gly Tyr Ser Asp Val Asp Asp Leu Leu Phe Asn Thr
145 150 155 160

Ile Gly Gly Leu Ile Gly Ala Ser Val Ala Ala Leu Val Ser Leu Lys
165 170 175

Ser Ser Lys Val Val Ser Gly Ile Ile Met Gly Gly Ser Leu Ser Val
180 185 190

Met Ala Met Met Met Tyr Ser Ser Phe Ile Ala
195 200

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<211> 1359
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 <223> RXN01873

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                                     Met Ser Gln Ala Ile
                                     1 5

gat agc aag gtc gag gca cac gaa ggc cac gaa ggc cac gaa ggc atc 163
Asp Ser Lys Val Glu Ala His Glu Gly His Glu Gly His Glu Gly Ile
                                     10 15 20

gag cga gga aca cgc aat tac aag cgc gct gtg ttt gcg atg ctg gcc 211
Glu Arg Gly Thr Arg Asn Tyr Lys Arg Ala Val Phe Ala Met Leu Ala
                                     25 30 35

gcc ggt ctt gct gct ttc aat ggt ctt tat tgc acg cag gca ttg ctt 259
Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys Thr Gln Ala Leu Leu
                                     40 45 50

ccc acc atg acg gaa gag ttg gga att acg ccc act gag tcc gcg ctg 307
Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro Thr Glu Ser Ala Leu
                                     55 60 65

acg gtg tcg gct acg act gga atg ttg gcg ctg tgt att gtt ccg gcg 355
Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu Cys Ile Val Pro Ala
                                     70 75 80 85

tcg ata ctt tcg gag aaa ttt ggt cgc ggt cgg gtg ctg aca att tca 403
Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg Val Leu Thr Ile Ser
                                     90 95 100

ctc acg ttg gcc atc atc gtg gga tta att ttg ccg ctt gtc ccc aat 451
Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu Pro Leu Val Pro Asn
                                     105 110 115

att act gct ctc atc ctg ctc aga ggt ctc caa ggt gcg ctg ctt gct 499
Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln Gly Ala Leu Leu Ala
                                     120 125 130

ggc act cca gcg gtg gcg atg acc tgg ttg tct gag gaa att cac ccc 547
Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser Glu Glu Ile His Pro
                                     135 140 145

aag gat att ggg cat gcg atg gga att tac atc gcg gga aat act gtc 595
Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile Ala Gly Asn Thr Val
150 155 160 165

ggc ggg ctc act gga cgt atg att ccg gcg gga cta ctt gaa gta act 643
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His	Trp	Gln	Asn	Ala	Leu	Leu	Gly	Ser	Ser	Ile	Ala	Ala	Leu	Ile	Phe		
			185					190					195				
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			200					205				210					
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Lys	Asn	Ile	Asn	Leu	Arg	His	Glu	Ile	Ser	Ala	Met	Ala	Ala	His	Trp		
			215				220				225						
cgg	aat	cct	cgt	ttg	gcg	ttg	ctt	ttt	ggc	act	gcg	ttt	ttg	ggc	atg	835	
Arg	Asn	Pro	Arg	Leu	Ala	Leu	Leu	Phe	Gly	Thr	Ala	Phe	Leu	Gly	Met		
					235					240					245		
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Gly	Thr	Phe	Val	Ser	Leu	Tyr	Asn	Tyr	Leu	Gly	Phe	Arg	Met	Ile	Asp		
				250					255					260			
cag	ttt	ggg	ctg	agt	gaa	gtg	ctg	gtt	ggc	gcg	gtg	ttc	atc	atg	tat	931	
Gln	Phe	Gly	Leu	Ser	Glu	Val	Leu	Val	Gly	Ala	Val	Phe	Ile	Met	Tyr		
			265					270					275				
ctg	gcc	ggg	acc	tgg	agt	tcc	acc	cag	gcg	ggc	gcg	ttg	agg	gag	aag	979	
Leu	Ala	Gly	Thr	Trp	Ser	Ser	Thr	Gln	Ala	Gly	Ala	Leu	Arg	Glu	Lys		
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Ile	Gly	Asn	Gly	Ser	Thr	Val	Ile	Phe	Leu	Ser	Leu	Thr	Met	Ile	Ala		
			295			300					305						
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Ser	Met	Ala	Leu	Met	Gly	Ile	Asn	Asn	Leu	Trp	Val	Thr	Leu	Val	Ala		
					315				320						325		
ctg	ttt	gtg	ttt	acc	gcg	gca	ttt	ttc	gca	ctg	cat	tcc	agt	gct	tgc	1123	
Leu	Phe	Val	Phe	Thr	Ala	Ala	Phe	Phe	Ala	Leu	His	Ser	Ser	Ala	Ser		
				330					335					340			
gga	tgg	atc	gga	atc	atc	gca	acg	aag	gat	cgc	gcg	gaa	gcc	tcc	agc	1171	
Gly	Trp	Ile	Gly	Ile	Ile	Ala	Thr	Lys	Asp	Arg	Ala	Glu	Ala	Ser	Ser		
			345					350					355				
atg	tat	ttg	ttc	tgt	tat	tac	gtg	gga	tcc	tgc	gtg	att	ggc	tgg	gtt	1219	
Met	Tyr	Leu	Phe	Cys	Tyr	Tyr	Val	Gly	Ser	Ser	Val	Ile	Gly	Trp	Val		
			360				365					370					
tct	gga	ttc	gcg	ttt	acg	cat	ttg	ccg	tgg	ttg	gcg	ttc	att	ggc	tgg	1267	
Ser	Gly	Phe	Ala	Phe	Thr	His	Leu	Pro	Trp	Leu	Ala	Phe	Ile	Gly	Trp		
			375			380					385						
ttg	att	ctg	ctt	ctt	tgc	gga	gtg	ctg	gcg	att	tgt	gtg	acg	ctg	gca	1315	
Leu	Ile	Leu	Leu	Leu	Cys	Gly	Val	Leu	Ala	Ile	Cys	Val	Thr	Leu	Ala		

390					395			400		405	
agg	ctt	gcc	cgc	aac	gcc	aat	taatac	gagt	ttgtcc	gtgt	tta
Arg	Leu	Ala	Arg	Asn	Ala	Asn					1359
				410							

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<212> PRT
<213> Corynebacterium glutamicum
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Gly	His	Glu	Gly 20	Ile	Glu	Arg	Gly	Thr 25	Arg	Asn	Tyr	Lys	Arg 30	Ala	Val
Phe	Ala	Met 35	Leu	Ala	Ala	Gly	Leu 40	Ala	Ala	Phe	Asn	Gly 45	Leu	Tyr	Cys
Thr	Gln 50	Ala	Leu	Leu	Pro	Thr 55	Met	Thr	Glu	Glu	Leu 60	Gly	Ile	Thr	Pro
Thr 65	Glu	Ser	Ala	Leu	Thr 70	Val	Ser	Ala	Thr	Thr 75	Gly	Met	Leu	Ala	Leu 80
Cys	Ile	Val	Pro	Ala 85	Ser	Ile	Leu	Ser	Glu 90	Lys	Phe	Gly	Arg	Gly 95	Arg
Val	Leu	Thr	Ile 100	Ser	Leu	Thr	Leu	Ala 105	Ile	Ile	Val	Gly	Leu 110	Ile	Leu
Pro	Leu	Val 115	Pro	Asn	Ile	Thr	Ala 120	Leu	Ile	Leu	Leu	Arg 125	Gly	Leu	Gln
Gly	Ala 130	Leu	Leu	Ala	Gly	Thr 135	Pro	Ala	Val	Ala	Met 140	Thr	Trp	Leu	Ser
Glu 145	Glu	Ile	His	Pro	Lys 150	Asp	Ile	Gly	His	Ala 155	Met	Gly	Ile	Tyr	Ile 160
Ala	Gly	Asn	Thr	Val 165	Gly	Gly	Leu	Thr	Gly 170	Arg	Met	Ile	Pro	Ala 175	Gly
Leu	Leu	Glu	Val 180	Thr	His	Trp	Gln	Asn 185	Ala	Leu	Leu	Gly	Ser 190	Ser	Ile
Ala	Ala	Leu 195	Ile	Phe	Gly	Val	Ile 200	Met	Val	Val	Leu	Leu	Pro	Lys	Gln
Arg	Lys 210	Phe	Gln	Pro	Lys	Asn 215	Ile	Asn	Leu	Arg	His 220	Glu	Ile	Ser	Ala
Met 225	Ala	Ala	His	Trp	Arg 230	Asn	Pro	Arg	Leu	Ala 235	Leu	Leu	Phe	Gly	Thr 240

Ala Phe Leu Gly Met Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly
 245 250 255

Phe Arg Met Ile Asp Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala
 260 265 270

Val Phe Ile Met Tyr Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly
 275 280 285

Ala Leu Arg Glu Lys Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser
 290 295 300

Leu Thr Met Ile Ala Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp
 305 310 315 320

Val Thr Leu Val Ala Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu
 325 330 335

His Ser Ser Ala Ser Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg
 340 345 350

Ala Glu Ala Ser Ser Met Tyr Leu Phe Cys Tyr Tyr Val Gly Ser Ser
 355 360 365

Val Ile Gly Trp Val Ser Gly Phe Ala Phe Thr His Leu Pro Trp Leu
 370 375 380

Ala Phe Ile Gly Trp Leu Ile Leu Leu Leu Cys Gly Val Leu Ala Ile
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Cys Val Thr Leu Ala Arg Leu Ala Arg Asn Ala Asn
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<210> 207
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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1192)
 <223> FRXA01873

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 Met Ser Gln Ala Ile
 1 5

gat agc aag gtc gag gca cac gaa ggc cac gaa ggc atc 163
 Asp Ser Lys Val Glu Ala His Glu Gly His Glu Gly Ile
 10 15 20

gag cga gga aca cgc aat tac aag cgc gct gtg ttt gcg atg ctg gcc 211

Glu Arg Gly Thr Arg Asn Tyr Lys Arg Ala Val Phe Ala Met Leu Ala	
25 30 35	
gcc ggt ctt gct gct ttc aat ggt ctt tat tgc acg cag gca ttg ctt	259
Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys Thr Gln Ala Leu Leu	
40 45 50	
ccc acc atg acg gaa gag ttg gga att acg ccc act gag tcc gcg ctg	307
Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro Thr Glu Ser Ala Leu	
55 60 65	
acg gtg tcg gct acg act gga atg ttg gcg ctg tgt att gtt ccg gcg	355
Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu Cys Ile Val Pro Ala	
70 75 80 85	
tcg ata ctt tcg gag aaa ttt ggt cgc ggt cgg gtg ctg aca att tca	403
Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg Val Leu Thr Ile Ser	
90 95 100	
ctc acg ttg gcc atc atc gtg gga tta att ttg ccg ctt gtc ccc aat	451
Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu Pro Leu Val Pro Asn	
105 110 115	
att act gct ctc atc ctg ctc aga ggt ctc caa ggt gcg ctg ctt gct	499
Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln Gly Ala Leu Leu Ala	
120 125 130	
ggc act cca gcg gtg gcg atg acc tgg ttg tct gag gaa att cac ccc	547
Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser Glu Glu Ile His Pro	
135 140 145	
aag gat att ggg cat gcg atg gga att tac atc gcg gga aat act gtc	595
Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile Ala Gly Asn Thr Val	
150 155 160 165	
ggc ggg ctc act gga cgt atg att ccg gcg gga cta ctt gaa gta act	643
Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly Leu Leu Glu Val Thr	
170 175 180	
cat tgg caa aac gca ctg ctg gga agt tct atc gct gcg ctg atc ttc	691
His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile Ala Ala Leu Ile Phe	
185 190 195	
ggc gta atc atg gtg gtg ttg ctt ccc aag cag ccg aaa ttc cag ccg	739
Gly Val Ile Met Val Val Leu Leu Pro Lys Gln Arg Lys Phe Gln Pro	
200 205 210	
aag aat atc aat ctg cgc cat gag att tcg gcg atg gct gct cat tgg	787
Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala Met Ala Ala His Trp	
215 220 225	
cgg aat cct cgt ttg gcg ttg ctt ttt ggt act gcg ttt ttg ggc atg	835
Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr Ala Phe Leu Gly Met	
230 235 240 245	
ggt act ttt gtg tcg ctg tac aac tat ttg ggt ttc cgc atg att gat	883
Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly Phe Arg Met Ile Asp	

250										255										260																			
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Gln	Phe	Gly	Leu	Ser	Glu	Val	Leu	Val	Gly	Ala	Val	Phe	Ile	Met	Tyr																								
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ctg	gcc	ggg	acc	tgg	agt	tcc	acc	cag	gcg	ggt	gcg	ttg	agg	gag	aag	979																							
Leu	Ala	Gly	Thr	Trp	Ser	Ser	Thr	Gln	Ala	Gly	Ala	Leu	Arg	Glu	Lys																								
280										285										290																			
atc	ggc	aat	ggg	tca	acg	gtt	att	ttc	ttg	agt	ctg	acg	atg	atc	gcg	1027																							
Ile	Gly	Asn	Gly	Ser	Thr	Val	Ile	Phe	Leu	Ser	Leu	Thr	Met	Ile	Ala																								
295										300										305																			
tcg	atg	gca	ctg	atg	ggg	att	aat	aat	ttg	tgg	gtc	acg	ttg	gtt	gcc	1075																							
Ser	Met	Ala	Leu	Met	Gly	Ile	Asn	Asn	Leu	Trp	Val	Thr	Leu	Val	Ala																								
310										315										320										325									
ctg	ttt	gtg	ttt	acc	gcg	gca	ttt	ttc	gca	ctg	cat	tcc	agt	gct	tcg	1123																							
Leu	Phe	Val	Phe	Thr	Ala	Ala	Phe	Phe	Ala	Leu	His	Ser	Ser	Ala	Ser																								
330										335										340																			
gga	tgg	atc	gga	atc	atc	gca	acg	aag	gat	cgc	gcg	gaa	gcc	tcc	agc	1171																							
Gly	Trp	Ile	Gly	Ile	Ile	Ala	Thr	Lys	Asp	Arg	Ala	Glu	Ala	Ser	Ser																								
345										350										355																			
atg	tat	ttg	ttc	tgt	gaa	tac	taggatacctc	ggtgattggt	ttg							1215																							
Met	Tyr	Leu	Phe	Cys	Glu	Tyr																																	
360																																							

<210> 208

<211> 364

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

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Gly	His	Glu	Gly	Ile	Glu	Arg	Gly	Thr	Arg	Asn	Tyr	Lys	Arg	Ala	Val																								
20										25										30																			
Phe	Ala	Met	Leu	Ala	Ala	Gly	Leu	Ala	Ala	Phe	Asn	Gly	Leu	Tyr	Cys																								
35										40										45																			
Thr	Gln	Ala	Leu	Leu	Pro	Thr	Met	Thr	Glu	Glu	Leu	Gly	Ile	Thr	Pro																								
50										55										60																			
Thr	Glu	Ser	Ala	Leu	Thr	Val	Ser	Ala	Thr	Thr	Gly	Met	Leu	Ala	Leu																								
65										70										75										80									
Cys	Ile	Val	Pro	Ala	Ser	Ile	Leu	Ser	Glu	Lys	Phe	Gly	Arg	Gly	Arg																								
85										90										95																			
Val	Leu	Thr	Ile	Ser	Leu	Thr	Leu	Ala	Ile	Ile	Val	Gly	Leu	Ile	Leu																								
100										105										110																			

Pro Leu Val Pro Asn Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln
 115 120 125
 Gly Ala Leu Leu Ala Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser
 130 135 140
 Glu Glu Ile His Pro Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile
 145 150 155 160
 Ala Gly Asn Thr Val Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly
 165 170 175
 Leu Leu Glu Val Thr His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile
 180 185 190
 Ala Ala Leu Ile Phe Gly Val Ile Met Val Val Leu Leu Pro Lys Gln
 195 200 205
 Arg Lys Phe Gln Pro Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala
 210 215 220
 Met Ala Ala His Trp Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr
 225 230 235 240
 Ala Phe Leu Gly Met Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly
 245 250 255
 Phe Arg Met Ile Asp Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala
 260 265 270
 Val Phe Ile Met Tyr Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly
 275 280 285
 Ala Leu Arg Glu Lys Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser
 290 295 300
 Leu Thr Met Ile Ala Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp
 305 310 315 320
 Val Thr Leu Val Ala Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu
 325 330 335
 His Ser Ser Ala Ser Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg
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 Ala Glu Ala Ser Ser Met Tyr Leu Phe Cys Glu Tyr
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<210> 209

<211> 1572

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1549)

<223> RXN00034

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 Met Ser Tyr Thr Ser
 1 5

ttt aaa ggc gat gat aaa gcc ctc atc ggc ata gtt tta tca gtt ctc 163
 Phe Lys Gly Asp Asp Lys Ala Leu Ile Gly Ile Val Leu Ser Val Leu
 10 15 20

aca ttt tgg ctt ttt gct cag tca acc cta aat atc ggc cca gat atg 211
 Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn Ile Gly Pro Asp Met
 25 30 35

gca act gat tta ggg atg agc gat ggc acc atg aac ata gct gtc gtg 259
 Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met Asn Ile Ala Val Val
 40 45 50

gcc gcc gcg tta ttc tgt gga aca ttt atc gtc gca gcc ggc ggc atc 307
 Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val Ala Ala Gly Gly Ile
 55 60 65

gca gat gtc ttt ggc cga gta cga atc atg atg att ggc aac atc ctt 355
 Ala Asp Val Phe Gly Arg Val Arg Ile Met Met Ile Gly Asn Ile Leu
 70 75 80 85

aac atc ctg gga tct ctc ctc atc gcc acg gca acg act tct tta gcc 403
 Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala Thr Thr Ser Leu Ala
 90 95 100

acc caa atg gtg atc acc ggc cga gtt ctc caa gga ctg gca gca gcg 451
 Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln Gly Leu Ala Ala Ala
 105 110 115

gcc atc atg tct gca tcc cta gca tta gtt aag aca tat tgg tta ggt 499
 Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys Thr Tyr Trp Leu Gly
 120 125 130

act gac cgc caa cga gca gtc tcc att tgg tcc att ggt tca tgg ggt 547
 Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser Ile Gly Ser Trp Gly
 135 140 145

ggc acc gga ttc tgc gcg ctt ttc gcg ggt ctt gtt gta gca agc ccc 595
 Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu Val Val Ala Ser Pro
 150 155 160 165

ttt ggt tgg aga gga atc ttc gcc ctc tgc gcg atc gtc tcc atc gtt 643
 Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala Ile Val Ser Ile Val
 170 175 180

gct att gcc ctt acc cgc cac atc ccg gaa tcc cgt ccg gct caa tcc 691
 Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser Arg Pro Ala Gln Ser
 185 190 195

att ggc atg cat ttg gat tgg agt ggc atc atc gtt ctt gcc ctc agt Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile Val Leu Ala Leu Ser 200 205 210	739
gtt cta tct ctt gaa ttg ttt att acc caa ggt gaa tca ctt ggc tgg Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly Glu Ser Leu Gly Trp 215 220 225	787
acg cac tgg atg acc tgg act ctc ctt gcc gtt tct ttg aca ttt ctt Thr His Trp Met Thr Trp Thr Leu Leu Ala Val Ser Leu Thr Phe Leu 230 235 240 245	835
gca gtt ttc gtc ttc att gaa cgc atc gcc agc tgg cca gtt ctc gac Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser Trp Pro Val Leu Asp 250 255 260	883
ttc aac ctt ttc aaa gac cac gcc ttc agc ggt gcg acc atc acc aac Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly Ala Thr Ile Thr Asn 265 270 275	931
ttc att atg agc gct act ggc gga gta gtt gcc gtt gtc atg tgg gtt Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala Val Val Met Trp Val 280 285 290	979
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atc ggc ttc gca gcc ttt gtc atc ctt ttc att cga gtt gga gaa aag Ile Gly Phe Ala Ala Phe Val Ile Leu Phe Ile Arg Val Gly Glu Lys 310 315 320 325	1075
gcc atg cag aaa gtt ggc gcc cga gca gtg atc atc acc gct ggc atc Ala Met Gln Lys Val Gly Ala Arg Ala Val Ile Ile Thr Ala Gly Ile 330 335 340	1123
ttg gta gcg acc gcg acc gcc ctc cta atg atc acc gcg gtc agc gag L u Val Ala Thr Ala Thr Ala Leu Leu Met Ile Thr Ala Val Ser Glu 345 350 355	1171
tca acg tac atc gtc atc tcc ctc gcc ggc ttc tcc ctt tat ggc ctt Ser Thr Tyr Ile Val Ile Ser Leu Ala Gly Phe Ser Leu Tyr Gly Leu 360 365 370	1219
ggc ctc gga ctc ttc gcc acc cca gtc acc gat act gcg ctt gga aca Gly Leu Gly Leu Phe Ala Thr Pro Val Thr Asp Thr Ala Leu Gly Thr 375 380 385	1267
ctt ccc aaa gac cgt acc ggc gct ggt gca ggt gta ttc aag atg tcc Leu Pro Lys Asp Arg Thr Gly Ala Gly Ala Gly Val Phe Lys Met Ser 390 395 400 405	1315
tct tcc ctc ggc gca gca ctc ggc atc gca atc tcc act tca gtg ttc Ser Ser Leu Gly Ala Ala Leu Gly Ile Ala Ile Ser Thr Ser Val Phe 410 415 420	1363

ctc gca ctt cgc gac ggc acc tcc atc aac tcc gac gtc gca ctc gcc 1411
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gga aca gtt tca ctt ggc atc aac gtt gta ttc gca gca aca gcc acc 1459
 Gly Thr Val Ser Leu Gly Ile Asn Val Val Phe Ala Ala Thr Ala Thr
 440 445 450

atc acc gca gca gtc ctt att cca aaa gcc gct ggc aaa gtc tca caa 1507
 Ile Thr Ala Ala Val Leu Ile Pro Lys Ala Ala Gly Lys Val Ser Gln
 455 460 465

acc agc atc acc ctt cct gag cca gct atc gct gta aaa atc 1549
 Thr Ser Ile Thr Leu Pro Glu Pro Ala Ile Ala Val Lys Ile
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taaaacttca ccaggacaga taa 1572

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<211> 483

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

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Ile Gly Pro Asp Met Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met
 35 40 45

Asn Ile Ala Val Val Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val
 50 55 60

Ala Ala Gly Gly Ile Ala Asp Val Phe Gly Arg Val Arg Ile Met Met
 65 70 75 80

Ile Gly Asn Ile Leu Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala
 85 90 95

Thr Thr Ser Leu Ala Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln
 100 105 110

Gly Leu Ala Ala Ala Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys
 115 120 125

Thr Tyr Trp Leu Gly Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser
 130 135 140

Ile Gly Ser Trp Gly Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu
 145 150 155 160

Val Val Ala Ser Pro Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala
 165 170 175

Ile Val Ser Ile Val Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser
 180 185 190
 Arg Pro Ala Gln Ser Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile
 195 200 205
 Val Leu Ala Leu Ser Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly
 210 215 220
 Glu Ser Leu Gly Trp Thr His Trp Met Thr Trp Thr Leu Leu Ala Val
 225 230 235 240
 Ser Leu Thr Phe Leu Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser
 245 250 255
 Trp Pro Val Leu Asp Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly
 260 265 270
 Ala Thr Ile Thr Asn Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala
 275 280 285
 Val Val Met Trp Val Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile
 290 295 300
 Ser Gly Leu Thr Ser Ile Gly Phe Ala Ala Phe Val Ile Leu Phe Ile
 305 310 315 320
 Arg Val Gly Glu Lys Ala Met Gln Lys Val Gly Ala Arg Ala Val Ile
 325 330 335
 Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu Leu Met Ile
 340 345 350
 Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu Ala Gly Phe
 355 360 365
 Ser Leu Tyr Gly Leu Gly Leu Gly Leu Phe Ala Thr Pro Val Thr Asp
 370 375 380
 Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala Gly Ala Gly
 385 390 395 400
 Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly Ile Ala Ile
 405 410 415
 Ser Thr Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser Ile Asn Ser
 420 425 430
 Asp Val Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn Val Val Phe
 435 440 445
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 450 455 460
 Gly Lys Val Ser Gln Thr Ser Ile Thr Leu Pro Glu Pro Ala Ile Ala
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Val Lys Ile

<210> 211

<211> 1045

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1045)

<223> FRXA02273

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Phe Lys Gly Asp Asp Lys Ala Leu Ile Gly Ile Val Leu Ser Val Leu
          10 15 20

aca ttt tgg ctt ttt gct cag tca acc cta aat atc ggc cca gat atg 211
Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn Ile Gly Pro Asp Met
          25 30 35

gca act gat tta ggg atg agc gat ggc acc atg aac ata gct gtc gtg 259
Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met Asn Ile Ala Val Val
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gcc gcc gcg tta ttc tgt gga aca ttt atc gtc gca gcc ggc ggc atc 307
Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val Ala Ala Gly Gly Ile
          55 60 65

gca gat gtc ttt ggc cga gta cga atc atg atg att ggc aac atc ctt 355
Ala Asp Val Phe Gly Arg Val Arg Ile Met Met Ile Gly Asn Ile Leu
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aac atc ctg gga tct ctc ctc atc gcc acg gca acg act tct tta gcc 403
Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala Thr Thr Ser Leu Ala
          90 95 100

acc caa atg gtg atc acc ggc cga gtt ctc caa gga ctg gca gca gcg 451
Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln Gly Leu Ala Ala Ala
          105 110 115

gcc atc atg tct gca tcc cta gca tta gtt aag aca tat tgg tta ggt 499
Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys Thr Tyr Trp Leu Gly
          120 125 130

act gac cgc caa cga gca gtc tcc att tgg tcc att ggt tca tgg ggt 547
Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser Ile Gly Ser Trp Gly
          135 140 145

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ttt ggt tgg aga gga atc ttc gcc ctc tgc gcg atc gtc tcc atc gtt 643
 Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala Ile Val Ser Ile Val
 170 175 180

gct att gcc ctt acc cgc cac atc ccg gaa tcc cgt ccg gct caa tcc 691
 Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser Arg Pro Ala Gln Ser
 185 190 195

att ggc atg cat ttg gat tgg agt ggc atc atc gtt ctt gcc ctc agt 739
 Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile Val Leu Ala Leu Ser
 200 205 210

gtt cta tct ctt gaa ttg ttt att acc caa ggt gaa tca ctt ggc tgg 787
 Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly Glu Ser Leu Gly Trp
 215 220 225

acg cac tgg atg acc tgg act ctc ctt gcc gtt tct ttg aca ttt ctt 835
 Thr His Trp Met Thr Trp Thr Leu Leu Ala Val Ser Leu Thr Phe Leu
 230 235 240 245

gca gtt ttc gtc ttc att gaa cgc atc gcc agc tgg cca gtt ctc gac 883
 Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser Trp Pro Val Leu Asp
 250 255 260

ttc aac ctt ttc aaa gac cac gcc ttc agc ggt gcg acc atc acc aac 931
 Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly Ala Thr Ile Thr Asn
 265 270 275

ttc att atg agc gct act ggc gga gta gtt gcc gtt gtc atg tgg gtt 979
 Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala Val Val Met Trp Val
 280 285 290

cag caa atg gga tgg ggt gtc tcc cca aca atc tcg gga ctc acc agc 1027
 Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile Ser Gly Leu Thr Ser
 295 300 305

atc ggc ttc gca gcc ttt 1045
 Ile Gly Phe Ala Ala Phe
 310 315

<210> 212

<211> 315

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

Met Ser Tyr Thr Ser Phe Lys Gly Asp Asp Lys Ala Leu Ile Gly Ile
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Val Leu Ser Val Leu Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn
 20 25 30

Ile Gly Pro Asp Met Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met
 35 40 45
 Asn Ile Ala Val Val Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val
 50 55 60
 Ala Ala Gly Gly Ile Ala Asp Val Phe Gly Arg Val Arg Ile Met Met
 65 70 75 80
 Ile Gly Asn Ile Leu Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala
 85 90 95
 Thr Thr Ser Leu Ala Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln
 100 105 110
 Gly Leu Ala Ala Ala Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys
 115 120 125
 Thr Tyr Trp Leu Gly Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser
 130 135 140
 Ile Gly Ser Trp Gly Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu
 145 150 155 160
 Val Val Ala Ser Pro Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala
 165 170 175
 Ile Val Ser Ile Val Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser
 180 185 190
 Arg Pro Ala Gln Ser Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile
 195 200 205
 Val Leu Ala Leu Ser Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly
 210 215 220
 Glu Ser Leu Gly Trp Thr His Trp Met Thr Trp Thr Leu Leu Ala Val
 225 230 235 240
 Ser Leu Thr Phe Leu Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser
 245 250 255
 Trp Pro Val Leu Asp Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly
 260 265 270
 Ala Thr Ile Thr Asn Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala
 275 280 285
 Val Val Met Trp Val Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile
 290 295 300
 Ser Gly Leu Thr Ser Ile Gly Phe Ala Ala Phe
 305 310 315

<210> 213

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Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala Glu Asp Arg Glu Lys
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gtc acc aat att ctt gat gaa tac gat gac ggc gat ctg act gtt gtc 691
 Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val
 185 190 195

tac aac ggc aac gtg ttt ggc gca gct gca acc agc ttg gac atg acc 739
 Tyr Asn Gly Asn Val Phe Gly Ala Ala Thr Ser Leu Asp Met Thr
 200 205 210

tct gag ctg atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc 787
 Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr
 215 220 225

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 Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu Ile Ser
 230 235 240

<210> 214
 <211> 242
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 214
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Trp Pro Phe Leu Ala Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr
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Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro
 35 40 45

Gly Leu Asp Ser Val Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro
 50 55 60

Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
 65 70 75 80

Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
 85 90 95

Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
 100 105 110

Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
 115 120 125

Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
 130 135 140

Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
 145 150 155 160

Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala

	165	170	175
Glu Asp Arg	Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly		
	180	185	190
Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr			
	195	200	205
Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val			
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Val Leu Ile Val Thr Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu			
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			240
Ile Ser			

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(826)
 <223> FRXA02907

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 agcccagaag aacagtcaac tcctagatta aaggataatc gtg gcg aaa ttc ctg 115
 Val Ala Lys Phe Leu 5
 1
 tat aag tta ggc tcc acg gcc tat caa aag aaa tgg ccg ttt ctt gcg 163
 Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys Trp Pro Phe Leu Ala 20
 10 15
 gtc tgg ctc gtg att ctc ata ggt atc acg acg ctg gcg ggg ctg tat 211
 Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr Leu Ala Gly Leu Tyr 35
 25 30
 gcc aag cca acg tcg agt agc ttc tct atc cct ggt ctt gat tct gtc 259
 Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro Gly Leu Asp Ser Val 50
 40 45
 acg acc atg gag aag atg cag gag cgt ttc cct ggt tcg gat gat gca 307
 Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro Gly Ser Asp Asp Ala 65
 55 60
 aca tcg gct ccc act ggt tct gtc gtc att cag gca ccg gaa ggc aag 355
 Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln Ala Pro Glu Gly Lys 85
 70 75 80
 acc ctc act gat cct gag gtt ggg gct gaa gta aac cag atg ctt gat 403
 Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val Asn Gln Met Leu Asp

90										95										100										
gag gtt cgg gcg act ggt gtg ctg aag gat gct gat tcc gtt gtg gat	451																													
Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala Asp Ser Val Val Asp																														
105 110 115																														
cct gtg ttg gct gcg cag ggt gtg gct gct cag atg acc cca gcc ctg	499																													
Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln Met Thr Pro Ala Leu																														
120 125 130																														
gag gct cag ggt gta cct gcg gag aag atc gcc gca gat att gag tcg	547																													
Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala Ala Asp Ile Glu Ser																														
135 140 145																														
att agt cca ctg agt gca gat gag act acc ggc atc atc tcg atg act	595																													
Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly Ile Ile Ser Met Thr																														
150 155 160 165																														
ttt gat gca gat tct gcc atg gat ata tcc gca gag gat cgt gag aag	643																													
Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala Glu Asp Arg Glu Lys																														
170 175 180																														
gtc acc aat att ctt gat gaa tac gat gac ggc gat ctg act gtt gtc	691																													
Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val																														
185 190 195																														
tac aac ggc aac gtg ttt ggc gca gct gca acc agc ttg gac atg acc	739																													
Tyr Asn Gly Asn Val Phe Gly Ala Ala Thr Ser Leu Asp Met Thr																														
200 205 210																														
tct gag ctc atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc	787																													
Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr																														
215 220 225																														
ttc ggt tcg ttc atc gct gcc ggt atg ccg ctg atc tct	826																													
Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu Ile Ser																														
230 235 240																														

<210> 216

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro	
35 40 45	
Gly Leu Asp Ser Val Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro	
50 55 60	

Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
 65 70 75 80
 Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
 85 90 95
 Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
 100 105 110
 Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
 115 120 125
 Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
 130 135 140
 Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
 145 150 155 160
 Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala
 165 170 175
 Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly
 180 185 190
 Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr
 195 200 205
 Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val
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 Val Leu Ile Val Thr Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu
 225 230 235 240
 Ile Ser

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2290)
 <223> RXA00479

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 Met Ser Thr Ser Ile
 1 5
 aca aca gag aac aag aag aaa tct ggt cct cct cgc ttg atg aga atc 163
 Thr Thr Glu Asn Lys Lys Lys Ser Gly Pro Pro Arg Leu Met Arg Ile
 10 15 20

ttt ctg ccc gcc ttg cta att tta gtt tgg ctt gta gga gct gga gtc	211
Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu Val Gly Ala Gly Val	
25 30 35	
ggc ggt cct tat ttt ggc aag gtt agt gag gtc tcc tcc aac agc cag	259
Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val Ser Ser Asn Ser Gln	
40 45 50	
acc aca tat ctg cca gaa tct gcc gat gcc act caa gta cag gaa cag	307
Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr Gln Val Gln Glu Gln	
55 60 65	
ttg gga gat ttt act gat tct gaa tcc atc cca gcc att gtc gta atg	355
Leu Gly Asp Phe Thr Asp Ser Glu Ser Ile Pro Ala Ile Val Val Met	
70 75 80 85	
gtc agc gat gaa ccc tta aca cag caa gac atc aca caa ctc aat gaa	403
Val Ser Asp Glu Pro Leu Thr Gln Gln Asp Ile Thr Gln Leu Asn Glu	
90 95 100	
gtt gtt gct ggg ctt tca gaa tta gac ata gtt tcc gat gaa gtc tcc	451
Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val Ser Asp Glu Val Ser	
105 110 115	
cct gct att cca tcc gag gac ggc aga gct gtc caa gtg ttt gtc ccc	499
Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val Gln Val Phe Val Pro	
120 125 130	
ctc aat cca tca gcg gag ctg acg gaa agc gtc gag aag ctc tct gag	547
Leu Asn Pro Ser Ala Glu Leu Thr Glu Ser Val Glu Lys Leu Ser Glu	
135 140 145	
acc ttg acc cag caa acg ccg gac tat gtg agc acc tat gtg acc gga	595
Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser Thr Tyr Val Thr Gly	
150 155 160 165	
ccg gct ggg ttt acc gct gat ctc agc gca gct ttc gcg ggt att gat	643
Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala Phe Ala Gly Ile Asp	
170 175 180	
ggg cta ctc cta gca gtc gcc ttg gct gcc gtc ctt gtc att ctt gtc	691
Gly Leu Leu Leu Ala Val Ala Leu Ala Ala Val Leu Val Ile Leu Val	
185 190 195	
atc gtc tat cgc tcc ttc att ctg ccc atc gcc gtg ctt gcc acc agt	739
Ile Val Tyr Arg Ser Phe Ile Leu Pro Ile Ala Val Leu Ala Thr Ser	
200 205 210	
ttg ttt gcg ctg act gta gct cta ttg gtg gtg tgg tgg cta gct aag	787
Leu Phe Ala Leu Thr Val Ala Leu Leu Val Val Trp Trp Leu Ala Lys	
215 220 225	
tgg gac atc ctg ctg ctt tcg ggt cag act caa ggc atc ctc ttc att	835
Trp Asp Ile Leu Leu Leu Ser Gly Gln Thr Gln Gly Ile Leu Phe Ile	
230 235 240 245	

ctg gtc att ggc gcc gcc acc gac tac tca ttg cta tac gtt gct cgt	883
Leu Val Ile Gly Ala Ala Thr Asp Tyr Ser Leu Leu Tyr Val Ala Arg	
250 255 260	
ttc cgt gaa gag tta cgc gtt caa caa gat aaa ggg ata gcc aca ggg	931
Phe Arg Glu Glu Leu Arg Val Gln Gln Asp Lys Gly Ile Ala Thr Gly	
265 270 275	
aaa gcc atc cgg gca tcg gtg gaa ccc att ctt gcc tcg ggc agc act	979
Lys Ala Ile Arg Ala Ser Val Glu Pro Ile Leu Ala Ser Gly Ser Thr	
280 285 290	
gtt att gcg ggc ctc ctt tgt ttg cta ttt agt gat ttg aaa tct aac	1027
Val Ile Ala Gly Leu Leu Cys Leu Leu Phe Ser Asp Leu Lys Ser Asn	
295 300 305	
tcc acg cta ggt cca gta gct tcg gtg ggc att att ttt gca atg ctt	1075
Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile Ile Phe Ala Met Leu	
310 315 320 325	
tct gct ctt act ctg cta cca gcc ctg ctg ttt gta ttc ggt cgg gtg	1123
Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe Val Phe Gly Arg Val	
330 335 340	
gcc ttt tgg ccc aag cga cca aaa tac gaa cct gaa aaa gcc cgt gcg	1171
Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro Glu Lys Ala Arg Ala	
345 350 355	
aaa aac gac atc ccc gcc agc ggg atc tgg tca aaa gtg gct gat tta	1219
Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser Lys Val Ala Asp Leu	
360 365 370	
gtg gag cag cat cct cgt gca atc tgg gta tct aca ctt att gtg ctt	1267
Val Glu Gln His Pro Arg Ala Ile Trp Val Ser Thr Leu Ile Val Leu	
375 380 385	
ctc ttg ggt gcg gct ttc gtt ccc aca cta aaa gcg gac ggt gtg tcc	1315
Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys Ala Asp Gly Val Ser	
390 395 400 405	
caa tcc gac cta gtt ctg ggt tcc tct gaa gca cgt gat ggc cag cag	1363
Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala Arg Asp Gly Gln Gln	
410 415 420	
gct tta ggc gaa cac ttc ccc ggt gga tcc ggc agt cct gct tat att	1411
Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly Ser Pro Ala Tyr Ile	
425 430 435	
atc gtt gat gaa aca cag gca gca cag gct gct gac gta gtc ctt aac	1459
Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala Asp Val Val Leu Asn	
440 445 450	
aac gac aat ttc gag act gta act gta act agt gct gac tcc ccc tct	1507
Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser Ala Asp Ser Pro Ser	
455 460 465	
ggc tca gcc cca atc acc gct gac ggt att gtg ccg tta ggt tct ggt	1555

Gly 470	Ser	Ala	Pro	Ile	Thr 475	Ala	Asp	Gly	Ile	Val 480	Pro	Leu	Gly	Ser	Gly 485	
aca	gct	cca	ggc	ccg	gta	ggt	gta	gaa	ggg	caa	gtc	ctt	tta	caa	gca	1603
Thr	Ala	Pro	Gly	Pro	Val	Val	Val	Glu	Gly	Gln	Val	Leu	Leu	Gln	Ala	
				490					495					500		
aca	ctt	gtc	gaa	gca	cca	gat	tcc	gaa	gaa	gct	caa	aaa	gct	att	cgc	1651
Thr	Leu	Val	Glu	Ala	Pro	Asp	Ser	Glu	Glu	Ala	Gln	Lys	Ala	Ile	Arg	
			505					510					515			
agt	atc	cgc	caa	act	ttt	gca	gat	gaa	aat	ata	tca	gcg	gta	gta	ggc	1699
Ser	Ile	Arg	Gln	Thr	Phe	Ala	Asp	Glu	Asn	Ile	Ser	Ala	Val	Val	Gly	
		520					525					530				
ggg	gtc	act	gca	act	tcc	gta	gac	act	aac	gat	gcc	tcc	atc	cat	gac	1747
Gly	Val	Thr	Ala	Thr	Ser	Val	Asp	Thr	Asn	Asp	Ala	Ser	Ile	His	Asp	
	535					540					545					
cgc	aac	ctg	atc	atc	cca	att	gta	ttg	ctg	gtc	att	ttg	ggt	att	ctc	1795
Arg	Asn	Leu	Ile	Ile	Pro	Ile	Val	Leu	Leu	Val	Ile	Leu	Val	Ile	Leu	
550					555					560					565	
atg	ctg	ttg	ctg	cgg	tct	att	gtc	gca	cca	ctc	ctg	cta	gta	gtc	acc	1843
Met	Leu	Leu	Leu	Arg	Ser	Ile	Val	Ala	Pro	Leu	Leu	Leu	Val	Val	Thr	
				570					575					580		
acc	gtg	gtg	tct	ttt	gct	act	gct	tta	ggc	gtg	gct	gct	tta	ctt	ttc	1891
Thr	Val	Val	Ser	Phe	Ala	Thr	Ala	Leu	Gly	Val	Ala	Ala	Leu	Leu	Phe	
			585					590					595			
aat	cac	gtt	ttc	agt	ttc	cca	gga	gca	gac	ccc	gca	gta	cct	ctc	tac	1939
Asn	His	Val	Phe	Ser	Phe	Pro	Gly	Ala	Asp	Pro	Ala	Val	Pro	Leu	Tyr	
		600					605					610				
gga	ttt	gta	ttt	tta	gta	gcc	ttg	ggc	atc	gac	tac	aac	att	ttc	tta	1987
Gly	Phe	Val	Phe	Leu	Val	Ala	Leu	Gly	Ile	Asp	Tyr	Asn	Ile	Phe	Leu	
	615					620					625					
gtc	acc	cga	atc	cgt	gaa	gaa	acc	aaa	acc	cac	ggc	aca	aga	ctt	gga	2035
Val	Thr	Arg	Ile	Arg	Glu	Glu	Thr	Lys	Thr	His	Gly	Thr	Arg	Leu	Gly	
630					635					640					645	
att	ctt	cga	ggc	ctg	aca	gta	acc	ggc	gga	gta	att	acc	tca	gct	gga	2083
Ile	Leu	Arg	Gly	Leu	Thr	Val	Thr	Gly	Gly	Val	Ile	Thr	Ser	Ala	Gly	
				650					655					660		
gta	gtt	ctc	gcc	gca	acg	ttc	gca	gca	ctc	tat	gtc	atc	cca	att	cta	2131
Val	Val	Leu	Ala	Ala	Thr	Phe	Ala	Ala	Leu	Tyr	Val	Ile	Pro	Ile	Leu	
			665					670					675			
ttc	ctg	gca	caa	att	gcc	ttc	att	gtc	gct	ttt	gga	gtt	ctt	att	gat	2179
Phe	Leu	Ala	Gln	Ile	Ala	Phe	Ile	Val	Ala	Phe	Gly	Val	Leu	Ile	Asp	
		680					685					690				
acc	ctg	ctc	gtt	cgc	gcc	ttc	ttg	gtg	cct	gct	ttg	ttc	tac	gac	atc	2227
Thr	Leu	Leu	Val	Arg	Ala	Phe	Leu	Val	Pro	Ala	Leu	Phe	Tyr	Asp	Ile	

695

700

705

gga ccg aaa atc tgg tgg ccg tca aaa ttg tcc aat cag aaa tac cag 2275
 Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser Asn Gln Lys Tyr Gln
 710 715 720 725

aag cag cct cag cta tgacacacca aaattcgcct ctc 2313
 Lys Gln Pro Gln Leu
 730

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<211> 730

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met Ser Thr Ser Ile Thr Thr Glu Asn Lys Lys Lys Ser Gly Pro Pro
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Val Gly Ala Gly Val Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val
 35 40 45

Ser Ser Asn Ser Gln Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr
 50 55 60

Gln Val Gln Glu Gln Leu Gly Asp Phe Thr Asp Ser Glu Ser Ile Pro
 65 70 75 80

Ala Ile Val Val Met Val Ser Asp Glu Pro Leu Thr Gln Gln Asp Ile
 85 90 95

Thr Gln Leu Asn Glu Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val
 100 105 110

Ser Asp Glu Val Ser Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val
 115 120 125

Gln Val Phe Val Pro Leu Asn Pro Ser Ala Glu Leu Thr Glu Ser Val
 130 135 140

Glu Lys Leu Ser Glu Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser
 145 150 155 160

Thr Tyr Val Thr Gly Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala
 165 170 175

Phe Ala Gly Ile Asp Gly Leu Leu Leu Ala Val Ala Leu Ala Ala Val
 180 185 190

Leu Val Ile Leu Val Ile Val Tyr Arg Ser Phe Ile Leu Pro Ile Ala
 195 200 205

Val Leu Ala Thr Ser Leu Phe Ala Leu Thr Val Ala Leu Leu Val Val

210	215	220
Trp Trp Leu Ala Lys Trp Asp Ile Leu Leu Leu Ser Gly Gln Thr Gln 225 230 235 240		
Gly Ile Leu Phe Ile Leu Val Ile Gly Ala Ala Thr Asp Tyr Ser Leu 245 250 255		
Leu Tyr Val Ala Arg Phe Arg Glu Glu Leu Arg Val Gln Gln Asp Lys 260 265 270		
Gly Ile Ala Thr Gly Lys Ala Ile Arg Ala Ser Val Glu Pro Ile Leu 275 280 285		
Ala Ser Gly Ser Thr Val Ile Ala Gly Leu Leu Cys Leu Leu Phe Ser 290 295 300		
Asp Leu Lys Ser Asn Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile 305 310 315 320		
Ile Phe Ala Met Leu Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe 325 330 335		
Val Phe Gly Arg Val Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro 340 345 350		
Glu Lys Ala Arg Ala Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser 355 360 365		
Lys Val Ala Asp Leu Val Glu Gln His Pro Arg Ala Ile Trp Val Ser 370 375 380		
Thr Leu Ile Val Leu Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys 385 390 395 400		
Ala Asp Gly Val Ser Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala 405 410 415		
Arg Asp Gly Gln Gln Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly 420 425 430		
Ser Pro Ala Tyr Ile Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala 435 440 445		
Asp Val Val Leu Asn Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser 450 455 460		
Ala Asp Ser Pro Ser Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val 465 470 475 480		
Pro Leu Gly Ser Gly Thr Ala Pro Gly Pro Val Val Val Glu Gly Gln 485 490 495		
Val Leu Leu Gln Ala Thr Leu Val Glu Ala Pro Asp Ser Glu Glu Ala 500 505 510		
Gln Lys Ala Ile Arg Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile		

515	520	525
Ser Ala Val Val Gly Gly Val Thr Ala Thr Ser Val Asp Thr Asn Asp 530 535 540		
Ala Ser Ile His Asp Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val 545 550 555 560		
Ile Leu Val Ile Leu Met Leu Leu Leu Arg Ser Ile Val Ala Pro Leu 565 570 575		
Leu Leu Val Val Thr Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val 580 585 590		
Ala Ala Leu Leu Phe Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro 595 600 605		
Ala Val Pro Leu Tyr Gly Phe Val Phe Leu Val Ala Leu Gly Ile Asp 610 615 620		
Tyr Asn Ile Phe Leu Val Thr Arg Ile Arg Glu Glu Thr Lys Thr His 625 630 635 640		
Gly Thr Arg Leu Gly Ile Leu Arg Gly Leu Thr Val Thr Gly Gly Val 645 650 655		
Ile Thr Ser Ala Gly Val Val Leu Ala Ala Thr Phe Ala Ala Leu Tyr 660 665 670		
Val Ile Pro Ile Leu Phe Leu Ala Gln Ile Ala Phe Ile Val Ala Phe 675 680 685		
Gly Val Leu Ile Asp Thr Leu Leu Val Arg Ala Phe Leu Val Pro Ala 690 695 700		
Leu Phe Tyr Asp Ile Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser 705 710 715 720		
Asn Gln Lys Tyr Gln Lys Gln Pro Gln Leu 725 730		

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 <211> 983
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(960)
 <223> RXN03124

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 Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp
 1 5 10 15

tac gcg cta ttt atc gtg tcc cgt ttc cgc aat gag ttg att tct cag	96
Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln	
20 25 30	
act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc	144
Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg	
35 40 45	
acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc	192
Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly	
50 55 60	
act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct	240
Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala	
65 70 75 80	
ctg gtt gct ctg tcg atc att aat att cca ttt cta acc gtg atg gcc	288
Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala	
85 90 95	
att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc	336
Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser	
100 105 110	
ttc ctc cca gct ctg ctt ggc ctg ctt ggc act cgc atc ttc gca gca	384
Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala	
115 120 125	
cgc gtg cct gga cct aag gtt ccg gat cct gag gac gag aag cca acg	432
Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr	
130 135 140	
atg ggt ctg aag tgg gtc cgc ctt gtg cgc aag atg ccg gtg gct tac	480
Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr	
145 150 155 160	
ctg ctg gtt ggc gtc gtt ttg ctt ggt gca atc gca att cct gcg acc	528
Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr	
165 170 175	
aat atg cgc ctg gcc atg ccg act gat ggc acc tcc acg ctg ggc acc	576
Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr	
180 185 190	
gcg ccg cgc acg ggg tat gac atg acg gca gat gcg ttc ggc ccg ggc	624
Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly	
195 200 205	
cgc aac gcg ccc atg att gcg ctt atc gac gca acc gac gtc cct gag	672
Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu	
210 215 220	
gaa gaa cgc cca ttg gtg ttt gga cag gcg gtg gag caa ttc ttg aac	720
Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn	
225 230 235 240	
act gat ggt gtg aag aat gct cag atc act cag acc acg gag aat ttc	768

Thr	Asp	Gly	Val	Lys	Asn	Ala	Gln	Ile	Thr	Gln	Thr	Thr	Glu	Asn	Ph		
				245					250					255			
gat	acc	gcg	cag	atc	ctg	tta	ccc	cag	aat	ttg	atg	cga	tcg	atg	agc	816	
Asp	Thr	Ala	Gln	Ile	Leu	Leu	Pro	Gln	Asn	Leu	Met	Arg	Ser	Met	Ser		
			260					265					270				
gca	cct	ctg	aga	ctc	tcg	caa	ctc	ttc	gtg	cag	atg	ctg	aga	cct	tcg	864	
Ala	Pro	Leu	Arg	Leu	Ser	Gln	Leu	Phe	Val	Gln	Met	Leu	Arg	Pro	Ser		
			275				280					285					
ctg	atg	aca	ccg	gcg	cga	cgt	atg	gca	tta	ctg	gcg	tca	ccc	caa	ttt	912	
Leu	Met	Thr	Pro	Ala	Arg	Arg	Met	Ala	Leu	Leu	Ala	Ser	Pro	Gln	Phe		
		290					295				300						
acg	atg	aca	tct	ctg	ctc	gcc	tcg	gcg	acg	tcc	tgg	ttc	ctt	acg	ttc	960	
Thr	Met	Thr	Ser	Leu	Leu	Ala	Ser	Ala	Thr	Ser	Trp	Phe	Leu	Thr	Phe		
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<210> 220

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

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Tyr	Ala	Leu	Phe	Ile	Val	Ser	Arg	Phe	Arg	Asn	Glu	Leu	Ile	Ser	Gln		
			20					25					30				
Thr	Gly	Ala	Asn	Asp	Leu	Glu	Pro	Lys	Glu	Leu	Ala	Glu	Arg	Leu	Arg		
			35				40					45					
Thr	Met	Pro	Leu	Ala	Ala	Arg	Ala	His	Ala	Met	Gly	Met	Ala	Val	Gly		
			50			55					60						
Thr	Ala	Gly	Ser	Ala	Val	Val	Phe	Ala	Gly	Thr	Thr	Val	Leu	Ile	Ala		
			65			70				75					80		
Leu	Val	Ala	Leu	Ser	Ile	Ile	Asn	Ile	Pro	Phe	Leu	Thr	Val	Met	Ala		
				85				90						95			
Ile	Ala	Ala	Ala	Ile	Thr	Val	Ala	Ile	Ala	Val	Leu	Val	Ala	Leu	Ser		
			100					105					110				
Phe	Leu	Pro	Ala	Leu	Leu	Gly	Leu	Leu	Gly	Thr	Arg	Ile	Phe	Ala	Ala		
			115				120					125					
Arg	Val	Pro	Gly	Pro	Lys	Val	Pro	Asp	Pro	Glu	Asp	Glu	Lys	Pro	Thr		
			130			135					140						
Met	Gly	Leu	Lys	Trp	Val	Arg	Leu	Val	Arg	Lys	Met	Pro	Val	Ala	Tyr		
145				150						155					160		

Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
 165 170 175
 Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
 180 185 190
 Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
 195 200 205
 Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
 210 215 220
 Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
 225 230 235 240
 Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe
 245 250 255
 Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser
 260 265 270
 Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser
 275 280 285
 Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe
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 Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe
 305 310 315 320

<210> 221
 <211> 762
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(762)
 <223> FRXA01180

<400> 221
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 tac gcg cta ttt atc gtg tcc cgt ttc cgc aat gag ttg att tct cag 96
 Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
 20 25 30
 act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc 144
 Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
 35 40 45

acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc	192
Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly	
50 55 60	
act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct	240
Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala	
65 70 75 80	
ctg gtt gct ctg tcg atc att aat att cca ttt cta acc gtg atg gcc	288
Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala	
85 90 95	
att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc	336
Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser	
100 105 110	
ttc ctc cca gct ctg ctt ggc ctg ctt ggc act cgc atc ttc gca gca	384
Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala	
115 120 125	
cgc gtg cct gga cct aag gtt ccg gat cct gag gac gag aag cca acg	432
Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr	
130 135 140	
atg ggt ctg aag tgg gtc cgc ctt gtg cgc aag atg ccg gtg gct tac	480
Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr	
145 150 155 160	
ctg ctg gtt ggc gtc gtt ttg ctt ggt gca atc gca att cct gcg acc	528
Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr	
165 170 175	
aat atg cgc ctg gcc atg ccg act gat ggc acc tcc acg ctg ggc acc	576
Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr	
180 185 190	
gcg ccg cgc acg ggg tat gac atg acg gca gat gcg ttc ggc ccg ggc	624
Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly	
195 200 205	
cgc aac gcg ccc atg att gcg ctt atc gac gca acc gac gtc cct gag	672
Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu	
210 215 220	
gaa gaa cgc cca ttg gtg ttt gga cag gcg gtg gag caa ttc ttg aac	720
Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn	
225 230 235 240	
act gat ggt gtg aag aat gct cag atc act cag acc acg gag	762
Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu	
245 250	

<210> 222

<211> 254

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 222

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Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
      20           25           30

Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
      35           40           45

Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
      50           55           60

Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
      65           70           75           80

Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
      85           90           95

Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
      100           105           110

Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
      115           120           125

Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
      130           135           140

Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
      145           150           155           160

Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
      165           170           175

Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
      180           185           190

Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
      195           200           205

Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
      210           215           220

Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
      225           230           235           240

Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu
      245           250

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<211> 393

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(370)

<223> RXA02586

<400> 223

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gatgccacca tcatccgcat gctgcttgtc ccccgccgtg atg cac ctg ctt cgc 115
                                     Met His Leu Leu Arg
                                     1 5

gac gac aac tgg tgg gca ccc ggc ttc gtt aaa aag gcc tac acc gtc 163
Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys Lys Ala Tyr Thr Val
                10                15                20

atg ggt cac ggc tct gag gtg gag gaa gca cct cgc cca acc acc cgt 211
Met Gly His Gly Ser Glu Val Glu Glu Ala Pro Arg Pro Thr Thr Arg
                25                30                35

cgc ctc aac gac gat gag gaa gtc acc gtg cat gaa gca gtt gtc gct 259
Arg Leu Asn Asp Asp Glu Glu Val Thr Val His Glu Ala Val Val Ala
                40                45                50

ggc gat acc gtg gca tct cgc ggt ggt ttg agc acg cag gaa aac cgt 307
Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser Thr Gln Glu Asn Arg
                55                60                65

gat ctg gtg tcc ttc gtg gaa ctt aag gct cgt ttg gaa aag cgc agg 355
Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg Leu Glu Lys Arg Arg
                70                75                80                85

ctt gag gat cta gat taaatctatg cgaggatttt tca 393
Leu Glu Asp Leu Asp
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<210> 224

<211> 90

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

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Met His Leu Leu Arg Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys
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Lys Ala Tyr Thr Val Met Gly His Gly Ser Glu Val Glu Glu Ala Pro
 20 25 30

Arg Pro Thr Thr Arg Arg Leu Asn Asp Asp Glu Glu Val Thr Val His
 35 40 45

Glu Ala Val Val Ala Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser
 50 55 60

Thr Gln Glu Asn Arg Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg
 65 70 75 80

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Leu Glu Lys Arg Arg Leu Glu Asp Leu Asp
85 90

<210> 225
<211> 2214
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(2191)
<223> RXA02587

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ttgttatcca accgccacaa ttcccaggag taatccaccc gtg ttt tct aaa tgg 115
Val Phe Ser Lys Trp
1 5
ggc cac ttt gct tac aga ttt agg cgc att gtt ccg tta gtc gtc atc 163
Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val Pro Leu Val Val Ile
10 15 20
gcc gcg att ttg gct ttg ttt gtc att ttc ggc acc aag ctg ggc gac 211
Ala Ala Ile Leu Ala Leu Phe Val Ile Phe Gly Thr Lys Leu Gly Asp
25 30 35
cgc atg agc cag gaa gga tgg gat gat cct ggt tct tcc tcg acc gct 259
Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly Ser Ser Ser Thr Ala
40 45 50
gcg gcg cgc atc gag ttg gag acc ttt ggg cgt gac aat gac ggc gat 307
Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg Asp Asn Asp Gly Asp
55 60 65
gtc gtg ttg ctg ttt act gcg cct gaa ggc act tct ttc gat gat gca 355
Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr Ser Phe Asp Asp Ala
70 75 80 85
gag gtg ttc tcc agc atc tct ggc tac tta gat ggg cta atc gag aac 403
Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp Gly Leu Ile Glu Asn
90 95 100
aac cct gat gaa gtc agc cac atc aac agc tac ttt gac act cgt aat 451
Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr Phe Asp Thr Arg Asn
105 110 115
caa aat ctc ctc agc aaa gac ggc acc caa acc ttt gca gct ctc ggg 499
Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr Phe Ala Ala Leu Gly
120 125 130
ctc aaa ggt gac ggc gag caa acg ctg aag gac ttc cgg gag att gaa 547
Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp Phe Arg Glu Ile Glu
135 140 145

gat	cag	ctc	cat	ccg	gac	aac	ctt	gcc	ggg	ggc	gtc	acc	act	gag	gtc	595
Asp	Gln	Leu	His	Pro	Asp	Asn	Leu	Ala	Gly	Gly	Val	Thr	Thr	Glu	Val	
150					155					160					165	
gcg	ggg	gcc	acc	gct	gta	gcc	gac	gca	ctc	gat	gag	ggc	atg	gct	ggc	643
Ala	Gly	Ala	Thr	Ala	Val	Ala	Asp	Ala	Leu	Asp	Glu	Gly	Met	Ala	Gly	
				170					175						180	
gat	att	tca	cgc	gcc	gaa	gtt	ttt	gcg	ctg	cct	ttc	gtg	gct	atc	ttg	691
Asp	Ile	Ser	Arg	Ala	Glu	Val	Phe	Ala	Leu	Pro	Phe	Val	Ala	Ile	Leu	
			185					190						195		
ctg	ctc	atc	gtg	ttt	ggc	tca	gtt	gtt	gcc	gcg	gcg	atg	cca	ttg	atc	739
Leu	Leu	Ile	Val	Phe	Gly	Ser	Val	Val	Ala	Ala	Ala	Met	Pro	Leu	Ile	
			200				205						210			
gtg	ggc	att	ttg	tcc	atc	ttg	ggg	tcg	ctg	ggc	atc	ttg	gca	att	ttg	787
Val	Gly	Ile	Leu	Ser	Ile	Leu	Gly	Ser	Leu	Gly	Ile	Leu	Ala	Ile	Leu	
	215					220					225					
gct	gga	ttc	ttc	cag	gtc	aac	gta	ttt	gca	caa	tct	gtt	gtg	acc	ctt	835
Ala	Gly	Phe	Phe	Gln	Val	Asn	Val	Phe	Ala	Gln	Ser	Val	Val	Thr	Leu	
230					235					240					245	
ctg	ggc	ttg	ggg	ctt	gcc	att	gac	tat	ggc	tta	ttc	atg	gtc	tct	cgt	883
Leu	Gly	Leu	Gly	Leu	Ala	Ile	Asp	Tyr	Gly	Leu	Phe	Met	Val	Ser	Arg	
				250					255						260	
ttc	cgt	gag	gaa	atg	gat	aag	ggc	acc	ccg	gtt	gaa	cag	gct	gtt	gcc	931
Phe	Arg	Glu	Glu	Met	Asp	Lys	Gly	Thr	Pro	Val	Glu	Gln	Ala	Val	Ala	
			265					270						275		
acc	act	acg	gcg	acc	gcg	ggg	aag	act	gtg	gtg	ttc	tct	gca	gcg	atg	979
Thr	Thr	Thr	Ala	Thr	Ala	Gly	Lys	Thr	Val	Val	Phe	Ser	Ala	Ala	Met	
			280				285					290				
gtg	gct	gtg	gcg	ctg	tcc	ggg	ttg	ttt	gtt	ttc	cca	cag	gct	ttc	ttg	1027
Val	Ala	Val	Ala	Leu	Ser	Gly	Leu	Phe	Val	Phe	Pro	Gln	Ala	Phe	Leu	
	295					300					305					
aag	tcg	gtg	gca	ttc	ggg	gcg	att	tcc	gcg	gtt	ggc	ctt	gct	gct	ttg	1075
Lys	Ser	Val	Ala	Phe	Gly	Ala	Ile	Ser	Ala	Val	Gly	Leu	Ala	Ala	Leu	
310					315					320					325	
atg	tcg	gtg	acg	gtg	ttg	ccg	tcg	ctg	ttc	agc	atg	ttg	ggg	aag	aat	1123
Met	Ser	Val	Thr	Val	Leu	Pro	Ser	Leu	Phe	Ser	Met	Leu	Gly	Lys	Asn	
				330					335						340	
atc	gat	aag	tgg	agt	ttg	cgt	cgc	act	gct	cga	aca	gcg	cgc	cgt	ttg	1171
Ile	Asp	Lys	Trp	Ser	Leu	Arg	Arg	Thr	Ala	Arg	Thr	Ala	Arg	Arg	Leu	
			345					350					355			
gaa	gac	acc	att	tgg	tac	cgc	gtg	ccg	gca	tgg	gca	atg	cgc	cat	gcc	1219
Glu	Asp	Thr	Ile	Trp	Tyr	Arg	Val	Pro	Ala	Trp	Ala	Met	Arg	His	Ala	
			360				365					370				

aag gca gtg acc gtg ggc gtc gta ttg ctc ttg ctt gct ctt aca gtg	1267
Lys Ala Val Thr Val Gly Val Val Leu Leu Leu Leu Ala Leu Thr Val	
375 380 385	
ccg ttg acg ggc gtg aaa ttc ggc ggc atc aat gaa acg tat ctg cca	1315
Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn Glu Thr Tyr Leu Pro	
390 395 400 405	
cca gct aac gac acc cgc gtc gcc caa gag cgt ttc gac gag gcg ttt	1363
Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg Phe Asp Glu Ala Phe	
410 415 420	
ccc gcc ttc cgc acc gag ccg gtc aag ctt gtg gtc acc ggg gcg gac	1411
Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val Val Thr Gly Ala Asp	
425 430 435	
aac aac cag ctg atc gat atc tat gtt cag gcc aac gaa gtt gag gga	1459
Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala Asn Glu Val Glu Gly	
440 445 450	
ctg aca gat cgt ttc acc gca ggt gcg act acc gat gat ggc acc acg	1507
Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr Asp Asp Gly Thr Thr	
455 460 465	
gtg ttg tct act ggt att cag gat cgt tcc ctc aat gag cag gta gtg	1555
Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu Asn Glu Gln Val Val	
470 475 480 485	
gag cag ctt cgc gct att tcc gtc cct gag ggc gtt gag gtg cag atc	1603
Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly Val Glu Val Gln Ile	
490 495 500	
ggt ggc act cca gcc atg gag atc gaa tcc att gag gcg ctc ttt gaa	1651
Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile Glu Ala Leu Phe Glu	
505 510 515	
aag ctc ctc tgg atg gct ctc tac att gtg ctg gcc act ttc atc ctc	1699
Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu Ala Thr Phe Ile Leu	
520 525 530	
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Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro Ala Lys Ala Ile Ile	
535 540 545	
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Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly Ile Leu Thr Leu Met	
550 555 560 565	
ttc gtc gat ggc gtg ggt gcc agc gca ttg aac ttc tcc cct ggc cca	1843
Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn Phe Ser Pro Gly Pro	
570 575 580	
ctg atg agt cca gtg ctg gtg ctg atc atg gct att att tac gga ctt	1891
Leu Met Ser Pro Val Leu Val Leu Met Ala Ile Ile Tyr Gly Leu	
585 590 595	
tcc acc gac tat gag gtg ttc ctg gta tct cgc atg gtg gag gcc cgc	1939

Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg Met Val Glu Ala Arg
600 605 610

gat aaa ggc gaa tcc acc gac gac gcc atc aga tac ggc act gca cac 1987
Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg Tyr Gly Thr Ala His
615 620 625

acc gga tct atc atc acc gcg gcc gca ctg atc atg att gtg gtc tgt 2035
Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile Met Ile Val Val Cys
630 635 640 645

gga gcg ttt ggt ttc tct gag atc gtc atg atg aag tac atc gcg ttc 2083
Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met Lys Tyr Ile Ala Phe
650 655 660

ggc atg atc gca gcg ctg att ctg gat gcc acc atc atc cgc atg ctg 2131
Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr Ile Ile Arg Met Leu
665 670 675

ctt gtc ccc cgc cgt gat gca cct gct tcg cga cga caa ctg gtg ggc 2179
Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg Arg Gln Leu Val Gly
680 685 690

acc cgg ctt cgt taaaaaggcc tacaccgtca tgg 2214
Thr Arg Leu Arg
695

<210> 226

<211> 697

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 226

Val Phe Ser Lys Trp Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val
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20 25 30

Thr Lys Leu Gly Asp Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly
35 40 45

Ser Ser Ser Thr Ala Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg
50 55 60

Asp Asn Asp Gly Asp Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr
65 70 75 80

Ser Phe Asp Asp Ala Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp
85 90 95

Gly Leu Ile Glu Asn Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr
100 105 110

Phe Asp Thr Arg Asn Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr
115 120 125

Phe Ala Ala Leu Gly Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp
 130 135 140
 Phe Arg Glu Ile Glu Asp Gln Leu His Pro Asp Asn L u Ala Gly Gly
 145 150 155 160
 Val Thr Thr Glu Val Ala Gly Ala Thr Ala Val Ala Asp Ala Leu Asp
 165 170 175
 Glu Gly Met Ala Gly Asp Ile Ser Arg Ala Glu Val Phe Ala Leu Pro
 180 185 190
 Phe Val Ala Ile Leu Leu Leu Ile Val Phe Gly Ser Val Val Ala Ala
 195 200 205
 Ala Met Pro Leu Ile Val Gly Ile Leu Ser Ile Leu Gly Ser Leu Gly
 210 215 220
 Ile Leu Ala Ile Leu Ala Gly Phe Phe Gln Val Asn Val Phe Ala Gln
 225 230 235 240
 Ser Val Val Thr Leu Leu Gly Leu Gly Leu Ala Ile Asp Tyr Gly Leu
 245 250 255
 Phe Met Val Ser Arg Phe Arg Glu Glu Met Asp Lys Gly Thr Pro Val
 260 265 270
 Glu Gln Ala Val Ala Thr Thr Thr Ala Thr Ala Gly Lys Thr Val Val
 275 280 285
 Phe Ser Ala Ala Met Val Ala Val Ala Leu Ser Gly Leu Phe Val Phe
 290 295 300
 Pro Gln Ala Phe Leu Lys Ser Val Ala Phe Gly Ala Ile Ser Ala Val
 305 310 315 320
 Gly Leu Ala Ala Leu Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser
 325 330 335
 Met Leu Gly Lys Asn Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg
 340 345 350
 Thr Ala Arg Arg Leu Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp
 355 360 365
 Ala Met Arg His Ala Lys Ala Val Thr Val Gly Val Val Leu Leu Leu
 370 375 380
 Leu Ala Leu Thr Val Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn
 385 390 395 400
 Glu Thr Tyr Leu Pro Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg
 405 410 415
 Phe Asp Glu Ala Phe Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val
 420 425 430

Val Thr Gly Ala Asp Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala
 435 440 445
 Asn Glu Val Glu Gly Leu Thr Asp Arg Ph Thr Ala Gly Ala Thr Thr
 450 455 460
 Asp Asp Gly Thr Thr Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu
 465 470 475 480
 Asn Glu Gln Val Val Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly
 485 490 495
 Val Glu Val Gln Ile Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile
 500 505 510
 Glu Ala Leu Phe Glu Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu
 515 520 525
 Ala Thr Phe Ile Leu Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro
 530 535 540
 Ala Lys Ala Ile Ile Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly
 545 550 555 560
 Ile Leu Thr Leu Met Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn
 565 570 575
 Phe Ser Pro Gly Pro Leu Met Ser Pro Val Leu Val Leu Ile Met Ala
 580 585 590
 Ile Ile Tyr Gly Leu Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg
 595 600 605
 Met Val Glu Ala Arg Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg
 610 615 620
 Tyr Gly Thr Ala His Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile
 625 630 635 640
 Met Ile Val Val Cys Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met
 645 650 655
 Lys Tyr Ile Ala Phe Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr
 660 665 670
 Ile Ile Arg Met Leu Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg
 675 680 685
 Arg Gln Leu Val Gly Thr Arg Leu Arg
 690 695

<210> 227

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXN03042

<400> 227

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tcgcctcggc gacgtcctgg ttccttacgt tctgatcggt ttg gtt cta gcg ttc 115
 Leu Val Leu Ala Phe
 1 5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163
 Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
 10 15 20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg 211
 Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
 25 30 35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259
 Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
 40 45 50

ctg ctg tcc ttc ttg ccg atc atg ctc atc ggc ctg gta ttt ggt ctg 307
 Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly Leu Val Phe Gly Leu
 55 60 65

gcc atg gat tac cag atc ttc ctc gtt act cgt atg cgt gag ggc ttc 355
 Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg Met Arg Glu Gly Phe
 70 75 80 85

acc aag ggc aag act gcg ggc aac gca acg tcg aat ggt ttc aag cac 403
 Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser Asn Gly Phe Lys His
 90 95 100

ggt gcc cgc gtg gtc act gct gcg gcg ctg atc atg gtg tct gtg ttc 451
 Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile Met Val Ser Val Phe
 105 110 115

gcg gca ttc ata gcg cag gac atg gcg ttt att aag acc atg ggc ttt 499
 Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile Lys Thr Met Gly Phe
 120 125 130

gct ctg gcc gtt gct gtg ttc ttc gat gcc ttc gtt gtt cgc atg atg 547
 Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe Val Val Arg Met Met
 135 140 145

att atc cct gca aca atg ttc ctg ctt gat gac aag gct tgg tgg cta 595
 Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp Lys Ala Trp Trp Leu
 150 155 160 165

cct aag tgg ttg gat aag att ctt ccc aac gtt gat gtt gaa ggt gag 643
 Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val Asp Val Glu Gly Glu
 170 175 180

ggt ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat 691
 Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn
 185 190 195

gta ggt gtc ggg gct tagagaaaca aaaaaggctg cta 729
 Val Gly Val Gly Ala
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<210> 228

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

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Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
 20 25 30

Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
 35 40 45

Asp Asp Pro Gln Pro Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly
 50 55 60

Leu Val Phe Gly Leu Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg
 65 70 75 80

Met Arg Glu Gly Phe Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser
 85 90 95

Asn Gly Phe Lys His Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile
 100 105 110

Met Val Ser Val Phe Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile
 115 120 125

Lys Thr Met Gly Phe Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe
 130 135 140

Val Val Arg Met Met Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp
 145 150 155 160

Lys Ala Trp Trp Leu Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val
 165 170 175

Asp Val Glu Gly Glu Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu
 180 185 190

Glu Leu Lys Glu Asn Val Gly Val Gly Ala
 195 200

<210> 229

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> FRXA02893

<400> 229

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tcgcctcggc gacgtcctgg ttccttacgt tctgatcggt ttg gtt cta gcg ttc 115
                                Leu Val Leu Ala Phe
                                1                               5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163
Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
                                10                               15                               20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg 211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
                                25                               30                               35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259
Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
                                40                               45                               50

ctg ctg tcc ttc ttg ccg atc atg ctc atc ggc ctg gta ttt ggt ctg 307
Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly Leu Val Phe Gly Leu
                                55                               60                               65

gcc atg gat tac cag atc ttc ctc gtt act cgt atg cgt gag ggc ttc 355
Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg Met Arg Glu Gly Phe
                                70                               75                               80                               85

acc aag ggc aag act gcg ggc aac gca acg tcg aat ggt ttc aag cac 403
Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser Asn Gly Phe Lys His
                                90                               95                               100

ggt gcc cgc gtg gtc act gct gcg gcg ctg atc atg gtg tct gtg ttc 451
Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile Met Val Ser Val Phe
                                105                               110                               115

gcg gca ttc ata gcg cag gac atg gcg ttt att aag acc atg ggc ttt 499
Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile Lys Thr Met Gly Phe
                                120                               125                               130

gct ctg gcc gtt gct gtg ttc ttc gat gcc ttc gtt gtt cgc atg atg 547
Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe Val Val Arg Met Met
                                135                               140                               145

att atc cct gca aca atg ttc ctg ctt gat gac aag gct tgg tgg cta 595
Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp Lys Ala Trp Trp Leu
                                150                               155                               160                               165

cct aag tgg ttg gat aag att ctt ccc aac gtt gat gtt gaa ggt gag 643
Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val Asp Val Glu Gly Glu

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170 175 180
 ggt ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat 691
 Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn
 185 190 195
 gta ggt gtc ggg gct tagagaaaca aaaaaggctg cta 729
 Val Gly Val Gly Ala
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 <210> 230
 <211> 202
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 230
 Leu Val Leu Ala Phe Leu Val Leu Leu Val Phe Arg Ser Ile Trp
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 Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
 20 25 30
 Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
 35 40 45
 Asp Asp Pro Gln Pro Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly
 50 55 60
 Leu Val Phe Gly Leu Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg
 65 70 75 80
 Met Arg Glu Gly Phe Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser
 85 90 95
 Asn Gly Phe Lys His Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile
 100 105 110
 Met Val Ser Val Phe Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile
 115 120 125
 Lys Thr Met Gly Phe Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe
 130 135 140
 Val Val Arg Met Met Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp
 145 150 155 160
 Lys Ala Trp Trp Leu Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val
 165 170 175
 Asp Val Glu Gly Glu Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu
 180 185 190
 Glu Leu Lys Glu Asn Val Gly Val Gly Ala
 195 200

<210> 231
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1582)
 <223> RXA01616

<400> 231

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gagttgtaac tgtaccgacc attcggtaca gttacgatcc atg act tca gaa acc 115
Met Thr Ser Glu Thr
1 5

tta cag gcg caa gcg cct acg aaa acc caa cgt tgg gct ttc ctc gcc 163
Leu Gln Ala Gln Ala Pro Thr Lys Thr Gln Arg Trp Ala Phe Leu Ala
10 15 20

gtt atc agc ggt ggt ctc ttt ctg atc ggt gta gac aac tcg att ctc 211
Val Ile Ser Gly Gly Leu Phe Leu Ile Gly Val Asp Asn Ser Ile Leu
25 30 35

tac acc gca ctc cct ctg ctg cgt gaa cag ctc gca gcc tcc gaa acc 259
Tyr Thr Ala Leu Pro Leu Leu Arg Glu Gln Leu Ala Ala Ser Glu Thr
40 45 50

caa gcg ttg tgg atc atc aac gca tat ccc ctg ctc atg gcg ggc ctt 307
Gln Ala Leu Trp Ile Ile Asn Ala Tyr Pro Leu Leu Met Ala Gly Leu
55 60 65

cgt ttg ggt gcc ggc act ttg ggt gac aaa aac ggc cac cgc cgg atg 355
Arg Leu Gly Ala Gly Thr Leu Gly Asp Lys Asn Gly His Arg Arg Met
70 75 80 85

ttc ctc atg ggc ttg agc att ttc gga atc gct tca ctt ggt gct gcg 403
Phe Leu Met Gly Leu Ser Ile Phe Gly Ile Ala Ser Leu Gly Ala Ala
90 95 100

ttt gct cca act gcg tgg gct ctt gtt gct gcg aga gct ttc ctt ggc 451
Phe Ala Pro Thr Ala Trp Ala Leu Val Ala Ala Arg Ala Phe Leu Gly
105 110 115

atc ggt gcg gca acg atg atg cct gca acc ttg gct ctg atc cgc att 499
Ile Gly Ala Ala Thr Met Met Pro Ala Thr Leu Ala Leu Ile Arg Ile
120 125 130

acg ttt gag gat gag cgt gag cgc aac act gca att ggt att tgg ggt 547
Thr Phe Glu Asp Glu Arg Glu Arg Asn Thr Ala Ile Gly Ile Trp Gly
135 140 145

tcc gtg gca att ctt ggc gct gcg gca ggc ccg atc att ggt ggt gcg 595
Ser Val Ala Ile Leu Gly Ala Ala Ala Gly Pro Ile Ile Gly Gly Ala
150 155 160 165
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ctg ttg gaa ttc ttc tgg tgg ggt tcg gtt ttc ctc att aac gtt ccg	643
Leu Leu Glu Phe Phe Trp Trp Gly Ser Val Phe Leu Ile Asn Val Pro	
170 175 180	
gtg gct gtt atc gcg ttg atc gct acg ctt ttt gtg gcg ccg gcc aat	691
Val Ala Val Ile Ala Leu Ile Ala Thr Leu Phe Val Ala Pro Ala Asn	
185 190 195	
atc gcg aat ccg tct aag cat tgg gat ttc ttg tcg tcg ttc tat gcg	739
Ile Ala Asn Pro Ser Lys His Trp Asp Phe Leu Ser Ser Phe Tyr Ala	
200 205 210	
ctg ctc aca ctt gct ggg ttg atc atc acg atc aag gaa tct gtg aat	787
Leu Leu Thr Leu Ala Gly Leu Ile Ile Thr Ile Lys Glu Ser Val Asn	
215 220 225	
act gca cgc cat atg cct ctt ctt ttg ggt gca gtc atc atg ttg atc	835
Thr Ala Arg His Met Pro Leu Leu Leu Gly Ala Val Ile Met Leu Ile	
230 235 240 245	
att ggt gcg gtg ttg ttt agc agt cgt cag aag aag atc gag gag cca	883
Ile Gly Ala Val Leu Phe Ser Ser Arg Gln Lys Lys Ile Glu Glu Pro	
250 255 260	
ctt cta gat ctg tcg ttg ttc cgt aat cgc ctt ttc tta ggc ggt gtg	931
Leu Leu Asp Leu Ser Leu Phe Arg Asn Arg Leu Phe Leu Gly Gly Val	
265 270 275	
gtt gct gcg ggc atg gcg atg ttt act gtg tcc ggt ttg gaa atg act	979
Val Ala Ala Gly Met Ala Met Phe Thr Val Ser Gly Leu Glu Met Thr	
280 285 290	
acc tcg cag cgt ttc cag ttg tct gtg ggt ttc act cca ctt gag gct	1027
Thr Ser Gln Arg Phe Gln Leu Ser Val Gly Phe Thr Pro Leu Glu Ala	
295 300 305	
ggg ttg ctc atg atc cca gct gca ttg ggt agc ttc ccg atg tct att	1075
Gly Leu Leu Met Ile Pro Ala Ala Leu Gly Ser Phe Pro Met Ser Ile	
310 315 320 325	
atc ggt ggt gca aac ctg cat cgt tgg ggc ttc aaa ccg ctg atc agt	1123
Ile Gly Gly Ala Asn Leu His Arg Trp Gly Phe Lys Pro Leu Ile Ser	
330 335 340	
ggg ggt ttt gct gcc act gcc gtt ggc atc gcc ctg tgt att tgg ggc	1171
Gly Gly Phe Ala Ala Thr Ala Val Gly Ile Ala Leu Cys Ile Trp Gly	
345 350 355	
gcg act cat act gat ggt ttg ccg ttt ttc atc gcg ggt cta ttc ttc	1219
Ala Thr His Thr Asp Gly Leu Pro Phe Phe Ile Ala Gly Leu Phe Phe	
360 365 370	
atg ggc gcg ggt gct ggt tcg gta atg tct gtg tct tcc act gcg att	1267
Met Gly Ala Gly Ala Gly Ser Val Met Ser Val Ser Ser Thr Ala Ile	
375 380 385	
atc ggt tcc gcg ccg gtg cgt aag gct ggc atg gcg tcg tcg atc gaa	1315

Ile Gly Ser Ala Pro Val Arg Lys Ala Gly Met Ala S r Ser Ile Glu
 390 395 400 405
 gag gtc tct tat gag ttc ggc acg ctg ttg tct gtc gcg att ttg ggt 1363
 Glu Val Ser Tyr Glu Phe Gly Thr Leu Leu Ser Val Ala Ile Leu Gly
 410 415 420
 agc ttg ttc cca ttc ttc tac tcg ctg cat gcc ccg gca gag gtt gcg 1411
 Ser Leu Phe Pro Phe Phe Tyr Ser Leu His Ala Pro Ala Glu Val Ala
 425 430 435
 gat aac ttc tcg gcg ggt gtt cac cac gcg att gat gcc gat gcg gcg 1459
 Asp Asn Phe Ser Ala Gly Val His His Ala Ile Asp Gly Asp Ala Ala
 440 445 450
 cgt gca tct ttg gac acc gca tac att aac gtg ttg atc att gcc cta 1507
 Arg Ala Ser Leu Asp Thr Ala Tyr Ile Asn Val Leu Ile Ile Ala Leu
 455 460 465
 gta tgc gca gta gcg gct gct ctg atc agc agt tac ctt ttc cgc gga 1555
 Val Cys Ala Val Ala Ala Ala Leu Ile Ser Ser Tyr Leu Phe Arg Gly
 470 475 480 485
 aat ccg aag gga gcc aat aat gcg cac tagtaaaaaa gagatgattc 1602
 Asn Pro Lys Gly Ala Asn Asn Ala His
 490
 tgc 1605

 <210> 232
 <211> 494
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 232
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 Asp Asn Ser Ile Leu Tyr Thr Ala Leu Pro Leu Leu Arg Glu Gln Leu
 35 40 45
 Ala Ala Ser Glu Thr Gln Ala Leu Trp Ile Ile Asn Ala Tyr Pro Leu
 50 55 60
 Leu Met Ala Gly Leu Arg Leu Gly Ala Gly Thr Leu Gly Asp Lys Asn
 65 70 75 80
 Gly His Arg Arg Met Phe Leu Met Gly Leu Ser Ile Phe Gly Ile Ala
 85 90 95
 Ser Leu Gly Ala Ala Phe Ala Pro Thr Ala Trp Ala Leu Val Ala Ala
 100 105 110

Arg Ala Phe Leu Gly Ile Gly Ala Ala Thr Met Met Pro Ala Thr Leu
 115 120 125
 Ala Leu Ile Arg Ile Thr Phe Glu Asp Glu Arg Glu Arg Asn Thr Ala
 130 135 140
 Ile Gly Ile Trp Gly Ser Val Ala Ile Leu Gly Ala Ala Ala Gly Pro
 145 150 155 160
 Ile Ile Gly Gly Ala Leu Leu Glu Phe Phe Trp Trp Gly Ser Val Phe
 165 170 175
 Leu Ile Asn Val Pro Val Ala Val Ile Ala Leu Ile Ala Thr Leu Phe
 180 185 190
 Val Ala Pro Ala Asn Ile Ala Asn Pro Ser Lys His Trp Asp Phe Leu
 195 200 205
 Ser Ser Phe Tyr Ala Leu Leu Thr Leu Ala Gly Leu Ile Ile Thr Ile
 210 215 220
 Lys Glu Ser Val Asn Thr Ala Arg His Met Pro Leu Leu Leu Gly Ala
 225 230 235 240
 Val Ile Met Leu Ile Ile Gly Ala Val Leu Phe Ser Ser Arg Gln Lys
 245 250 255
 Lys Ile Glu Glu Pro Leu Leu Asp Leu Ser Leu Phe Arg Asn Arg Leu
 260 265 270
 Phe Leu Gly Gly Val Val Ala Ala Gly Met Ala Met Phe Thr Val Ser
 275 280 285
 Gly Leu Glu Met Thr Thr Ser Gln Arg Phe Gln Leu Ser Val Gly Phe
 290 295 300
 Thr Pro Leu Glu Ala Gly Leu Leu Met Ile Pro Ala Ala Leu Gly Ser
 305 310 315 320
 Phe Pro Met Ser Ile Ile Gly Gly Ala Asn Leu His Arg Trp Gly Phe
 325 330 335
 Lys Pro Leu Ile Ser Gly Gly Phe Ala Ala Thr Ala Val Gly Ile Ala
 340 345 350
 Leu Cys Ile Trp Gly Ala Thr His Thr Asp Gly Leu Pro Phe Phe Ile
 355 360 365
 Ala Gly Leu Phe Phe Met Gly Ala Gly Ala Gly Ser Val Met Ser Val
 370 375 380
 Ser Ser Thr Ala Ile Ile Gly Ser Ala Pro Val Arg Lys Ala Gly Met
 385 390 395 400
 Ala Ser Ser Ile Glu Glu Val Ser Tyr Glu Phe Gly Thr Leu Leu Ser
 405 410 415

Val Ala Ile Leu Gly Ser Leu Phe Pro Phe Phe Tyr Ser Leu His Ala
 420 425 430

Pro Ala Glu Val Ala Asp Asn Phe Ser Ala Gly Val His His Ala Ile
 435 440 445

Asp Gly Asp Ala Ala Arg Ala Ser Leu Asp Thr Ala Tyr Ile Asn Val
 450 455 460

Leu Ile Ile Ala Leu Val Cys Ala Val Ala Ala Ala Leu Ile Ser Ser
 465 470 475 480

Tyr Leu Phe Arg Gly Asn Pro Lys Gly Ala Asn Asn Ala His
 485 490

<210> 233

<211> 1500

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1477)

<223> RXA01666

<400> 233

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agtttgaggg tttttgctcc ccattcttag gagacacccc gtg tcc acg ttt cat 115
 Val Ser Thr Phe His
 1 5

aaa gtt ttg atc aac acc atg atc tcc aac gtc acc act gga ttt ctg 163
 Lys Val Leu Ile Asn Thr Met Ile Ser Asn Val Thr Thr Gly Phe Leu
 10 15 20

ttc ttt gcc gtg gtg ttt tgg atg tat ctt tcc act ggc aac gtc gca 211
 Phe Phe Ala Val Val Phe Trp Met Tyr Leu Ser Thr Gly Asn Val Ala
 25 30 35

ctg acc ggc atc gtc agt gga att tac atg ggt ttg atc gcc gtt tgt 259
 Leu Thr Gly Ile Val Ser Gly Ile Tyr Met Gly Leu Ile Ala Val Cys
 40 45 50

tcc atc ttt ttc gga acc gtt gtt gat cac aat cgc aag aag tcc gtc 307
 Ser Ile Phe Phe Gly Thr Val Val Asp His Asn Arg Lys Lys Ser Val
 55 60 65

atg ctg ttt tcc agc gtc acc aca ctc gtg ttt tat tgt ctc agt gcc 355
 Met Leu Phe Ser Ser Val Thr Thr Leu Val Phe Tyr Cys Leu Ser Ala
 70 75 80 85

ctg gtg tgg gtg ttt tgg ctg gag gaa gac ggc ctg agc atc gga aat 403
 Leu Val Trp Val Phe Trp Leu Glu Glu Asp Gly Leu Ser Ile Gly Asn
 90 95 100

acc gcc ctg tgg gtg ttc gtt tct ttc atc ctc atc gga tca atc gtg	451
Thr Ala Leu Trp Val Phe Val Ser Phe Ile Leu Il Gly Ser Ile Val	
105 110 115	
gaa cac atg cgc aac atc gca ctg tcc acc gtg gtc acg ctg ttg gtt	499
Glu His Met Arg Asn Ile Ala Leu Ser Thr Val Val Thr Leu Leu Val	
120 125 130	
cct gaa gct gaa cgc gac aaa gca aac ggc ctg gta gga gcc gtg caa	547
Pro Glu Ala Glu Arg Asp Lys Ala Asn Gly Leu Val Gly Ala Val Gln	
135 140 145	
ggg gtt gga ttt tta gtc acc agc gtc att gct ggt tcc gcc atc ggg	595
Gly Val Gly Phe Leu Val Thr Ser Val Ile Ala Gly Ser Ala Ile Gly	
150 155 160 165	
ttc ttg ggc atg gaa atc acc ctg tgg atc tgc ctt ggg ctc tca ctt	643
Phe Leu Gly Met Glu Ile Thr Leu Trp Ile Cys Leu Gly Leu Ser Leu	
170 175 180	
gtc gcg ctg ctg cac ctg ctg ccg att cgc gtc gac gaa ccg gaa atc	691
Val Ala Leu Leu His Leu Leu Pro Ile Arg Val Asp Glu Pro Glu Ile	
185 190 195	
atc acc caa gaa gac gca cag cct act gtt tct gac gat tca gtt ccc	739
Ile Thr Gln Glu Asp Ala Gln Pro Thr Val Ser Asp Asp Ser Val Pro	
200 205 210	
aca cct acc tcc gat ttg gcg atc gtg tcc aaa ggc atc gac cta aaa	787
Thr Pro Thr Ser Asp Leu Ala Ile Val Ser Lys Gly Ile Asp Leu Lys	
215 220 225	
gga tca atg aaa atc atc ctg agt gtt ccg gga ctg ctc gcg ctt gtg	835
Gly Ser Met Lys Ile Ile Leu Ser Val Pro Gly Leu Leu Ala Leu Val	
230 235 240 245	
ttg ttt gcg tcc ttc aac aac ctc atc ggc ggc gtg tac tcc gca ctc	883
Leu Phe Ala Ser Phe Asn Asn Leu Ile Gly Gly Val Tyr Ser Ala Leu	
250 255 260	
atg gac cct tac ggc ctg gaa ctt ttc agc cca cag ctg tgg ggg cta	931
Met Asp Pro Tyr Gly Leu Glu Leu Phe Ser Pro Gln Leu Trp Gly Leu	
265 270 275	
ctg ctt gga ctc acc agc ctc ggc ttc atc gtt ggt ggt gct gtg atc	979
Leu Leu Gly Leu Thr Ser Leu Gly Phe Ile Val Gly Gly Ala Val Ile	
280 285 290	
tcc aaa act ggc ttg ggc aaa aac cct gtg cgc acc ttg ctg ctg gtt	1027
Ser Lys Thr Gly Leu Gly Lys Asn Pro Val Arg Thr Leu Leu Leu Val	
295 300 305	
aat gtt ggt gtg gct ttt gtt ggc atg tta ttt gcc att cgc gaa tgg	1075
Asn Val Gly Val Ala Phe Val Gly Met Leu Phe Ala Ile Arg Glu Trp	
310 315 320 325	
tgg tgg ctc tac atc ctg ggc att ttc atc ttc atg gct atc acc cca	1123

Trp Trp Leu Tyr Ile Leu Gly Ile Phe Ile Phe Met Ala Ile Thr Pro
 330 335 340
 gct gcc gaa gcc gca gaa caa acc atc ctt caa cga gtc gtc cca ttc 1171
 Ala Ala Glu Ala Ala Glu Gln Thr Ile Leu Gln Arg Val Val Pro Phe
 345 350 355
 cgc caa caa ggc cgc gta ttt gga cta gcc atg gca gtg gaa atg gca 1219
 Arg Gln Gln Gly Arg Val Phe Gly Leu Ala Met Ala Val Glu Met Ala
 360 365 370
 gcc aac ccg ctc tcc aca gtg atc gtg gcg att ttg gcc gaa gcc tac 1267
 Ala Asn Pro Leu Ser Thr Val Ile Val Ala Ile Leu Ala Glu Ala Tyr
 375 380 385
 ctc att cca tgg atg gct ggc ccc ggc gcg gac acc atc tgg ggc gtg 1315
 Leu Ile Pro Trp Met Ala Gly Pro Gly Ala Asp Thr Ile Trp Gly Val
 390 395 400 405
 atc ctc ggc gag ggt aaa gct cgc ggc atg gca ctg atg ttc ctc gca 1363
 Ile Leu Gly Glu Gly Lys Ala Arg Gly Met Ala Leu Met Phe Leu Ala
 410 415 420
 tca ggt gcc atc atg ttg gtt gtc gtg ctg ttg gca ttc atg tcg agg 1411
 Ser Gly Ala Ile Met Leu Val Val Val Leu Leu Ala Phe Met Ser Arg
 425 430 435
 tcc tac cgg aaa ctc agc cag tac tac gcc acc acc agc caa gac att 1459
 Ser Tyr Arg Lys Leu Ser Gln Tyr Tyr Ala Thr Thr Ser Gln Asp Ile
 440 445 450
 gcg gga gct gct gag aag taagtgtct agaccgttgt ttg 1500
 Ala Gly Ala Ala Glu Lys
 455

<210> 234

<211> 459

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 234

Val Ser Thr Phe His Lys Val Leu Ile Asn Thr Met Ile Ser Asn Val
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 Thr Thr Gly Phe Leu Phe Phe Ala Val Val Phe Trp Met Tyr Leu Ser
 20 25 30
 Thr Gly Asn Val Ala Leu Thr Gly Ile Val Ser Gly Ile Tyr Met Gly
 35 40 45
 Leu Ile Ala Val Cys Ser Ile Phe Phe Gly Thr Val Val Asp His Asn
 50 55 60
 Arg Lys Lys Ser Val Met Leu Phe Ser Ser Val Thr Thr Leu Val Phe
 65 70 75 80

Tyr Cys Leu Ser Ala Leu Val Trp Val Phe Trp Leu Glu Glu Asp Gly
 85 90 95
 Leu Ser Ile Gly Asn Thr Ala Leu Trp Val Phe Val Ser Phe Ile Leu
 100 105 110
 Ile Gly Ser Ile Val Glu His Met Arg Asn Ile Ala Leu Ser Thr Val
 115 120 125
 Val Thr Leu Leu Val Pro Glu Ala Glu Arg Asp Lys Ala Asn Gly Leu
 130 135 140
 Val Gly Ala Val Gln Gly Val Gly Phe Leu Val Thr Ser Val Ile Ala
 145 150 155 160
 Gly Ser Ala Ile Gly Phe Leu Gly Met Glu Ile Thr Leu Trp Ile Cys
 165 170 175
 Leu Gly Leu Ser Leu Val Ala Leu Leu His Leu Leu Pro Ile Arg Val
 180 185 190
 Asp Glu Pro Glu Ile Ile Thr Gln Glu Asp Ala Gln Pro Thr Val Ser
 195 200 205
 Asp Asp Ser Val Pro Thr Pro Thr Ser Asp Leu Ala Ile Val Ser Lys
 210 215 220
 Gly Ile Asp Leu Lys Gly Ser Met Lys Ile Ile Leu Ser Val Pro Gly
 225 230 235 240
 Leu Leu Ala Leu Val Leu Phe Ala Ser Phe Asn Asn Leu Ile Gly Gly
 245 250 255
 Val Tyr Ser Ala Leu Met Asp Pro Tyr Gly Leu Glu Leu Phe Ser Pro
 260 265 270
 Gln Leu Trp Gly Leu Leu Leu Gly Leu Thr Ser Leu Gly Phe Ile Val
 275 280 285
 Gly Gly Ala Val Ile Ser Lys Thr Gly Leu Gly Lys Asn Pro Val Arg
 290 295 300
 Thr Leu Leu Leu Val Asn Val Gly Val Ala Phe Val Gly Met Leu Phe
 305 310 315 320
 Ala Ile Arg Glu Trp Trp Trp Leu Tyr Ile Leu Gly Ile Phe Ile Phe
 325 330 335
 Met Ala Ile Thr Pro Ala Ala Glu Ala Ala Glu Gln Thr Ile Leu Gln
 340 345 350
 Arg Val Val Pro Phe Arg Gln Gln Gly Arg Val Phe Gly Leu Ala Met
 355 360 365
 Ala Val Glu Met Ala Ala Asn Pro Leu Ser Thr Val Ile Val Ala Ile
 370 375 380

Leu Ala Glu Ala Tyr Leu Ile Pro Trp Met Ala Gly Pro Gly Ala Asp
385 390 395 400

Thr Ile Trp Gly Val Ile Leu Gly Glu Gly Lys Ala Arg Gly Met Ala
405 410 415

Leu Met Phe Leu Ala Ser Gly Ala Ile Met Leu Val Val Val Leu Leu
420 425 430

Ala Phe Met Ser Arg Ser Tyr Arg Lys Leu Ser Gln Tyr Tyr Ala Thr
435 440 445

Thr Ser Gln Asp Ile Ala Gly Ala Ala Glu Lys
450 455

<210> 235

<211> 1521

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1498)

<223> RXA00062

<400> 235

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tcactgttgc gttttcttgc tgccatcaaa aattagtcac atg att tta agc atc 115
Met Ile Leu Ser Ile
1 5

gtc ctt ttg ggc tac ttc atg att ctg ctt gac acc tcc atc gtc att 163
Val Leu Leu Gly Tyr Phe Met Ile Leu Leu Asp Thr Ser Ile Val Ile
10 15 20

acg ggt cta cct gcc atc ggc agt gaa ctt ggc atc gat ccc gtg cac 211
Thr Gly Leu Pro Ala Ile Gly Ser Glu Leu Gly Ile Asp Pro Val His
25 30 35

ctg tca tgg gtg cag agt tcc tac aca tta gtc ttc ggc gca ctt ctt 259
Leu Ser Trp Val Gln Ser Ser Tyr Thr Leu Val Phe Gly Ala Leu Leu
40 45 50

ctg ctg gga gct cgt gcc ggt gat atc ttc ggc cga aag aaa gtg ctc 307
Leu Leu Gly Ala Arg Ala Gly Asp Ile Phe Gly Arg Lys Lys Val Leu
55 60 65

tac att ggt ctc gcg ttg ttt gcg gct tca tcg ttg gca att gcg ctt 355
Tyr Ile Gly Leu Ala Leu Phe Ala Ala Ser Ser Leu Ala Ile Ala Leu
70 75 80 85

tct cca aat gct gcg gtc ctc att gga gca cgc gta gtt caa ggc gcg 403
Ser Pro Asn Ala Ala Val Leu Ile Gly Ala Arg Val Val Gln Gly Ala
90 95 100

gga gct gcg att atc gct cca gcg aca ctt gcg ttg att act gag ttc	451
Gly Ala Ala Ile Ile Ala Pro Ala Thr Leu Ala Leu Ile Thr Glu Phe	
105 110 115	
ttc ccc gaa ggc cca gct cgc ctt cgt gct acc tct gct tat ggt gct	499
Phe Pro Glu Gly Pro Ala Arg Leu Arg Ala Thr Ser Ala Tyr Gly Ala	
120 125 130	
gtt gcc ggc atc ggt gtg gca gca ggc cta gtg atc ggc ggc gta ttt	547
Val Ala Gly Ile Gly Val Ala Ala Gly Leu Val Ile Gly Gly Val Phe	
135 140 145	
gct gat ctt ttg tcg tgg cgc atc ggc ttc ttt atc aac gtc ccc atc	595
Ala Asp Leu Leu Ser Trp Arg Ile Gly Phe Phe Ile Asn Val Pro Ile	
150 155 160 165	
gcc gca gtg ttg gcc tac ata gtg cac aaa gcc att ccc gca acc ttc	643
Ala Ala Val Leu Ala Tyr Ile Val His Lys Ala Ile Pro Ala Thr Phe	
170 175 180	
agc agg cct gga tca ctc gac atc ttc gga gca att acc tcc acg gca	691
Ser Arg Pro Gly Ser Leu Asp Ile Phe Gly Ala Ile Thr Ser Thr Ala	
185 190 195	
ggt atc gcc gcg gtg ctc tac gca att gtc cgc agc gcc gat tac agc	739
Gly Ile Ala Ala Val Leu Tyr Ala Ile Val Arg Ser Ala Asp Tyr Ser	
200 205 210	
tgg aca gat ccg ttt gtg ttg att tcc ctc gtg ctg ggc atc gca gtg	787
Trp Thr Asp Pro Phe Val Leu Ile Ser Leu Val Leu Gly Ile Ala Val	
215 220 225	
ttc atc tgg ttc ctg cgc cat gaa tcc tca gcc aaa gaa cca ctt ctg	835
Phe Ile Trp Phe Leu Arg His Glu Ser Ser Ala Lys Glu Pro Leu Leu	
230 235 240 245	
ccc ctg ggg ctc ttt aaa aac cgc agg cga aac acc atc ttg gcc agc	883
Pro Leu Gly Leu Phe Lys Asn Arg Arg Arg Asn Thr Ile Leu Ala Ser	
250 255 260	
cgc ttt ctt ctg gtt ggc tcc gtg atg tca ttc ttc ttc ttt gcc acc	931
Arg Phe Leu Leu Val Gly Ser Val Met Ser Phe Phe Phe Phe Ala Thr	
265 270 275	
cag ctg ttc cag gac acc atg gga atg aat gct ctc cag gca ggc ctt	979
Gln Leu Phe Gln Asp Thr Met Gly Met Asn Ala Leu Gln Ala Gly Leu	
280 285 290	
gcg ttc atg ccg cta tct ctg ctg cag ttt gcc agc gcc gcg atg gtg	1027
Ala Phe Met Pro Leu Ser Leu Leu Gln Phe Ala Ser Ala Ala Met Val	
295 300 305	
cca cgg ctt tcc cga gca ggc gta tct gat tcc atg ctc acc gtc atc	1075
Pro Arg Leu Ser Arg Ala Gly Val Ser Asp Ser Met Leu Thr Val Ile	
310 315 320 325	
ggt ttc gcc atc atg gtc atc ggc atg gca ggc ctc gca ttt gta cca	1123

Gly Phe Ala Ile Met Val Ile Gly Met Ala Gly Leu Ala Phe Val Pro
 330 335 340

aac acg atg atc gcg ctg atc cta cca ata gtt ttg gtg gga ttt ggc 1171
 Asn Thr Met Ile Ala Leu Ile Leu Pro Ile Val Leu Val Gly Phe Gly
 345 350 355

caa ggc ttc gct ttc gga cca atg aca gct ctg gca gtt caa ggt gca 1219
 Gln Gly Phe Ala Phe Gly Pro Met Thr Ala Leu Ala Val Gln Gly Ala
 360 365 370

ccg aag gac caa tcc ggc gcc gtt tct ggc ctg gtg aat tcc ctt cac 1267
 Pro Lys Asp Gln Ser Gly Ala Val Ser Gly Leu Val Asn Ser Leu His
 375 380 385

caa atc ggc ggc acc ttc ggt ttg ggt gtg ttc tcc tcc ttg gct gtc 1315
 Gln Ile Gly Gly Thr Phe Gly Leu Gly Val Phe Ser Ser Leu Ala Val
 390 395 400 405

gct gtc atc gga cat gat gca aca tca gag atg atc agc gac cgc gca 1363
 Ala Val Ile Gly His Asp Ala Thr Ser Glu Met Ile Ser Asp Arg Ala
 410 415 420

cac ttc gga ttc ttg ctc tcc acc gtg acg ctg acg ctg gcc acc atc 1411
 His Phe Gly Phe Leu Leu Ser Thr Val Thr Leu Thr Leu Ala Thr Ile
 425 430 435

ttt gcg gtc aca ctg ctg aag cgc cac gaa acc cga aag agt agc gag 1459
 Phe Ala Val Thr Leu Leu Lys Arg His Glu Thr Arg Lys Ser Ser Glu
 440 445 450

cgc cca acc cag ctc gtc gac gaa aag gca gtt acc tct tagtgcgctg 1508
 Arg Pro Thr Gln Leu Val Asp Glu Lys Ala Val Thr Ser
 455 460 465

cagcatccca gtt 1521

<210> 236

<211> 466

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 236

Met Ile Leu Ser Ile Val Leu Leu Gly Tyr Phe Met Ile Leu Leu Asp
 1 5 10 15

Thr Ser Ile Val Ile Thr Gly Leu Pro Ala Ile Gly Ser Glu Leu Gly
 20 25 30

Ile Asp Pro Val His Leu Ser Trp Val Gln Ser Ser Tyr Thr Leu Val
 35 40 45

Phe Gly Ala Leu Leu Leu Leu Gly Ala Arg Ala Gly Asp Ile Phe Gly
 50 55 60

Arg Lys Lys Val Leu Tyr Ile Gly Leu Ala Leu Phe Ala Ala Ser Ser

65	70	75	80
Leu Ala Ile Ala	Leu Ser Pro Asn Ala	Ala Val Leu Ile Gly	Ala Arg
	85	90	95
Val Val Gln Gly	Ala Gly Ala Ala	Ile Ile Ala Pro	Ala Thr Leu Ala
	100	105	110
Leu Ile Thr Glu	Phe Phe Pro Glu	Gly Pro Ala Arg	Leu Arg Ala Thr
	115	120	125
Ser Ala Tyr Gly	Ala Val Ala Gly	Ile Gly Val Ala	Ala Gly Leu Val
	130	135	140
Ile Gly Gly Val	Phe Ala Asp Leu	Leu Ser Trp Arg	Ile Gly Phe Phe
	145	150	155
Ile Asn Val Pro	Ile Ala Ala Val	Leu Ala Tyr Ile	Val His Lys Ala
	165	170	175
Ile Pro Ala Thr	Phe Ser Arg Pro	Gly Ser Leu Asp	Ile Phe Gly Ala
	180	185	190
Ile Thr Ser Thr	Ala Gly Ile Ala	Ala Val Leu Tyr	Ala Ile Val Arg
	195	200	205
Ser Ala Asp Tyr	Ser Trp Thr Asp	Pro Phe Val Leu	Ile Ser Leu Val
	210	215	220
Leu Gly Ile Ala	Val Phe Ile Trp	Phe Leu Arg His	Glu Ser Ser Ala
	225	230	235
Lys Glu Pro Leu	Leu Pro Leu Gly	Leu Phe Lys Asn	Arg Arg Arg Asn
	245	250	255
Thr Ile Leu Ala	Ser Arg Phe Leu	Leu Val Gly Ser	Val Met Ser Phe
	260	265	270
Phe Phe Phe Ala	Thr Gln Leu Phe	Gln Asp Thr Met	Gly Met Asn Ala
	275	280	285
Leu Gln Ala Gly	Leu Ala Phe Met	Pro Leu Ser Leu	Leu Gln Phe Ala
	290	295	300
Ser Ala Ala Met	Val Pro Arg Leu	Ser Arg Ala Gly	Val Ser Asp Ser
	305	310	315
Met Leu Thr Val	Ile Gly Phe Ala	Ile Met Val Ile	Gly Met Ala Gly
	325	330	335
Leu Ala Phe Val	Pro Asn Thr Met	Ile Ala Leu Ile	Leu Pro Ile Val
	340	345	350
Leu Val Gly Phe	Gly Gln Gly Phe	Ala Phe Gly Pro	Met Thr Ala Leu
	355	360	365
Ala Val Gln Gly	Ala Pro Lys Asp	Gln Ser Gly Ala	Val Ser Gly Leu

370

375

380

Val Asn Ser Leu His Gln Ile Gly Gly Thr Phe Gly Leu Gly Val Phe
 385 390 395 400

Ser Ser Leu Ala Val Ala Val Ile Gly His Asp Ala Thr Ser Glu Met
 405 410 415

Ile Ser Asp Arg Ala His Phe Gly Phe Leu Leu Ser Thr Val Thr Leu
 420 425 430

Thr Leu Ala Thr Ile Phe Ala Val Thr Leu Leu Lys Arg His Glu Thr
 435 440 445

Arg Lys Ser Ser Glu Arg Pro Thr Gln Leu Val Asp Glu Lys Ala Val
 450 455 460

Thr Ser
 465

<210> 237

<211> 1584

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1561)

<223> RXA00215

<400> 237

cagtgcacaaac tgacccccgca tcctaaaccg cgccagattt ctacctcaaa gaattgaagg 60

ccttttccag gcgcccctcgt gcgtgaaaga ataactcaac gtg tct gac aaa aag 115
 Val Ser Asp Lys Lys
 1 5

cag gat cta aca tcc tcc gca gca ggt agt gct gca ccc caa acc aag 163
 Gln Asp Leu Thr Ser Ser Ala Ala Gly Ser Ala Ala Pro Gln Thr Lys
 10 15 20

gcc tac ccc gcc atg ccc ttg cct gaa aag caa gct tgg cca gct cta 211
 Ala Tyr Pro Ala Met Pro Leu Pro Glu Lys Gln Ala Trp Pro Ala Leu
 25 30 35

att gcc ttg tgc att ggg ttt ttc atg atc ctg ttg gat caa acc atc 259
 Ile Ala Leu Cys Ile Gly Phe Phe Met Ile Leu Leu Asp Gln Thr Ile
 40 45 50

gtg gcc gtc tct acc cca gcg tta cag gca gac atg ggc gcg tcc tac 307
 Val Ala Val Ser Thr Pro Ala Leu Gln Ala Asp Met Gly Ala Ser Tyr
 55 60 65

aac gag gtc atc tgg gta acc tcg gtg tat ctc ctc act ttc gcg gtg 355
 Asn Glu Val Ile Trp Val Thr Ser Val Tyr Leu Leu Thr Phe Ala Val
 70 75 80 85

cca ctg ctt gtt act ggc cgt ttg ggc gac aag tac ggt ccg aaa aat	403
Pro Leu Leu Val Thr Gly Arg Leu Gly Asp Lys Tyr Gly Pro Lys Asn	
90 95 100	
gtc tat gtc gca ggc atg gtt atc ttc aca gtg agc tct ttg gcc tgt	451
Val Tyr Val Ala Gly Met Val Ile Phe Thr Val Ser Ser Leu Ala Cys	
105 110 115	
ggc ttg gcc cca gac atg ttc acg ttg att atc gct cgt ggc gtt caa	499
Gly Leu Ala Pro Asp Met Phe Thr Leu Ile Ile Ala Arg Gly Val Gln	
120 125 130	
ggc ttg ggc gca gcc ctt ttg act cca caa acc atg gca aca atc aac	547
Gly Leu Gly Ala Ala Leu Leu Thr Pro Gln Thr Met Ala Thr Ile Asn	
135 140 145	
cgc atc ttt gct ttt gag cgc cgc ggt gca gct ctt gga gtg tgg ggt	595
Arg Ile Phe Ala Phe Glu Arg Arg Gly Ala Ala Leu Gly Val Trp Gly	
150 155 160 165	
tct aca gct ggc ctt gca tcc cta gca gga ccg atc ctg ggt ggt gtc	643
Ser Thr Ala Gly Leu Ala Ser Leu Ala Gly Pro Ile Leu Gly Gly Val	
170 175 180	
atc acc gaa aac tgg ggt tgg caa tgg gtc ttc tac atc aac gtg ccc	691
Ile Thr Glu Asn Trp Gly Trp Gln Trp Val Phe Tyr Ile Asn Val Pro	
185 190 195	
atc ggc gtg atc tcg gtg atc gca gta atg aag tac gtt cct gaa ttc	739
Ile Gly Val Ile Ser Val Ile Ala Val Met Lys Tyr Val Pro Glu Phe	
200 205 210	
cca ccg ctg acc cga ccg ctt gat ccg ctt tct atc gtg ttg tcc atc	787
Pro Pro Leu Thr Arg Pro Leu Asp Pro Leu Ser Ile Val Leu Ser Ile	
215 220 225	
gtg gcc gtg ttc ttc ctg gtg ttt gct ttc cag gaa ggc gaa ggc gct	835
Val Ala Val Phe Phe Leu Val Phe Ala Phe Gln Glu Gly Glu Gly Ala	
230 235 240 245	
ggc tgg gcg gca tgg gtg tgg atc atg atc gta gcc gcc ttt gcg ctc	883
Gly Trp Ala Ala Trp Val Trp Ile Met Ile Val Ala Ala Phe Ala Leu	
250 255 260	
ttt gcg tgg ttt atc tac caa caa agc agg gcc gag aaa tcc gga aac	931
Phe Ala Trp Phe Ile Tyr Gln Gln Ser Arg Ala Glu Lys Ser Gly Asn	
265 270 275	
gat cct ctc gtc cca ctg gag att ttc aag ttt aga aac ttc agc ctc	979
Asp Pro Leu Val Pro Leu Glu Ile Phe Lys Phe Arg Asn Phe Ser Leu	
280 285 290	
ggc aat atc tgc atc atg gcc atg gga ttc acc gtg gct ggt act cct	1027
Gly Asn Ile Cys Ile Met Ala Met Gly Phe Thr Val Ala Gly Thr Pro	
295 300 305	

ctg ccc atc atg ttg tac ttc cag caa gca cac gga atg aac gcc atg	1075
Leu Pro Ile Met Leu Tyr Phe Gln Gln Ala His Gly Met Asn Ala Met	
310 315 320 325	
 gaa gcg ggt ttc atg atg gtg cct caa gct ctc atg gca gca gta ctg	1123
Glu Ala Gly Phe Met Met Val Pro Gln Ala Leu Met Ala Ala Val Leu	
330 335 340	
 tca cca ttt gtt gga aag ctg gtt gat cga tcc aac cct gga ctc atg	1171
Ser Pro Phe Val Gly Lys Leu Val Asp Arg Ser Asn Pro Gly Leu Met	
345 350 355	
 gca gcc ctc ggt ttt agc aca gtg gct gtg tcc att gta ctg ctg tca	1219
Ala Ala Leu Gly Phe Ser Thr Val Ala Val Ser Ile Val Leu Leu Ser	
360 365 370	
 atg gta atg att ttc gat acg ggt cta gtc tgg gca ctt gtt tcg atg	1267
Met Val Met Ile Phe Asp Thr Gly Leu Val Trp Ala Leu Val Ser Met	
375 380 385	
 act ttg ctc ggc atc gga aac gcc ttt gtg tgg gca ccg aac tcg acc	1315
Thr Leu Leu Gly Ile Gly Asn Ala Phe Val Trp Ala Pro Asn Ser Thr	
390 395 400 405	
 tcc act atg cgc gac ctg cca cac aag ttc atg gga gcg ggc tct ggc	1363
Ser Thr Met Arg Asp Leu Pro His Lys Phe Met Gly Ala Gly Ser Gly	
410 415 420	
 gtg ttc aat aca acc cgc caa tta ggt tca gtc atc ggc gcc gct gcc	1411
Val Phe Asn Thr Thr Arg Gln Leu Gly Ser Val Ile Gly Ala Ala Ala	
425 430 435	
 atc ggc gcg gta atg cag att cga ctg gca gca ggc gat gag ggc gca	1459
Ile Gly Ala Val Met Gln Ile Arg Leu Ala Ala Gly Asp Glu Gly Ala	
440 445 450	
 gct ttt ggt caa gca ctt cta ctt gcc gct gcg gtg ctg gtt atc ggc	1507
Ala Phe Gly Gln Ala Leu Leu Leu Ala Ala Ala Val Leu Val Ile Gly	
455 460 465	
 att gtg gca tca acg atg gca gga aaa aat gca cac cca gcg ccg gta	1555
Ile Val Ala Ser Thr Met Ala Gly Lys Asn Ala His Pro Ala Pro Val	
470 475 480 485	
 aag cct taaaggcgc atgaatcctt cga	1584
Lys Pro	

<210> 238

<211> 487

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

Val Ser Asp Lys Lys Gln Asp Leu Thr Ser Ser Ala Ala Gly Ser Ala
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Ala Pro Gln Thr Lys Ala Tyr Pro Ala Met Pro Leu Pro Glu Lys Gln
 20 25 30
 Ala Trp Pro Ala Leu Ile Ala Leu Cys Ile Gly Phe Phe Met Ile Leu
 35 40 45
 Leu Asp Gln Thr Ile Val Ala Val Ser Thr Pro Ala Leu Gln Ala Asp
 50 55 60
 Met Gly Ala Ser Tyr Asn Glu Val Ile Trp Val Thr Ser Val Tyr Leu
 65 70 75 80
 Leu Thr Phe Ala Val Pro Leu Leu Val Thr Gly Arg Leu Gly Asp Lys
 85 90 95
 Tyr Gly Pro Lys Asn Val Tyr Val Ala Gly Met Val Ile Phe Thr Val
 100 105 110
 Ser Ser Leu Ala Cys Gly Leu Ala Pro Asp Met Phe Thr Leu Ile Ile
 115 120 125
 Ala Arg Gly Val Gln Gly Leu Gly Ala Ala Leu Leu Thr Pro Gln Thr
 130 135 140
 Met Ala Thr Ile Asn Arg Ile Phe Ala Phe Glu Arg Arg Gly Ala Ala
 145 150 155 160
 Leu Gly Val Trp Gly Ser Thr Ala Gly Leu Ala Ser Leu Ala Gly Pro
 165 170 175
 Ile Leu Gly Gly Val Ile Thr Glu Asn Trp Gly Trp Gln Trp Val Phe
 180 185 190
 Tyr Ile Asn Val Pro Ile Gly Val Ile Ser Val Ile Ala Val Met Lys
 195 200 205
 Tyr Val Pro Glu Phe Pro Pro Leu Thr Arg Pro Leu Asp Pro Leu Ser
 210 215 220
 Ile Val Leu Ser Ile Val Ala Val Phe Phe Leu Val Phe Ala Phe Gln
 225 230 235 240
 Glu Gly Glu Gly Ala Gly Trp Ala Ala Trp Val Trp Ile Met Ile Val
 245 250 255
 Ala Ala Phe Ala Leu Phe Ala Trp Phe Ile Tyr Gln Gln Ser Arg Ala
 260 265 270
 Glu Lys Ser Gly Asn Asp Pro Leu Val Pro Leu Glu Ile Phe Lys Phe
 275 280 285
 Arg Asn Phe Ser Leu Gly Asn Ile Cys Ile Met Ala Met Gly Phe Thr
 290 295 300
 Val Ala Gly Thr Pro Leu Pro Ile Met Leu Tyr Phe Gln Gln Ala His
 305 310 315 320

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<210> 239
<211> 1455
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1432)  
<223> RXN03064
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<400> 239
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tgtcatcatc ttggctgtat tagtttttac agcctttgtc atg atg ttg aat gag 115
                                         Met Met Leu Asn Glu
                                         1                               5

act act ctg gca gtc gcg ttg ccg tcg atc atg gcg gac ttt gac att 163
Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met Ala Asp Phe Asp Ile
                        10                        15                        20

gag gcg aat act gcg cag tgg ttg ctc act ggt ttt atg ttg acc atg 211

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Glu	Ala	Asn	Thr	Ala	Gln	Trp	Leu	Leu	Thr	Gly	Phe	Met	Leu	Thr	Met		
			25				30						35				
gct	gtg	gtt	ctt	cca	gct	act	ggt	tgg	atg	ttg	gaa	cgt	ttt	acc	act	259	
Ala	Val	Val	Leu	Pro	Ala	Thr	Gly	Trp	Met	Leu	Glu	Arg	Phe	Thr	Thr		
		40					45					50					
cgt	agt	gtg	ttt	att	ttc	gcc	acg	gtg	gtc	ttc	ctg	atc	ggt	act	gtg	307	
Arg	Ser	Val	Phe	Ile	Phe	Ala	Thr	Val	Val	Phe	Leu	Ile	Gly	Thr	Val		
	55					60					65						
acg	gct	gcg	ttg	tct	cct	act	ttt	gcg	att	atg	ctt	gca	gcc	cgc	gtc	355	
Thr	Ala	Ala	Leu	Ser	Pro	Thr	Phe	Ala	Ile	Met	Leu	Ala	Ala	Arg	Val		
	70				75					80					85		
gct	cag	gcg	att	ggt	acc	gct	gtg	atc	atg	ccg	ctg	ctg	atg	act	gtc	403	
Ala	Gln	Ala	Ile	Gly	Thr	Ala	Val	Ile	Met	Pro	Leu	Leu	Met	Thr	Val		
			90					95						100			
gcg	atg	acc	gtt	gtt	cct	cca	gag	cgc	cgt	ggc	gcc	gtc	atg	ggt	ttg	451	
Ala	Met	Thr	Val	Val	Pro	Pro	Glu	Arg	Arg	Gly	Ala	Val	Met	Gly	Leu		
			105					110					115				
att	gcg	gtc	gtg	atg	gcc	gtt	ggt	cct	gct	ctt	gga	cct	agt	gtg	gct	499	
Ile	Ala	Val	Val	Met	Ala	Val	Gly	Pro	Ala	Leu	Gly	Pro	Ser	Val	Ala		
		120					125					130					
ggt	ttc	gta	ctc	agc	ttg	tct	tcg	tgg	cac	gcg	att	ttc	tgg	gtc	atg	547	
Gly	Phe	Val	Leu	Ser	Leu	Ser	Ser	Trp	His	Ala	Ile	Phe	Trp	Val	Met		
	135					140						145					
gtt	ccg	ttg	gtg	ttt	gtg	gca	agc	ctg	atc	ggt	acc	ctg	cgt	ctg	acc	595	
Val	Pro	Leu	Val	Phe	Val	Ala	Ser	Leu	Ile	Gly	Thr	Leu	Arg	Leu	Thr		
	150				155				160						165		
aac	gtc	agt	gag	cct	aaa	aag	act	cct	ttg	gat	gtt	att	tcc	ttc	ctg	643	
Asn	Val	Ser	Glu	Pro	Lys	Lys	Thr	Pro	Leu	Asp	Val	Ile	Ser	Phe	Leu		
				170					175					180			
att	tcc	gca	gtg	gct	ttc	ggt	ggc	ctt	gtg	tac	gcc	ttg	agc	tcg	att	691	
Ile	Ser	Ala	Val	Ala	Phe	Gly	Gly	Leu	Val	Tyr	Ala	Leu	Ser	Ser	Ile		
		185						190					195				
ggc	atc	att	ttg	gaa	ggt	gac	aga	agc	gct	ttg	gtc	gtg	ttg	gct	gtc	739	
Gly	Ile	Ile	Leu	Glu	Gly	Asp	Arg	Ser	Ala	Leu	Val	Val	Leu	Ala	Val		
		200				205						210					
ggc	atc	att	gcg	ttg	gtg	gtg	ttt	gtg	tgg	cgc	cag	att	gcc	atg	ggt	787	
Gly	Ile	Ile	Ala	Leu	Val	Val	Phe	Val	Trp	Arg	Gln	Ile	Ala	Met	Gly		
	215					220					225						
aag	cag	gat	aag	gcg	ctg	ttg	gat	ctg	cgt	ccg	ttg	gcg	att	cgt	gag	835	
Lys	Gln	Asp	Lys	Ala	Leu	Leu	Asp	Leu	Arg	Pro	Leu	Ala	Ile	Arg	Glu		
	230				235				240						245		
tac	acc	att	ccg	ctg	gtt	gtg	ctt	ttg	acg	ctg	ttc	ggt	gcg	ctg	ctc	883	
Tyr	Thr	Ile	Pro	Leu	Val	Val	Leu	Leu	Thr	Leu	Phe	Gly	Ala	Leu	Leu		

250	255	260	
ggt gtc atg aat aca ctg ccg ctc tac ctg cag gga tcc ttg atg gtc Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln Gly Ser Leu Met Val 265 270 275			931
acc gcc ttg gtc gcg ggt cta gtg ctg ttg cca ggt ggt ctt ttg gaa Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro Gly Gly Leu Leu Glu 280 285 290			979
ggt gtg ctg tcg cca ttt gtg ggt cga att tat gat cgt cat ggt cca Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr Asp Arg His Gly Pro 295 300 305			1027
cgc gga ctc gtg atc ggc ggt atg tca ctc gtt gtg atc tcc ctg ttt Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val Val Ile Ser Leu Phe 310 315 320 325			1075
gca ctg tcc acc gtc gat gag ttc gcc aac gtg tgg ttc atc atc ggc Ala Leu Ser Thr Val Asp Glu Phe Ala Asn Val Trp Phe Ile Ile Gly 330 335 340			1123
gta cac atc gtg ttc tcc atc ggc ctt gcg ctg ctg ttc acc cca ctg Val His Ile Val Phe Ser Ile Gly Leu Ala Leu Leu Phe Thr Pro Leu 345 350 355			1171
atg aca gtc gcg ctc gca tcc gtc ccc gac aac atg tac ggc cac ggc Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn Met Tyr Gly His Gly 360 365 370			1219
tcc gcg atc ctc aac acc ctc caa cag ctc gcc ggc gcc gca ggc acc Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala Gly Ala Ala Gly Thr 375 380 385			1267
gcg gtc atg att gcg gtt tat tcc acc gtc agc aac aac gcg ctt atc Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser Asn Asn Ala Leu Ile 390 395 400 405			1315
gac ggc gca acc caa caa acc gcc ctc gcc gac ggc gcc aac tct gca Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp Gly Ala Asn Ser Ala 410 415 420			1363
ttc ttc gcc tca gcg tgc gtg gca gtg ttt gca ctg atc gtg ggc ttc Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala Leu Ile Val Gly Phe 425 430 435			1411
ttt gta aag agg cca gcc cgc taagctagggt cgcatgatca gca Phe Val Lys Arg Pro Ala Arg 440			1455

<210> 240

<211> 444

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Met	Met	Leu	Asn	Glu	Thr	Thr	Leu	Ala	Val	Ala	Leu	Pro	Ser	Ile	Met	1	5	10	15
Ala	Asp	Phe	Asp	Ile	Glu	Ala	Asn	Thr	Ala	Gln	Trp	Leu	Leu	Thr	Gly	20	25	30	
Ph	Met	Leu	Thr	Met	Ala	Val	Val	Leu	Pro	Ala	Thr	Gly	Trp	Met	Leu	35	40	45	
Glu	Arg	Phe	Thr	Thr	Arg	Ser	Val	Phe	Ile	Phe	Ala	Thr	Val	Val	Phe	50	55	60	
Leu	Ile	Gly	Thr	Val	Thr	Ala	Ala	Leu	Ser	Pro	Thr	Phe	Ala	Ile	Met	65	70	75	
Leu	Ala	Ala	Arg	Val	Ala	Gln	Ala	Ile	Gly	Thr	Ala	Val	Ile	Met	Pro	85	90	95	
Leu	Leu	Met	Thr	Val	Ala	Met	Thr	Val	Val	Pro	Pro	Glu	Arg	Arg	Gly	100	105	110	
Ala	Val	Met	Gly	Leu	Ile	Ala	Val	Val	Met	Ala	Val	Gly	Pro	Ala	Leu	115	120	125	
Gly	Pro	Ser	Val	Ala	Gly	Phe	Val	Leu	Ser	Leu	Ser	Ser	Trp	His	Ala	130	135	140	
Ile	Phe	Trp	Val	Met	Val	Pro	Leu	Val	Phe	Val	Ala	Ser	Leu	Ile	Gly	145	150	155	
Thr	Leu	Arg	Leu	Thr	Asn	Val	Ser	Glu	Pro	Lys	Lys	Thr	Pro	Leu	Asp	165	170	175	
Val	Ile	Ser	Phe	Leu	Ile	Ser	Ala	Val	Ala	Phe	Gly	Gly	Leu	Val	Tyr	180	185	190	
Ala	Leu	Ser	Ser	Ile	Gly	Ile	Ile	Leu	Glu	Gly	Asp	Arg	Ser	Ala	Leu	195	200	205	
Val	Val	Leu	Ala	Val	Gly	Ile	Ile	Ala	Leu	Val	Val	Phe	Val	Trp	Arg	210	215	220	
Gln	Ile	Ala	Met	Gly	Lys	Gln	Asp	Lys	Ala	Leu	Leu	Asp	Leu	Arg	Pro	225	230	235	
Leu	Ala	Ile	Arg	Glu	Tyr	Thr	Ile	Pro	Leu	Val	Val	Leu	Leu	Thr	Leu	245	250	255	
Phe	Gly	Ala	Leu	Leu	Gly	Val	Met	Asn	Thr	Leu	Pro	Leu	Tyr	Leu	Gln	260	265	270	
Gly	Ser	Leu	Met	Val	Thr	Ala	Leu	Val	Ala	Gly	Leu	Val	Leu	Leu	Pro	275	280	285	
Gly	Gly	Leu	Leu	Glu	Gly	Val	Leu	Ser	Pro	Phe	Val	Gly	Arg	Ile	Tyr	290	295	300	

Asp Arg His Gly Pro Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val
 305 310 315 320
 Val Ile Ser Leu Phe Ala Leu Ser Thr Val Asp Glu Phe Ala Asn Val
 325 330 335
 Trp Phe Ile Ile Gly Val His Ile Val Phe Ser Ile Gly Leu Ala Leu
 340 345 350
 Leu Phe Thr Pro Leu Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn
 355 360 365
 Met Tyr Gly His Gly Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala
 370 375 380
 Gly Ala Ala Gly Thr Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser
 385 390 395 400
 Asn Asn Ala Leu Ile Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp
 405 410 415
 Gly Ala Asn Ser Ala Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala
 420 425 430
 Leu Ile Val Gly Phe Phe Val Lys Arg Pro Ala Arg
 435 440

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1093)
 <223> FRXA00565

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 tgtcatcatc ttggctgtat tagttttttac agcctttgtc atg atg ttg aat gag 115
 Met Met Leu Asn Glu
 1 5
 act act ctg gca gtc gcg ttg ccg tcg atc atg gcg gac ttt gac att 163
 Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met Ala Asp Phe Asp Ile
 10 15 20
 gag gcg aat act gcg cag tgg ttg ctc act ggt ttt atg ttg acc atg 211
 Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly Phe Met Leu Thr Met
 25 30 35
 gct gtg gtt ctt cca gct act ggt tgg atg ttg gaa cgt ttt acc act 259
 Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu Glu Arg Phe Thr Thr
 40 45 50

cgt agt gtg ttt att ttc gcc acg gtg gtc ttc ctg atc ggt act gtg Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe Leu Ile Gly Thr Val 55 60 65	307
acg gct gcg ttg tct cct act ttt gcg att atg ctt gca gcc cgc gtc Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met Leu Ala Ala Arg Val 70 75 80 85	355
gct cag gcg att ggt acc gct gtg atc atg ccg ctg ctg atg act gtc Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro Leu Leu Met Thr Val 90 95 100	403
gcg atg acc gtt gtt cct cca gag cgc cgt ggc gcc gtc atg ggt ttg Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly Ala Val Met Gly Leu 105 110 115	451
att gcg gtc gtg atg gcc gtt ggt cct gct ctt gga cct agt gtg gct Ile Ala Val Val Met Ala Val Gly Pro Ala Leu Gly Pro Ser Val Ala 120 125 130	499
ggt ttc gta ctc agc ttg tct tcg tgg cac gcg att ttc tgg gtc atg Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala Ile Phe Trp Val Met 135 140 145	547
gtt ccg ttg gtg ttt gtg gca agc ctg atc ggt acc ctg cgt ctg acc Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly Thr Leu Arg Leu Thr 150 155 160 165	595
aac gtc agt gag cct aaa aag act cct ttg gat gtt att tcc ttc ctg Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp Val Ile Ser Phe Leu 170 175 180	643
att tcc gca gtg gct ttc ggt ggc ctt gtg tac gcc ttg agc tcg att Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr Ala Leu Ser Ser Ile 185 190 195	691
ggc atc att ttg gaa ggt gac aga agc gct ttg gtc gtg ttg gct gtc Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu Val Val Leu Ala Val 200 205 210	739
ggc atc att gcg ttg gtg gtg ttt gtg tgg cgc cag att gcc atg ggt Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg Gln Ile Ala Met Gly 215 220 225	787
aag cag gat aag gcg ctg ttg gat ctg cgt ccg ttg gcg att cgt gag Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro Leu Ala Ile Arg Glu 230 235 240 245	835
tac acc att ccg ctg gtt gtg ctt ttg acg ctg ttc ggt gcg ctg ctc Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu Phe Gly Ala Leu Leu 250 255 260	883
ggt gtc atg aat aca ctg ccg ctc tac ctg cag gga tcc ttg atg gtc Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln Gly Ser Leu Met Val 265 270 275	931
acc gcc ttg gtc gcg ggt cta gtg ctg ttg cca ggt ggt ctt ttg gaa	979

Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro Gly Gly Leu Leu Glu
 280 285 290

ggt gtg ctg tcg cca ttt gtg ggt cga att tat gat cgt cat ggt cca 1027
 Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr Asp Arg His Gly Pro
 295 300 305

cgc gga ctc gtg atc ggc ggt atg tca ctc gtt gtg atc tcc ctg ttt 1075
 Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val Val Ile Ser Leu Phe
 310 315 320 325

gca ctg tcc acc gtc gat 1093
 Ala Leu Ser Thr Val Asp
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<210> 242
 <211> 331
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 242
 Met Met Leu Asn Glu Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met
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Ala Asp Phe Asp Ile Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly
 20 25 30

Phe Met Leu Thr Met Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu
 35 40 45

Glu Arg Phe Thr Thr Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe
 50 55 60

Leu Ile Gly Thr Val Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met
 65 70 75 80

Leu Ala Ala Arg Val Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro
 85 90 95

Leu Leu Met Thr Val Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly
 100 105 110

Ala Val Met Gly Leu Ile Ala Val Val Met Ala Val Gly Pro Ala Leu
 115 120 125

Gly Pro Ser Val Ala Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala
 130 135 140

Ile Phe Trp Val Met Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly
 145 150 155 160

Thr Leu Arg Leu Thr Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp
 165 170 175

Val Ile Ser Phe Leu Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr
 180 185 190

Ala Leu Ser Ser Ile Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu
 195 200 205

Val Val Leu Ala Val Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg
 210 215 220

Gln Ile Ala Met Gly Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro
 225 230 235 240

Leu Ala Ile Arg Glu Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu
 245 250 255

Phe Gly Ala Leu Leu Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln
 260 265 270

Gly Ser Leu Met Val Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro
 275 280 285

Gly Gly Leu Leu Glu Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr
 290 295 300

Asp Arg His Gly Pro Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val
 305 310 315 320

Val Ile Ser Leu Phe Ala Leu Ser Thr Val Asp
 325 330

<210> 243
 <211> 380
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(357)
 <223> FRXA02878

<400> 243
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 Cys Leu Ser Thr Val Asp Glu Phe Ala Thr Cys Trp Ser Ser Phe Ala
 1 5 10 15

gac aca tcg tgg ttc tca tcg gcc ctt gcg ctg ctg ttc acc cca ctg 96
 Asp Thr Ser Trp Phe Ser Ser Ala Leu Ala Leu Leu Phe Thr Pro Leu
 20 25 30

atg aca gtc gcg ctc gca tcc gtc ccc gac aac atg tac ggc cac ggc 144
 Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn Met Tyr Gly His Gly
 35 40 45

tcc gcg atc ctc aac acc ctc caa cag ctc gcc ggc gcc gca ggc acc 192
 Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala Gly Ala Ala Gly Thr
 50 55 60

gcg gtc atg att gcg gtt tat tcc acc gtc agc aac aac gcg ctt atc 240

Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser Asn Asn Ala L u Ile
 65 70 75 80

gac ggc gca acc caa caa acc gcc ctc gcc gac ggc gcc aac tct gca 288
 Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp Gly Ala Asn S r Ala
 85 90 95

ttc ttc gcc tca gcg tgc gtg gca gtg ttt gca ctg atc gtg ggc ttc 336
 Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala Leu Ile Val Gly Phe
 100 105 110

ttt gta aag agg cca gcc cgc taagctaggt cgc atgatca gca 380
 Phe Val Lys Arg Pro Ala Arg
 115

<210> 244
 <211> 119
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 244
 Cys Leu Ser Thr Val Asp Glu Phe Ala Thr Cys Trp Ser Ser Phe Ala
 1 5 10 15

Asp Thr Ser Trp Phe Ser Ser Ala Leu Ala Leu Leu Phe Thr Pro Leu
 20 25 30

Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn Met Tyr Gly His Gly
 35 40 45

Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala Gly Ala Ala Gly Thr
 50 55 60

Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser Asn Asn Ala Leu Ile
 65 70 75 80

Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp Gly Ala Asn Ser Ala
 85 90 95

Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala Leu Ile Val Gly Phe
 100 105 110

Phe Val Lys Arg Pro Ala Arg
 115

<210> 245
 <211> 1533
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1510)
 <223> RXA00648

<400> 245

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tcccgaatca	gccacaccac	agatcaaata	cggcctgctg	gtg	gtc	act	ctc	gcc	115
				Val	Val	Thr	Leu	Ala	
				1				5	

tca	gct	ggt	atc	act	gtt	tcc	cta	gcg	cag	acc	ctg	gtt	att	ccg	atc	163
Ser	Ala	Gly	Ile	Thr	Val	Ser	Leu	Ala	Gln	Thr	Leu	Val	Ile	Pro	Ile	
			10					15					20			

att	ggt	cgg	ttg	ccc	gag	atc	ttc	aac	acc	acg	gct	gct	aat	gcc	tct	211
Ile	Gly	Arg	Leu	Pro	Glu	Ile	Phe	Asn	Thr	Thr	Ala	Ala	Asn	Ala	Ser	
			25					30					35			

tgg	atc	att	act	gtg	acg	ctg	ttg	gtg	ggc	gca	gtg	gcg	act	cct	gtg	259
Trp	Ile	Ile	Thr	Val	Thr	Leu	Leu	Val	Gly	Ala	Val	Ala	Thr	Pro	Val	
		40					45					50				

atg	ggc	agg	ctt	gca	gat	atg	tac	ggc	aag	aaa	aag	atg	atg	ctc	atc	307
Met	Gly	Arg	Leu	Ala	Asp	Met	Tyr	Gly	Lys	Lys	Lys	Met	Met	Leu	Ile	
	55					60					65					

tca	ctt	gtc	ccg	ttc	att	ctt	gga	tca	gtg	atc	tgc	gct	gtg	tcg	gtg	355
Ser	Leu	Val	Pro	Phe	Ile	Leu	Gly	Ser	Val	Ile	Cys	Ala	Val	Ser	Val	
	70				75					80					85	

gat	ttg	att	ccg	atg	atc	atc	ggc	cgt	ggg	ttt	cag	ggg	ctt	ggc	tct	403
Asp	Leu	Ile	Pro	Met	Ile	Ile	Gly	Arg	Gly	Phe	Gln	Gly	Leu	Gly	Ser	
				90					95					100		

ggc	ctg	att	cct	ctt	ggc	att	tct	ctc	atg	cat	gat	ttg	ttg	ccc	cgg	451
Gly	Leu	Ile	Pro	Leu	Gly	Ile	Ser	Leu	Met	His	Asp	Leu	Leu	Pro	Arg	
			105					110					115			

gag	aaa	gca	ggg	tct	gcc	att	gct	ttg	atg	agt	tct	tcc	atg	ggc	att	499
Glu	Lys	Ala	Gly	Ser	Ala	Ile	Ala	Leu	Met	Ser	Ser	Ser	Met	Gly	Ile	
		120					125					130				

ggc	ggt	gca	ctc	ggt	cta	ccg	ctg	gct	gct	gct	att	gcc	cag	ttt	gcg	547
Gly	Gly	Ala	Leu	Gly	Leu	Pro	Leu	Ala	Ala	Ala	Ile	Ala	Gln	Phe	Ala	
		135				140					145					

tcc	tgg	cgg	gtg	ctg	ttc	tgg	ttc	acc	gct	ctg	gta	gcg	ctt	aca	gtt	595
Ser	Trp	Arg	Val	Leu	Phe	Trp	Phe	Thr	Ala	Leu	Val	Ala	Leu	Thr	Val	
	150				155					160					165	

ggc	gcg	gtc	att	tgg	aag	gcg	att	cct	gct	aga	ccc	agg	atc	gtg	agg	643
Gly	Ala	Val	Ile	Trp	Lys	Ala	Ile	Pro	Ala	Arg	Pro	Arg	Ile	Val	Arg	
			170					175						180		

agt	ggc	ggc	ttt	gat	tat	ttc	ggt	gct	ctc	ggc	ctt	gca	atg	gga	ctt	691
Ser	Gly	Gly	Phe	Asp	Tyr	Phe	Gly	Ala	Leu	Gly	Leu	Ala	Met	Gly	Leu	
			185				190					195				

atc	gca	ttg	ttg	ctc	gcg	gtg	tcc	aag	gga	tca	gaa	tgg	ggc	tgg	aga	739
Ile	Ala	Leu	Leu	Leu	Ala	Val	Ser	Lys	Gly	Ser	Glu	Trp	Gly	Trp	Arg	

200	205	210	
agt gcc ctg acc att ggg tta ttc gtg gca gcg ctg gtg att ttg gtg Ser Ala Leu Thr Ile Gly Leu Phe Val Ala Ala Leu Val Ile Leu Val 215 220 225			787
ggt tgg ggc tgg ttc gaa acc cgc cag aaa tcc cct ttg att gat ctg Gly Trp Gly Trp Phe Glu Thr Arg Gln Lys Ser Pro Leu Ile Asp Leu 230 235 240 245			835
cgc acc act att cgg gcg acc gtg ttg atg aca aat att gcg tcc atc Arg Thr Thr Ile Arg Ala Thr Val Leu Met Thr Asn Ile Ala Ser Ile 250 255 260			883
ctc atc ggt ttc acc atg tat gga atg aat ctg atc ctg cct cag gtc Leu Ile Gly Phe Thr Met Tyr Gly Met Asn Leu Ile Leu Pro Gln Val 265 270 275			931
atg cag ctg cct gta att ctg ggc tac ggt cta ggc cag agc atg ctt Met Gln Leu Pro Val Ile Leu Gly Tyr Gly Leu Gly Gln Ser Met Leu 280 285 290			979
cag atg ggc atc tgg ctg atc ccg atg ggt cta ggc atg atg ttg att Gln Met Gly Ile Trp Leu Ile Pro Met Gly Leu Gly Met Met Leu Ile 295 300 305			1027
tcg aat gca ggt gca gcc att agc gct gct cat ggt cct cgt gtg acg Ser Asn Ala Gly Ala Ala Ile Ser Ala Ala His Gly Pro Arg Val Thr 310 315 320 325			1075
ctg aca att gcg ggt gtt gtg atc gca gtc ggt tat gca ctt act gcc Leu Thr Ile Ala Gly Val Val Ile Ala Val Gly Tyr Ala Leu Thr Ala 330 335 340			1123
aca gtg ttg ttc act atc ggc aac cgc aca ccg gga gga gat gca gac Thr Val Leu Phe Thr Ile Gly Asn Arg Thr Pro Gly Gly Asp Ala Asp 345 350 355			1171
aac gca ctt att ttg acc acc ctg gtg ctg ttc tca gtg tgt agt ctc Asn Ala Leu Ile Leu Thr Thr Leu Val Leu Phe Ser Val Cys Ser Leu 360 365 370			1219
gtg gtc ggt atc ggc att ggc ctg gca ttt ggt tcc atg cct gcc ttg Val Val Gly Ile Gly Ile Gly Leu Ala Phe Gly Ser Met Pro Ala Leu 375 380 385			1267
atc atg ggt gcc gta cca gcc acg gag aaa gcc gca gcg aat ggt ttc Ile Met Gly Ala Val Pro Ala Thr Glu Lys Ala Ala Ala Asn Gly Phe 390 395 400 405			1315
aac tct ctt atg cgt tca ctg ggc acc acc ggc tca tca gct gtc atc Asn Ser Leu Met Arg Ser Leu Gly Thr Thr Gly Ser Ser Ala Val Ile 410 415 420			1363
ggt gca gtg ttg gcc gga atg atg agt ggc gga gta ccc acc tta ggg Gly Ala Val Leu Ala Gly Met Met Ser Gly Gly Val Pro Thr Leu Gly 425 430 435			1411

gga ttc atg acc act ctg atc atc gga tgc tgc gcc gcg ctt gtg gct 1459
 Gly Phe Met Thr Thr Leu Ile Ile Gly Cys Cys Ala Ala Leu Val Ala
 440 445 450

gcg gtc atc tcc tat ttc atc ccc acc aca acc act gtg gtg gaa gca 1507
 Ala Val Ile Ser Tyr Phe Ile Pro Thr Thr Thr Thr Val Val Glu Ala
 455 460 465

aaa taatcccggc agcgactcga cca 1533
 Lys
 470

<210> 246

<211> 470

<212> PRT

<213> Corynebacterium glutamicum

<400> 246

Val Val Thr Leu Ala Ser Ala Gly Ile Thr Val Ser Leu Ala Gln Thr
 1 5 10 15

Leu Val Ile Pro Ile Ile Gly Arg Leu Pro Glu Ile Phe Asn Thr Thr
 20 25 30

Ala Ala Asn Ala Ser Trp Ile Ile Thr Val Thr Leu Leu Val Gly Ala
 35 40 45

Val Ala Thr Pro Val Met Gly Arg Leu Ala Asp Met Tyr Gly Lys Lys
 50 55 60

Lys Met Met Leu Ile Ser Leu Val Pro Phe Ile Leu Gly Ser Val Ile
 65 70 75 80

Cys Ala Val Ser Val Asp Leu Ile Pro Met Ile Ile Gly Arg Gly Phe
 85 90 95

Gln Gly Leu Gly Ser Gly Leu Ile Pro Leu Gly Ile Ser Leu Met His
 100 105 110

Asp Leu Leu Pro Arg Glu Lys Ala Gly Ser Ala Ile Ala Leu Met Ser
 115 120 125

Ser Ser Met Gly Ile Gly Gly Ala Leu Gly Leu Pro Leu Ala Ala Ala
 130 135 140

Ile Ala Gln Phe Ala Ser Trp Arg Val Leu Phe Trp Phe Thr Ala Leu
 145 150 155 160

Val Ala Leu Thr Val Gly Ala Val Ile Trp Lys Ala Ile Pro Ala Arg
 165 170 175

Pro Arg Ile Val Arg Ser Gly Gly Phe Asp Tyr Phe Gly Ala Leu Gly
 180 185 190

Leu Ala Met Gly Leu Ile Ala Leu Leu Leu Ala Val Ser Lys Gly Ser

195	200	205
Glu Trp Gly Trp Arg S r Ala Leu Thr Ile Gly Leu Phe Val Ala Ala		
210	215	220
Leu Val Ile Leu Val Gly Trp Gly Trp Phe Glu Thr Arg Gln Lys Ser		
225	230	235
Pro Leu Ile Asp Leu Arg Thr Thr Ile Arg Ala Thr Val Leu Met Thr		
	245	250
Asn Ile Ala Ser Ile Leu Ile Gly Phe Thr Met Tyr Gly Met Asn Leu		
	260	270
Ile Leu Pro Gln Val Met Gln Leu Pro Val Ile Leu Gly Tyr Gly Leu		
	275	280
Gly Gln Ser Met Leu Gln Met Gly Ile Trp Leu Ile Pro Met Gly Leu		
	290	295
Gly Met Met Leu Ile Ser Asn Ala Gly Ala Ala Ile Ser Ala Ala His		
305	310	315
Gly Pro Arg Val Thr Leu Thr Ile Ala Gly Val Val Ile Ala Val Gly		
	325	330
Tyr Ala Leu Thr Ala Thr Val Leu Phe Thr Ile Gly Asn Arg Thr Pro		
	340	345
Gly Gly Asp Ala Asp Asn Ala Leu Ile Leu Thr Thr Leu Val Leu Phe		
	355	360
Ser Val Cys Ser Leu Val Val Gly Ile Gly Ile Gly Leu Ala Phe Gly		
	370	375
Ser Met Pro Ala Leu Ile Met Gly Ala Val Pro Ala Thr Glu Lys Ala		
385	390	395
Ala Ala Asn Gly Phe Asn Ser Leu Met Arg Ser Leu Gly Thr Thr Gly		
	405	410
Ser Ser Ala Val Ile Gly Ala Val Leu Ala Gly Met Met Ser Gly Gly		
	420	425
Val Pro Thr Leu Gly Gly Phe Met Thr Thr Leu Ile Ile Gly Cys Cys		
	435	440
Ala Ala Leu Val Ala Ala Val Ile Ser Tyr Phe Ile Pro Thr Thr Thr		
	450	455
Thr Val Val Glu Ala Lys		
465	470	

<210> 247
 <211> 1770
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1747)

<223> RXN01320

<400> 247

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								Met	Thr	Ser	Gln	Val	
								1				5	

aag	ccg	gac	gac	gaa	cgt	ccg	gta	aca	aca	att	tca	aaa	agt	ggt	gca	163
Lys	Pro	Asp	Asp	Glu	Arg	Pro	Val	Thr	Thr	Ile	Ser	Lys	Ser	Gly	Ala	
				10						15					20	

cct	tcg	gcc	cac	acc	tca	gca	cca	tat	ggt	gca	gca	gca	act	gaa	gaa	211
Pro	Ser	Ala	His	Thr	Ser	Ala	Pro	Tyr	Gly	Ala	Ala	Ala	Thr	Glu	Glu	
			25					30					35			

gct	gtc	gag	gaa	aaa	acc	aaa	ggt	cgc	ggt	gga	ttt	atc	atc	gca	gcc	259
Ala	Val	Glu	Glu	Lys	Thr	Lys	Gly	Arg	Val	Gly	Phe	Ile	Ile	Ala	Ala	
		40					45					50				

ctc	atg	ttg	gcg	atg	ctt	ctt	agc	tcc	ttg	ggt	cag	acc	att	ttc	ggt	307
Leu	Met	Leu	Ala	Met	Leu	Leu	Ser	Ser	Leu	Gly	Gln	Thr	Ile	Phe	Gly	
	55				60					65						

tct	gcc	ctg	cca	acg	att	ggt	ggt	gag	ctt	ggc	ggc	ggt	aac	cac	atg	355
Ser	Ala	Leu	Pro	Thr	Ile	Val	Gly	Glu	Leu	Gly	Gly	Val	Asn	His	Met	
	70				75					80					85	

acc	tgg	gtg	att	acc	gcc	ttc	ctc	ttg	ggc	cag	acc	att	tca	ttg	cct	403
Thr	Trp	Val	Ile	Thr	Ala	Phe	Leu	Leu	Gly	Gln	Thr	Ile	Ser	Leu	Pro	
				90					95					100		

att	ttc	ggc	aag	ttg	ggt	gac	cag	ttt	ggt	cgc	aaa	tac	ctc	ttc	atg	451
Ile	Phe	Gly	Lys	Leu	Gly	Asp	Gln	Phe	Gly	Arg	Lys	Tyr	Leu	Phe	Met	
		105						110					115			

ttt	gcc	atc	gca	ctg	ttc	gtg	gtg	ggt	tcc	atc	atc	ggt	gct	ttg	gct	499
Phe	Ala	Ile	Ala	Leu	Phe	Val	Val	Gly	Ser	Ile	Ile	Gly	Ala	Leu	Ala	
		120					125					130				

cag	aac	atg	acc	acc	ttg	att	gtg	gct	cgt	gca	ctg	cag	ggt	atc	gcc	547
Gln	Asn	Met	Thr	Thr	Leu	Ile	Val	Ala	Arg	Ala	Leu	Gln	Gly	Ile	Ala	
	135					140					145					

ggt	ggt	ggc	ttg	atg	att	ctt	tct	cag	gca	att	acc	gct	gat	gtc	acc	595
Gly	Gly	Gly	Leu	Met	Ile	Leu	Ser	Gln	Ala	Ile	Thr	Ala	Asp	Val	Thr	
150					155					160					165	

acc	gcc	cgt	gag	cgt	gca	aag	tac	atg	ggc	atc	atg	ggt	tcc	ggt	ttc	643
Thr	Ala	Arg	Glu	Arg	Ala	Lys	Tyr	Met	Gly	Ile	Met	Gly	Ser	Val	Phe	
			170						175					180		

gga ctg tcc tcc atc ctt ggc cca ttg ctt ggt ggc tgg ttc act gac	691
Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Asp	
185 190 195	
ggt cca ggc tgg cgt tgg ggt ctg tgg ttg aac gtt cca atc ggc atc	739
Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn Val Pro Ile Gly Ile	
200 205 210	
atc gca ctg gtt gct atc gct gtg ctg ctg aaa ctt cca gct cgt gaa	787
Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys Leu Pro Ala Arg Glu	
215 220 225	
cgt ggc aag gtc tcc gtt gac tgg ttg gga agc atc ttc atg gct atc	835
Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser Ile Phe Met Ala Ile	
230 235 240 245	
gcc acc acc gca ttt gtc ctc gca gtg acc tgg ggt ggc aat gaa tat	883
Ala Thr Thr Ala Phe Val Leu Ala Val Thr Trp Gly Gly Asn Glu Tyr	
250 255 260	
gag tgg gca tca cca atg atc atc ggt ttg ttc atc acg aca ttg gtc	931
Glu Trp Ala Ser Pro Met Ile Ile Gly Leu Phe Ile Thr Thr Leu Val	
265 270 275	
gct gcg ata gtg ttc gtt ttc gtc gaa aag cgt gct gtt gac cca ctg	979
Ala Ala Ile Val Phe Val Phe Val Glu Lys Arg Ala Val Asp Pro Leu	
280 285 290	
gtc ccc atg ggc ctt ttc tcg aac cgc aac ttc gtg ctc acc gcc gtc	1027
Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe Val Leu Thr Ala Val	
295 300 305	
gcc ggt atc ggc gta ggc ctg ttt atg atg ggc acc atc gcg tac atg	1075
Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly Thr Ile Ala Tyr Met	
310 315 320 325	
cct acc tac ctg cag atg gtt cat ggt ctg aac cca acg caa gct ggt	1123
Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn Pro Thr Gln Ala Gly	
330 335 340	
ctg atg ctg atc cca atg atg atc ggc ctg att ggt aca tcc act gtg	1171
Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile Gly Thr Ser Thr Val	
345 350 355	
gtg ggc aac atc gtg tcc aag act ggc aag tac aag tgg tac cca ttc	1219
Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys Trp Tyr Pro Phe	
360 365 370	
atc ggc atg ctc atc atg gtc ctt gcc cta gta ctg cta tcg acg ctg	1267
Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu Leu Ser Thr Leu	
375 380 385	
aca cct tcg gca agc ttg gct ctc att gga ctg tac ttc ttc gtc ttc	1315
Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr Phe Phe Val Phe	
390 395 400 405	

gga ttc ggc ctg ggc tgt gca atg cag att ttg gtt ctc atc gtg cag 1363
 Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val Leu Ile Val Gln
 410 415 420
 aac tcc ttc cca atc acc atg gtt ggc acc gcg acc ggt tcc aac aac 1411
 Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala Thr Gly Ser Asn Asn
 425 430 435
 ttc ttc cgc caa atc ggt gga gca gta ggt tcc gca ctg atc ggt ggc 1459
 Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala Leu Ile Gly Gly
 440 445 450
 ctg ttt atc tcc aac ctg tcc gac cga ttc acc gaa aac gtc ccc gca 1507
 Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu Asn Val Pro Ala
 455 460 465
 gca gtg gct tcc atg ggt gaa gaa ggc gca caa tac gcc tca gca atg 1555
 Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr Ala Ser Ala Met
 470 475 480 485
 tcc gat ttc tcc ggt gca tcc aac ctc act cca cac ctt gtt gaa tca 1603
 Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His Leu Val Glu Ser
 490 495 500
 ctt cca caa gca ctc cgt gaa gca att caa ctt tct tac aac gac gcc 1651
 Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu Ser Tyr Asn Asp Ala
 505 510 515
 ctg aca cca atc ttc ttg gcg ctc acc ccg atc gca gta gtc gcc gcg 1699
 Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile Ala Val Val Ala Ala
 520 525 530
 atc ctc ctc ttt ttc atc cgt gaa gat cac ctc aag gaa acg cac gaa 1747
 Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu Lys Glu Thr His Glu
 535 540 545
 taatgacaca cgaaacttcc gtc 1770

<210> 248

<211> 549

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 248

Met Thr Ser Gln Val Lys Pro Asp Asp Glu Arg Pro Val Thr Thr Ile
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 Ser Lys Ser Gly Ala Pro Ser Ala His Thr Ser Ala Pro Tyr Gly Ala
 20 25 30
 Ala Ala Thr Glu Glu Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly
 35 40 45
 Phe Ile Ile Ala Ala Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly
 50 55 60

Gln Thr Ile Ph Gly Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly
 65 70 75 80
 Gly Val Asn His Met Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln
 85 90 95
 Thr Ile Ser Leu Pro Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg
 100 105 110
 Lys Tyr Leu Phe Met Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile
 115 120 125
 Ile Gly Ala Leu Ala Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala
 130 135 140
 Leu Gln Gly Ile Ala Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile
 145 150 155 160
 Thr Ala Asp Val Thr Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile
 165 170 175
 Met Gly Ser Val Phe Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly
 180 185 190
 Gly Trp Phe Thr Asp Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn
 195 200 205
 Val Pro Ile Gly Ile Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys
 210 215 220
 Leu Pro Ala Arg Glu Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser
 225 230 235 240
 Ile Phe Met Ala Ile Ala Thr Thr Ala Phe Val Leu Ala Val Thr Trp
 245 250 255
 Gly Gly Asn Glu Tyr Glu Trp Ala Ser Pro Met Ile Ile Gly Leu Phe
 260 265 270
 Ile Thr Thr Leu Val Ala Ala Ile Val Phe Val Phe Val Glu Lys Arg
 275 280 285
 Ala Val Asp Pro Leu Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe
 290 295 300
 Val Leu Thr Ala Val Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly
 305 310 315 320
 Thr Ile Ala Tyr Met Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn
 325 330 335
 Pro Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile
 340 345 350
 Gly Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr
 355 360 365

Lys Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val
 370 375 380
 Leu Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu
 385 390 395 400
 Tyr Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu
 405 410 415
 Val Leu Ile Val Gln Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala
 420 425 430
 Thr Gly Ser Asn Asn Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser
 435 440 445
 Ala Leu Ile Gly Gly Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr
 450 455 460
 Glu Asn Val Pro Ala Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln
 465 470 475 480
 Tyr Ala Ser Ala Met Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro
 485 490 495
 His Leu Val Glu Ser Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu
 500 505 510
 Ser Tyr Asn Asp Ala Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile
 515 520 525
 Ala Val Val Ala Ala Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu
 530 535 540
 Lys Glu Thr His Glu
 545
 <210> 249
 <211> 841
 <212> DNA
 <213> *Corynebacterium glutamicum*
 <220>
 <221> CDS
 <222> (101)..(841)
 <223> FRXA01314
 <400> 249
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 caattaaaaa tacttttctt cttagagggtg gattttcaga atg aca tca cag gtc 115
 Met Thr Ser Gln Val
 1 5
 aag ccg gac gac gaa cgt ccg gta aca aca att tca aaa agt ggt gca 163
 Lys Pro Asp Asp Glu Arg Pro Val Thr Thr Ile Ser Lys Ser Gly Ala
 10 15 20

cct tgc gcc cac acc tca gca cca tat ggt gca gca gca act gaa gaa	211
Pro Ser Ala His Thr Ser Ala Pro Tyr Gly Ala Ala Ala Thr Glu Glu	
25 30 35	
gct gtc gag gaa aaa acc aaa ggt cgc gtt gga ttt atc atc gca gcc	259
Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly Phe Ile Ile Ala Ala	
40 45 50	
ctc atg ttg gcg atg ctt ctt agc tcc ttg ggt cag acc att ttc ggt	307
Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly Gln Thr Ile Phe Gly	
55 60 65	
tct gcc ctg cca acg att gtt ggt gag ctt ggc ggc gtt aac cac atg	355
Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asn His Met	
70 75 80 85	
acc tgg gtg att acc gcc ttc ctc ttg ggc cag acc att tca ttg cct	403
Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln Thr Ile Ser Leu Pro	
90 95 100	
att ttc ggc aag ttg ggt gac cag ttt ggt cgc aaa tac ctc ttc atg	451
Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg Lys Tyr Leu Phe Met	
105 110 115	
ttt gcc atc gca ctg ttc gtg gtg ggt tcc atc atc ggt gct ttg gct	499
Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile Ile Gly Ala Leu Ala	
120 125 130	
cag aac atg acc acc ttg att gtg gct cgt gca ctg cag ggt atc gcc	547
Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala Leu Gln Gly Ile Ala	
135 140 145	
ggt ggt ggc ttg atg att ctt tct cag gca att acc gct gat gtc acc	595
Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Thr Ala Asp Val Thr	
150 155 160 165	
acc gcc cgt gag cgt gca aag tac atg ggc atc atg ggt tcc gtt ttc	643
Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile Met Gly Ser Val Phe	
170 175 180	
gga ctg tcc tcc atc ctt ggc cca ttg ctt ggt ggc tgg ttc act gac	691
Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Asp	
185 190 195	
ggt cca ggc tgg cgt tgg ggt ctg tgg ttg aac gtt cca atc ggc atc	739
Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn Val Pro Ile Gly Ile	
200 205 210	
atc gca ctg gtt gct atc gct gtg ctg ctg aaa ctt cca gct cgt gaa	787
Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys Leu Pro Ala Arg Glu	
215 220 225	
cgt ggc aag gtc tcc gtt gac tgg ttg gga agc atc ttc atg gct atc	835
Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser Ile Phe Met Ala Ile	
230 235 240 245	

gcc acc
Ala Thr

841

<210> 250
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 250

Met	Thr	Ser	Gln	Val	Lys	Pro	Asp	Asp	Glu	Arg	Pro	Val	Thr	Thr	Ile
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Ser	Lys	Ser	Gly	Ala	Pro	Ser	Ala	His	Thr	Ser	Ala	Pro	Tyr	Gly	Ala
			20					25					30		
Ala	Ala	Thr	Glu	Glu	Ala	Val	Glu	Glu	Lys	Thr	Lys	Gly	Arg	Val	Gly
		35					40					45			
Phe	Ile	Ile	Ala	Ala	Leu	Met	Leu	Ala	Met	Leu	Leu	Ser	Ser	Leu	Gly
	50					55					60				
Gln	Thr	Ile	Phe	Gly	Ser	Ala	Leu	Pro	Thr	Ile	Val	Gly	Glu	Leu	Gly
65					70					75					80
Gly	Val	Asn	His	Met	Thr	Trp	Val	Ile	Thr	Ala	Phe	Leu	Leu	Gly	Gln
				85					90					95	
Thr	Ile	Ser	Leu	Pro	Ile	Phe	Gly	Lys	Leu	Gly	Asp	Gln	Phe	Gly	Arg
			100					105					110		
Lys	Tyr	Leu	Phe	Met	Phe	Ala	Ile	Ala	Leu	Phe	Val	Val	Gly	Ser	Ile
		115					120					125			
Ile	Gly	Ala	Leu	Ala	Gln	Asn	Met	Thr	Thr	Leu	Ile	Val	Ala	Arg	Ala
	130					135					140				
Leu	Gln	Gly	Ile	Ala	Gly	Gly	Gly	Leu	Met	Ile	Leu	Ser	Gln	Ala	Ile
145					150					155					160
Thr	Ala	Asp	Val	Thr	Thr	Ala	Arg	Glu	Arg	Ala	Lys	Tyr	Met	Gly	Ile
				165					170					175	
Met	Gly	Ser	Val	Phe	Gly	Leu	Ser	Ser	Ile	Leu	Gly	Pro	Leu	Leu	Gly
			180					185					190		
Gly	Trp	Phe	Thr	Asp	Gly	Pro	Gly	Trp	Arg	Trp	Gly	Leu	Trp	Leu	Asn
		195					200					205			
Val	Pro	Ile	Gly	Ile	Ile	Ala	Leu	Val	Ala	Ile	Ala	Val	Leu	Leu	Lys
		210				215					220				
Leu	Pro	Ala	Arg	Glu	Arg	Gly	Lys	Val	Ser	Val	Asp	Trp	Leu	Gly	Ser
225					230					235					240
Ile	Phe	Met	Ala	Ile	Ala	Thr									

245

<210> 251
 <211> 803
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(780)
 <223> FRXA01320

<400> 251

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Val Asp Pro Leu Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe Val	
1 5 10 15	
ctc acc gcc gtc gcc ggt atc ggc gta ggc ctg ttt atg atg ggc acc	96
Leu Thr Ala Val Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly Thr	
20 25 30	
atc gcg tac atg cct acc tac ctg cag atg gtt cat ggt ctg aac cca	144
Ile Ala Tyr Met Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn Pro	
35 40 45	
acg caa gct ggt ctg atg ctg atc cca atg atg atc ggc ctg att ggt	192
Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile Gly	
50 55 60	
aca tcc act gtg gtg ggc aac atc gtg tcc aag act ggc aag tac aag	240
Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys	
65 70 75 80	
tgg tac cca ttc atc ggc atg ctc atc atg gtc ctt gcc cta gta ctg	288
Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu	
85 90 95	
cta tcg acg ctg aca cct tcg gca agc ttg gct ctc att gga ctg tac	336
Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr	
100 105 110	
ttc ttc gtc ttc gga ttc ggc ctg ggc tgt gca atg cag att ttg gtt	384
Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val	
115 120 125	
ctc atc gtg cag aac tcc ttc cca atc acc atg gtt ggc acc gcg acc	432
Leu Ile Val Gln Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala Thr	
130 135 140	
ggt tcc aac aac ttc ttc cgc caa atc ggt gga gca gta ggt tcc gca	480
Gly Ser Asn Asn Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala	
145 150 155 160	
ctg atc ggt ggc ctg ttt atc tcc aac ctg tcc gac cga ttc acc gaa	528
Leu Ile Gly Gly Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu	
165 170 175	

aac gtc ccc gca gca gtg gct tcc atg ggt gaa gaa ggc gca caa tac 576
 Asn Val Pro Ala Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr
 180 185 190
 gcc tca gca atg tcc gat ttc tcc ggt gca tcc aac ctc act cca cac 624
 Ala Ser Ala Met Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His
 195 200 205
 ctt gtt gaa tca ctt cca caa gca ctc cgt gaa gca att caa ctt tct 672
 Leu Val Glu Ser Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu Ser
 210 215 220
 tac aac gac gcc ctg aca cca atc ttc ttg gcg ctc acc ccg atc gca 720
 Tyr Asn Asp Ala Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile Ala
 225 230 235 240
 gta gtc gcc gcg atc ctc ctc ttt ttc atc cgt gaa gat cac ctc aag 768
 Val Val Ala Ala Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu Lys
 245 250 255
 gaa acg cac gaa taatgacaca cgaaacttcc gtc 803
 Glu Thr His Glu
 260

<210> 252

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Val Asp Pro Leu Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe Val
 1 5 10 15
 Leu Thr Ala Val Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly Thr
 20 25 30
 Ile Ala Tyr Met Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn Pro
 35 40 45
 Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile Gly
 50 55 60
 Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys
 65 70 75 80
 Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu
 85 90 95
 Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr
 100 105 110
 Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val
 115 120 125
 Leu Ile Val Gln Asn Ser Phe Pro Il Thr Met Val Gly Thr Ala Thr

130 135 140

Gly Ser Asn Asn Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala
 145 150 155 160

Leu Ile Gly Gly Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu
 165 170 175

Asn Val Pro Ala Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr
 180 185 190

Ala Ser Ala Met Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His
 195 200 205

Leu Val Glu Ser Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu Ser
 210 215 220

Tyr Asn Asp Ala Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile Ala
 225 230 235 240

Val Val Ala Ala Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu Lys
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Glu Thr His Glu
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 <223> RXN02926

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 Met Thr His Glu Thr
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tcc gtc ccc gga cct gcc gac gcg cag gtc gca gga gat acg aag ctg 163
 Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala Gly Asp Thr Lys Leu
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cgc aaa ggc cgc gcg aag aag gaa aaa act cct tca tca atg acg cct 211
 Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro Ser Ser Met Thr Pro
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gaa caa caa aag aaa gtc tgg tgg gtc ctc agc gcg ctg atg gtc gcc 259
 Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser Ala Leu Met Val Ala
 40 45 50

atg atg atg gcc tcc ctt gac cag atg att ttc ggc aca gcc ctg cca 307

Met Met Met Ala Ser Leu Asp Gln Met Ile Phe Gly Thr Ala Leu Pro	
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aca atc gtc ggt gaa ctc ggc ggc gtt gac cac atg atg tgg gtc atc	355
Thr Ile Val Gly Glu Leu Gly Gly Val Asp His Met Met Trp Val Ile	
70 75 80 85	
acc gca tac cta ctt gcc gaa acc atc atg ctg ccg atc tac gga aag	403
Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu Pro Ile Tyr Gly Lys	
90 95 100	
ctc ggc gac ctg gtt gga cgt aaa ggt ctc ttc atc gga gcc ctc ggc	451
Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe Ile Gly Ala Leu Gly	
105 110 115	
atc ttc ctg atc ggc tcc gtc atc ggc ggg ctt gca gga aat atg acc	499
Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu Ala Gly Asn Met Thr	
120 125 130	
tgg ttg atc gtc ggc cgt gcc gta cag ggc atc ggt ggc ggt gga ctg	547
Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile Gly Gly Gly Gly Leu	
135 140 145	
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Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val Val Pro Ala Arg Glu	
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cgt ggc cgc tac atg ggt gtc atg ggt gga gtc ttc gga ctc tct gca	643
Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val Phe Gly Leu Ser Ala	
170 175 180	
gtt ctt ggc cca cta ctc ggt ggc tgg ttc acc gaa gga cca ggc tgg	691
Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Glu Gly Pro Gly Trp	
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Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly Ile Ile Ala Ile Gly	
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gtc gcc att tac ttc ctg gac att cca aag aag agc gtc aag ttc cgc	787
Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys Ser Val Lys Phe Arg	
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Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val Ala Ala Thr Ser Leu	
230 235 240 245	
atc ctg ttc acc acc tgg ggt gga tcc cag tac gag tgg tct gat cca	883
Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr Glu Trp Ser Asp Pro	
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atc atc att gga ctg atc atc acc acc atc gtt gcc gct gca ctg ctg	931
Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val Ala Ala Leu Leu	
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Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu Val Pro Met Ser Phe	

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ggt atc gca atg ttc ggc atc atc ggc tac ctt ccg acc tac ctc cag Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu Pro Thr Tyr Leu Gln 310 315 320 325			1075
atg gtc cac gga atc aac gcc acc gaa gcc ggc tac atg ctg atc cca Met Val His Gly Ile Asn Ala Thr Glu Ala Gly Tyr Met Leu Ile Pro 330 335 340			1123
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cta gcc atg cag gtt ctg gtc ctg atc gtt cag aac acc ctg cca acc Leu Ala Met Gln Val Leu Val Leu Ile Val Gln Asn Thr Leu Pro Thr 410 415 420			1363
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aac gaa ttg acg ccg gca atc gtc aat caa ttg cca acc gcg ctc cac Asn Glu Leu Thr Pro Ala Ile Val Asn Gln Leu Pro Thr Ala Leu His 490 495 500			1603
gat gcg ttc gcc ggt tcc tac aac gac gca ctc atc cca gtg ttc tac Asp Ala Phe Ala Gly Ser Tyr Asn Asp Ala Leu Ile Pro Val Phe Tyr 505 510 515			1651

gtg atg atg cca ctg atc ggc atc gcg ctg ctt ctc ttg ctg ttt att 1699
 Val Met Met Pro Leu Ile Gly Ile Ala Leu Leu Leu Leu Leu Phe Ile
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cct 1755

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 35 40 45

Ala Leu Met Val Ala Met Met Met Ala Ser Leu Asp Gln Met Ile Phe
 50 55 60

Gly Thr Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asp His
 65 70 75 80

Met Met Trp Val Ile Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu
 85 90 95

Pro Ile Tyr Gly Lys Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe
 100 105 110

Ile Gly Ala Leu Gly Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu
 115 120 125

Ala Gly Asn Met Thr Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile
 130 135 140

Gly Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val
 145 150 155 160

Val Pro Ala Arg Glu Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val
 165 170 175

Phe Gly Leu Ser Ala Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr
 180 185 190

Glu Gly Pro Gly Trp Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly
 195 200 205

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Ile Ile Ala Ile Gly Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys
210                               215                               220

Ser Val Lys Phe Arg Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val
225                               230                               235                               240

Ala Ala Thr Ser Leu Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr
245                               250                               255

Glu Trp Ser Asp Pro Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val
260                               265                               270

Ala Ala Ala Leu Leu Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu
275                               280                               285

Val Pro Met Ser Phe Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile
290                               295                               300

Ala Gly Leu Ile Leu Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu
305                               310                               315                               320

Pro Thr Tyr Leu Gln Met Val His Gly Ile Asn Ala Thr Glu Ala Gly
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Tyr Met Leu Ile Pro Met Met Val Gly Met Met Gly Thr Ser Ile Trp
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Thr Gly Ile Arg Ile Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro
355                               360                               365

Ile Gly Met Val Val Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met
370                               375                               380

Glu Val Ser Thr Thr Leu Trp Gln Ile Gly Ile Tyr Leu Phe Val Leu
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Gly Val Gly Leu Gly Leu Ala Met Gln Val Leu Val Leu Ile Val Gln
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Asn Thr Leu Pro Thr Ala Val Val Gly Ser Ala Thr Ala Val Asn Asn
420                               425                               430

Phe Phe Arg Gln Ile Gly Ser Ser Leu Gly Ser Ala Leu Val Gly Gly
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Met Phe Val Gly Asn Leu Gly Thr Leu Met Glu Glu Arg Met Pro Ala
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Ala Met Ala Gln Leu Ser Pro Glu Glu Gln Ala Ala Met Ala Ala Gln
465                               470                               475                               480

Gly Gly Leu Asp Ser Asn Glu Leu Thr Pro Ala Ile Val Asn Gln Leu
485                               490                               495

Pro Thr Ala Leu His Asp Ala Phe Ala Gly Ser Tyr Asn Asp Ala Leu
500                               505                               510

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 Met Thr His Glu Thr
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 Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala Gly Asp Thr Lys Leu
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 cgc aaa ggc cgc gcg aag aag gaa aaa act cct tca tca atg acg cct 211
 Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro Ser Ser Met Thr Pro
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 gaa caa caa aag aaa gtc tgg tgg gtc ctc agc gcg ctg atg gtc gcc 259
 Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser Ala Leu Met Val Ala
 40 45 50
 atg atg atg gcc tcc ctt gac cag atg att ttc ggc aca gcc ctg cca 307
 Met Met Met Ala Ser Leu Asp Gln Met Ile Phe Gly Thr Ala Leu Pro
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 aca atc gtc ggt gaa ctc ggc ggc gtt gac cac atg atg tgg gtc atc 355
 Thr Ile Val Gly Glu Leu Gly Gly Val Asp His Met Met Trp Val Ile
 70 75 80 85
 acc gca tac cta ctt gcc gaa acc atc atg ctg ccg atc tac gga aag 403
 Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu Pro Ile Tyr Gly Lys
 90 95 100
 ctc ggc gac ctg gtt gga cgt aaa ggt ctc ttc atc gga gcc ctc ggc 451
 Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe Ile Gly Ala Leu Gly
 105 110 115
 atc ttc ctg atc ggc tcc gtc atc ggc ggg ctt gca gga aat atg acc 499
 Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu Ala Gly Asn Met Thr

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Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile Gly Gly Gly Gly Leu			
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Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val Val Pro Ala Arg Glu			
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cgt ggc cgc tac atg ggt gtc atg ggt gga gtc ttc gga ctc tct gca			643
Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val Phe Gly Leu Ser Ala			
170	175		180
gtt ctt ggc cca cta ctc ggt ggc tgg ttc acc gaa gga cca ggc tgg			691
Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Glu Gly Pro Gly Trp			
185	190		195
cgc tgg gca ttc tgg atg aac atc cca ctg gga atc atc gcc atc ggt			739
Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly Ile Ile Ala Ile Gly			
200	205		210
gtc gcc att tac ttc ctg gac att cca aag aag agc gtc aag ttc cgc			787
Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys Ser Val Lys Phe Arg			
215	220		225
tgg gat tac ctg ggc act ttc ttc atg atc gtt gcc gca acc agc ctg			835
Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val Ala Ala Thr Ser Leu			
230	235	240	245
atc ctg ttc acc acc tgg ggt gga tcc cag tac gag tgg tct gat cca			883
Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr Glu Trp Ser Asp Pro			
250	255		260
atc atc att gga ctg atc atc acc acc atc gtt gcc gct gca ctg ctg			931
Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val Ala Ala Leu Leu			
265	270		275
gtt gtt gtg gaa ctg cgc gca aaa gat cca ttg gtt cca atg tcc ttc			979
Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu Val Pro Met Ser Phe			
280	285		290
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Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile Ala Gly Leu Ile Leu			
295	300		305
ggt atc gca atg ttc ggc atc atc ggc tac ctt ccg acc tac ctc cag			1075
Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu Pro Thr Tyr Leu Gln			
310	315	320	325
atg gtc cac gga atc aac gcc acc gaa gcc ggc tac atg ctg atc cca			1123
Met Val His Gly Ile Asn Ala Thr Glu Ala Gly Tyr Met Leu Ile Pro			
330	335		340
atg atg gtc ggc atg atg ggt acc tcc atc tgg act ggt atc cgc atc			1171
Met Met Val Gly Met Met Gly Thr Ser Ile Trp Thr Gly Ile Arg Ile			
345	350		355

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 Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro Ile Gly Met Val Val
 360 365 370

acc ttc gtg gca ctg atc ttc ttt gcc cga atg gaa gtg tcc acc acc 1267
 Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met Glu Val Ser Thr Thr
 375 380 385

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Ser Ser Met Thr Pro Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser
 35 40 45

Ala Leu Met Val Ala Met Met Met Ala Ser Leu Asp Gln Met Ile Phe
 50 55 60

Gly Thr Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asp His
 65 70 75 80

Met Met Trp Val Ile Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu
 85 90 95

Pro Ile Tyr Gly Lys Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe
 100 105 110

Ile Gly Ala Leu Gly Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu
 115 120 125

Ala Gly Asn Met Thr Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile
 130 135 140

Gly Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val
 145 150 155 160

Val Pro Ala Arg Glu Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val
 165 170 175

Phe Gly Leu Ser Ala Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr
 180 185 190

Glu Gly Pro Gly Trp Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly

195	200	205	
Ile Ile Ala Ile Gly Val	Ala Ile Tyr Phe Leu Asp	Ile Pro Lys Lys	
210	215	220	
Ser Val Lys Phe Arg Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val			
225	230	235	240
Ala Ala Thr Ser Leu Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr			
245	250	255	
Glu Trp Ser Asp Pro Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val			
260	265	270	
Ala Ala Ala Leu Leu Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu			
275	280	285	
Val Pro Met Ser Phe Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile			
290	295	300	
Ala Gly Leu Ile Leu Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu			
305	310	315	320
Pro Thr Tyr Leu Gln Met Val His Gly Ile Asn Ala Thr Glu Ala Gly			
325	330	335	
Tyr Met Leu Ile Pro Met Met Val Gly Met Met Gly Thr Ser Ile Trp			
340	345	350	
Thr Gly Ile Arg Ile Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro			
355	360	365	
Ile Gly Met Val Val Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met			
370	375	380	
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Met Ile Ala Leu Leu Val Ala			
1 5			
gta ttc gcc ttc cag etc aac gcc tcc atg ctg gcg ccg gca ctg gcc 161			

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Thr	Met	Glu	Thr	Glu	Leu	Asn	Ala	Thr	Ala	Ala	Gln	Ile	Gly	Met	Thr		
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cag	act	gct	ttc	ttc	acc	gcg	gcg	gcg	ctg	ttt	tcc	ctg	ttc	ctg	cca	257	
Gln	Thr	Ala	Phe	Phe	Thr	Ala	Ala	Ala	Leu	Phe	Ser	Leu	Phe	Leu	Pro		
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cgt	tgg	ggc	gat	ctg	att	ggc	cgc	cgc	aaa	gtg	ctg	gtc	ggc	atg	atg	305	
Arg	Trp	Gly	Asp	Leu	Ile	Gly	Arg	Arg	Lys	Val	Leu	Val	Gly	Met	Met		
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Ile	Val	Thr	Gly	Ile	Gly	Cys	Val	Val	Ala	Ala	Phe	Ala	Pro	Asn	Val		
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acc	atc	ctc	ttc	ctg	ggc	cgc	ctg	att	caa	ggc	gtt	gct	ggc	cca	acc	401	
Thr	Ile	Leu	Phe	Leu	Gly	Arg	Leu	Ile	Gln	Gly	Val	Ala	Gly	Pro	Thr		
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gtg	cca	ctg	tgt	ctg	atc	att	ctg	cgc	cag	cag	gta	acc	aat	gaa	aag	449	
Val	Pro	Leu	Cys	Leu	Ile	Ile	Leu	Arg	Gln	Gln	Val	Thr	Asn	Glu	Lys		
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caa	tat	gcg	cta	ctt	ctc	gga	att	gtt	acc	tct	gtc	aac	ggc	ggc	atc	497	
Gln	Tyr	Ala	Leu	Leu	Leu	Gly	Ile	Val	Thr	Ser	Val	Asn	Gly	Gly	Ile		
	120				125				130						135		
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Phe	Arg	Ser	Ile	Phe	Trp	Val	Met	Ala	Ala	Phe	Cys	Ala	Val	Ala	Ala		
			155					160					165				
ctc	gca	ctg	cct	ttc	agc	gtg	aag	gaa	tcc	acc	gct	gaa	gaa	acc	ccg	641	
Leu	Ala	Leu	Pro	Phe	Ser	Val	Lys	Glu	Ser	Thr	Ala	Glu	Glu	Thr	Pro		
		170					175					180					
aag	atg	gac	tgg	ctt	ggc	gtg	ctg	cca	ctg	gcg	gtg	tcc	att	gga	tct	689	
Lys	Met	Asp	Trp	Leu	Gly	Val	Leu	Pro	Leu	Ala	Val	Ser	Ile	Gly	Ser		
	185					190					195						
ttg	ctc	atg	gct	ttc	aac	gag	gcc	ggc	aaa	ctc	ggc	gcc	gcg	aac	tgg	737	
Leu	Leu	Met	Ala	Phe	Asn	Glu	Ala	Gly	Lys	Leu	Gly	Ala	Ala	Asn	Trp		
	200				205					210					215		
att	ctg	gtg	gtt	gtg	ctg	ttc	atc	atc	ggc	atc	gcc	gga	gtc	atc	ttc	785	
Ile	Leu	Val	Val	Val	Leu	Phe	Ile	Ile	Gly	Ile	Ala	Gly	Val	Ile	Phe		
				220					225					230			
ttc	tac	aac	att	gaa	aag	cgc	gtt	aag	cac	ccg	ctg	gtc	agt	gtt	gaa	833	
Ph	Tyr	Asn	Ile	Glu	Lys	Arg	Val	Lys	His	Pro	Leu	Val	Ser	Val	Glu		

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aca atg acc ggt gta ttc gcc gta atg aat ggt ctg ctg ccc aac ctt Thr Met Thr Gly Val Phe Ala Val Met Asn Gly Leu Leu Pro Asn Leu 265 270 275			929
gcg cag gat gct gcc aac ggt gcc ggc atg tca gcg agc gtg gtg tcc Ala Gln Asp Ala Ala Asn Gly Ala Gly Met Ser Ala Ser Val Val Ser 280 285 290 295			977
tgg tgg aca ctt acc cca tat gcg ctg gct ggc ttg gta ttc ggt cca Trp Trp Thr Leu Thr Pro Tyr Ala Leu Ala Gly Leu Val Phe Gly Pro 300 305 310			1025
atc gcc gga att ctc gcc gga aaa ttt gga tac aag atc gtc ctg caa Ile Ala Gly Ile Leu Ala Gly Lys Phe Gly Tyr Lys Ile Val Leu Gln 315 320 325			1073
att ggt atc gct gcc acc atc atc ggc gtt gcc gga gcc acc ttc tta Ile Gly Ile Ala Ala Thr Ile Ile Gly Val Ala Gly Ala Thr Phe Leu 330 335 340			1121
gtc gga agc acc tcg cat ctc gcg tac ctc ggc atc tcc atc ttc gtg Val Gly Ser Thr Ser His Leu Ala Tyr Leu Gly Ile Ser Ile Phe Val 345 350 355			1169
ggt att acc tat gca ggt att gcc aac atc atg ctc aac ggc ctg ggc Gly Ile Thr Tyr Ala Gly Ile Ala Asn Ile Met Leu Asn Gly Leu Gly 360 365 370 375			1217
atc gtg ctc tcc cct gct aac aac caa ggc tat ctg cct ggc atg aac Ile Val Leu Ser Pro Ala Asn Asn Gln Gly Tyr Leu Pro Gly Met Asn 380 385 390			1265
gca ggt gcc ttc aac cta ggt gca ggt att tcc ttc gcc atc ctc ttc Ala Gly Ala Phe Asn Leu Gly Ala Gly Ile Ser Phe Ala Ile Leu Phe 395 400 405			1313
gca gtt tcc acg gca ttc agt gac aac ggc gga gga tac gcc gca ggc Ala Val Ser Thr Ala Phe Ser Asp Asn Gly Gly Gly Tyr Ala Ala Gly 410 415 420			1361
atg tgg gct ggc gtg atc atc ttg gtc cta gcc ttc ctc tgc tcc ctg Met Trp Ala Gly Val Ile Ile Leu Val Leu Ala Phe Leu Cys Ser Leu 425 430 435			1409
ctg atc cca cgc cca gaa tca atc acc gat aca gtg gca gcc aaa gtc Leu Ile Pro Arg Pro Glu Ser Ile Thr Asp Thr Val Ala Ala Lys Val 440 445 450 455			1457
cag gct gaa gaa gcc gct caa gcc gcc agc taaatccaca aactgaacta Gln Ala Glu Glu Ala Ala Gln Ala Ala Ser 460 465			1507

agg

1510

<210> 258

<211> 465

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

Met Ile Ala Leu Leu Val Ala Val Phe Ala Phe Gln Leu Asn Ala Ser
 1 5 10 15

Met Leu Ala Pro Ala Leu Ala Thr Met Glu Thr Glu Leu Asn Ala Thr
 20 25 30

Ala Ala Gln Ile Gly Met Thr Gln Thr Ala Phe Phe Thr Ala Ala Ala
 35 40 45

Leu Phe Ser Leu Phe Leu Pro Arg Trp Gly Asp Leu Ile Gly Arg Arg
 50 55 60

Lys Val Leu Val Gly Met Met Ile Val Thr Gly Ile Gly Cys Val Val
 65 70 75 80

Ala Ala Phe Ala Pro Asn Val Thr Ile Leu Phe Leu Gly Arg Leu Ile
 85 90 95

Gln Gly Val Ala Gly Pro Thr Val Pro Leu Cys Leu Ile Ile Leu Arg
 100 105 110

Gln Gln Val Thr Asn Glu Lys Gln Tyr Ala Leu Leu Leu Gly Ile Val
 115 120 125

Thr Ser Val Asn Gly Gly Ile Gly Gly Val Asp Ala Leu Ala Gly Gly
 130 135 140

Trp Leu Ala Glu Thr Leu Gly Phe Arg Ser Ile Phe Trp Val Met Ala
 145 150 155 160

Ala Phe Cys Ala Val Ala Ala Leu Ala Leu Pro Phe Ser Val Lys Glu
 165 170 175

Ser Thr Ala Glu Glu Thr Pro Lys Met Asp Trp Leu Gly Val Leu Pro
 180 185 190

Leu Ala Val Ser Ile Gly Ser Leu Leu Met Ala Phe Asn Glu Ala Gly
 195 200 205

Lys Leu Gly Ala Ala Asn Trp Ile Leu Val Val Val Leu Phe Ile Ile
 210 215 220

Gly Ile Ala Gly Val Ile Phe Phe Tyr Asn Ile Glu Lys Arg Val Lys
 225 230 235 240

His Pro Leu Val Ser Val Glu Tyr Leu Gly Gln Arg Arg Thr Trp Ala
 245 250 255

Leu Leu Leu Ser Thr Leu Leu Thr Met Thr Gly Val Phe Ala Val Met
 260 265 270
 Asn Gly Leu Leu Pro Asn Leu Ala Gln Asp Ala Ala Asn Gly Ala Gly
 275 280 285
 Met Ser Ala Ser Val Val Ser Trp Trp Thr Leu Thr Pro Tyr Ala Leu
 290 295 300
 Ala Gly Leu Val Phe Gly Pro Ile Ala Gly Ile Leu Ala Gly Lys Phe
 305 310 315 320
 Gly Tyr Lys Ile Val Leu Gln Ile Gly Ile Ala Ala Thr Ile Ile Gly
 325 330 335
 Val Ala Gly Ala Thr Phe Leu Val Gly Ser Thr Ser His Leu Ala Tyr
 340 345 350
 Leu Gly Ile Ser Ile Phe Val Gly Ile Thr Tyr Ala Gly Ile Ala Asn
 355 360 365
 Ile Met Leu Asn Gly Leu Gly Ile Val Leu Ser Pro Ala Asn Asn Gln
 370 375 380
 Gly Tyr Leu Pro Gly Met Asn Ala Gly Ala Phe Asn Leu Gly Ala Gly
 385 390 395 400
 Ile Ser Phe Ala Ile Leu Phe Ala Val Ser Thr Ala Phe Ser Asp Asn
 405 410 415
 Gly Gly Gly Tyr Ala Ala Gly Met Trp Ala Gly Val Ile Ile Leu Val
 420 425 430
 Leu Ala Phe Leu Cys Ser Leu Leu Ile Pro Arg Pro Glu Ser Ile Thr
 435 440 445
 Asp Thr Val Ala Ala Lys Val Gln Ala Glu Glu Ala Ala Gln Ala Ala
 450 455 460
 Ser
 465

<210> 259

<211> 1470

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1447)

<223> RXA02087

<400> 259

aatcggtatc atgctgtgtg gtgtgatcag ttgctggct gcggtcgcat ggatcttcgg 60

ccgggagacg	ctgccaacgg	cgaaagtcga	gcaggtataa	atg	acg	cca	att	gtg	115							
				Met	Thr	Pro	Ile	Val								
				1				5								
gag	tcc	agg	gcg	tgg	aaa	gct	ctg	ggc	gct	tta	agt	gtt	ggg	ctg	ttt	163
Glu	Ser	Arg	Ala	Trp	Lys	Ala	Leu	Gly	Ala	Leu	Ser	Val	Gly	Leu	Phe	
			10					15						20		
ctc	aca	ctg	ctt	gac	caa	tcg	ttg	gtg	gct	gtc	gcg	ctg	cca	aag	att	211
Leu	Thr	Leu	Leu	Asp	Gln	Ser	Leu	Val	Ala	Val	Ala	Leu	Pro	Lys	Ile	
			25					30					35			
caa	gag	gat	ttg	ggc	gcg	agc	ctg	aac	caa	gcg	gtg	tgg	gtg	tca	gcg	259
Gln	Glu	Asp	Leu	Gly	Ala	Ser	Leu	Asn	Gln	Ala	Val	Trp	Val	Ser	Ala	
		40					45					50				
gtt	tat	ttg	ctc	act	ttt	gcg	gtg	cca	ctg	ttg	att	act	ggg	cgc	ttg	307
Val	Tyr	Leu	Leu	Thr	Phe	Ala	Val	Pro	Leu	Leu	Ile	Thr	Gly	Arg	Leu	
	55					60					65					
ggc	gat	cgt	tat	gga	cag	cga	aat	att	tat	ctt	gcc	ggc	atg	gct	gtg	355
Gly	Asp	Arg	Tyr	Gly	Gln	Arg	Asn	Ile	Tyr	Leu	Ala	Gly	Met	Ala	Val	
70					75					80					85	
ttt	acc	ctc	gcg	gcg	ttg	gcc	tgt	gta	ttt	gca	cca	agc	atc	gaa	tgg	403
Phe	Thr	Leu	Ala	Ala	Leu	Ala	Cys	Val	Phe	Ala	Pro	Ser	Ile	Glu	Trp	
			90					95						100		
ttg	att	gct	gct	cgc	gcg	gtg	cag	ggc	ctg	ggc	gga	tct	ctt	ctt	aat	451
Leu	Ile	Ala	Ala	Arg	Ala	Val	Gln	Gly	Leu	Gly	Gly	Ser	Leu	Leu	Asn	
		105						110					115			
ccg	cag	ccc	ctg	agc	atc	att	cac	aag	att	ttc	gcg	cat	gat	cgt	agg	499
Pro	Gln	Pro	Leu	Ser	Ile	Ile	His	Lys	Ile	Phe	Ala	His	Asp	Arg	Arg	
		120					125					130				
gga	gcc	gcc	acc	ggg	gtg	tgg	agt	gct	gtt	gcc	tca	tca	gct	gga	ctt	547
Gly	Ala	Ala	Thr	Gly	Val	Trp	Ser	Ala	Val	Ala	Ser	Ser	Ala	Gly	Leu	
	135					140				145						
ttc	ggg	cca	gtt	atc	ggc	ggc	gtt	ctg	gtg	ggg	tgg	atc	agc	tgg	cgt	595
Phe	Gly	Pro	Val	Ile	Gly	Gly	Val	Leu	Val	Gly	Trp	Ile	Ser	Trp	Arg	
150					155					160				165		
gct	gtg	ttc	ttg	gtt	tat	gtg	ccg	ctc	gga	ttg	atc	tcc	cta	ttt	atg	643
Ala	Val	Phe	Leu	Val	Tyr	Val	Pro	Leu	Gly	Leu	Ile	Ser	Leu	Phe	Met	
			170						175					180		
gtg	gcg	cgt	tat	gtg	cct	aaa	ctt	ccc	acg	gga	acc	tcg	aag	atc	gat	691
Val	Ala	Arg	Tyr	Val	Pro	Lys	Leu	Pro	Thr	Gly	Thr	Ser	Lys	Ile	Asp	
			185					190					195			
tgg	ctc	tcg	ggc	gcg	gtc	tca	ctt	gtt	gct	gta	ctt	ggc	gtg	gtt	ctt	739
Trp	Leu	Ser	Gly	Ala	Val	Ser	Leu	Val	Ala	Val	Leu	Gly	Val	Val	Leu	
	200						205					210				
gcc	ttg	cag	cag	ggg	cca	gaa	ctt	ggg	tgg	gga	aca	ctg	att	tgg	gtg	787

Ala Leu Gln Gln Gly Pro Glu Leu Gly Trp Gly Thr Leu Ile Trp Val	
215 220 225	
tcc ctt gcc gtt ggt att gct gca gct gtg ctc ttt ata tgg atg caa	835
Ser Leu Ala Val Gly Ile Ala Ala Ala Val Leu Phe Ile Trp Met Gln	
230 235 240 245	
aca aga tcc aag gcg cca ctg atg ccg ttg agg att ttc aag acg cgc	883
Thr Arg Ser Lys Ala Pro Leu Met Pro Leu Arg Ile Phe Lys Thr Arg	
250 255 260	
aac ttc gcg atc ggt gca ttt tcg atc ttc agc ctg ggc ttt acg gtg	931
Asn Phe Ala Ile Gly Ala Phe Ser Ile Phe Ser Leu Gly Phe Thr Val	
265 270 275	
tat tcc gtt aat ttg ccc atc atg ttg tat ctg caa acg gct cag gga	979
Tyr Ser Val Asn Leu Pro Ile Met Leu Tyr Leu Gln Thr Ala Gln Gly	
280 285 290	
atg tcg tcg cag ttg gcc ggt ttg atg ttg gtt ccg atg ggc atc atc	1027
Met Ser Ser Gln Leu Ala Gly Leu Met Leu Val Pro Met Gly Ile Ile	
295 300 305	
tct gtg gtg atg tca cca gta att gga cga ttg gtg gat cgc ctg gca	1075
Ser Val Val Met Ser Pro Val Ile Gly Arg Leu Val Asp Arg Leu Ala	
310 315 320 325	
cca gga atg atc tcc aag atc gga ttc ggc gcg ctg att ttc tcg atg	1123
Pro Gly Met Ile Ser Lys Ile Gly Phe Gly Ala Leu Ile Phe Ser Met	
330 335 340	
gcg ttg atg gct gtc ttt atg atc gcc aac cta tcg ccg tgg tgg cta	1171
Ala Leu Met Ala Val Phe Met Ile Ala Asn Leu Ser Pro Trp Trp Leu	
345 350 355	
ctc atc ccg att att ttg ttc ggt agc tcc aac gcg atg agt ttt gca	1219
Leu Ile Pro Ile Ile Leu Phe Gly Ser Ser Asn Ala Met Ser Phe Ala	
360 365 370	
ccg aac tct gtg att gct ctg cgt gat gtt ccg cag gat tta gtg ggc	1267
Pro Asn Ser Val Ile Ala Leu Arg Asp Val Pro Gln Asp Leu Val Gly	
375 380 385	
tct gct tct ggt ttt tac aac acc tca cgc cag gtg ggc gct gtt ttg	1315
Ser Ala Ser Gly Phe Tyr Asn Thr Ser Arg Gln Val Gly Ala Val Leu	
390 395 400 405	
ggc gcc gct acc ttg ggc gct gtg atg caa ata gga gtg ggc acg gtg	1363
Gly Ala Ala Thr Leu Gly Ala Val Met Gln Ile Gly Val Gly Thr Val	
410 415 420	
tcc ttc ggt gtt gcc atg ggt gcg gca atc ctg gtg aca ctc gtg ccc	1411
Ser Phe Gly Val Ala Met Gly Ala Ala Ile Leu Val Thr Leu Val Pro	
425 430 435	
tta atc ttt ggg ttc cta gcg gta acc caa ttt aga tagttgctcc	1457
Leu Ile Phe Gly Phe Leu Ala Val Thr Gln Phe Arg	

440

445

gattttctca cga

1470

<210> 260

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

Met Thr Pro Ile Val Glu Ser Arg Ala Trp Lys Ala Leu Gly Ala Leu
 1 5 10 15

Ser Val Gly Leu Phe Leu Thr Leu Leu Asp Gln Ser Leu Val Ala Val
 20 25 30

Ala Leu Pro Lys Ile Gln Glu Asp Leu Gly Ala Ser Leu Asn Gln Ala
 35 40 45

Val Trp Val Ser Ala Val Tyr Leu Leu Thr Phe Ala Val Pro Leu Leu
 50 55 60

Ile Thr Gly Arg Leu Gly Asp Arg Tyr Gly Gln Arg Asn Ile Tyr Leu
 65 70 75 80

Ala Gly Met Ala Val Phe Thr Leu Ala Ala Leu Ala Cys Val Phe Ala
 85 90 95

Pro Ser Ile Glu Trp Leu Ile Ala Ala Arg Ala Val Gln Gly Leu Gly
 100 105 110

Gly Ser Leu Leu Asn Pro Gln Pro Leu Ser Ile Ile His Lys Ile Phe
 115 120 125

Ala His Asp Arg Arg Gly Ala Ala Thr Gly Val Trp Ser Ala Val Ala
 130 135 140

Ser Ser Ala Gly Leu Phe Gly Pro Val Ile Gly Gly Val Leu Val Gly
 145 150 155 160

Trp Ile Ser Trp Arg Ala Val Phe Leu Val Tyr Val Pro Leu Gly Leu
 165 170 175

Ile Ser Leu Phe Met Val Ala Arg Tyr Val Pro Lys Leu Pro Thr Gly
 180 185 190

Thr Ser Lys Ile Asp Trp Leu Ser Gly Ala Val Ser Leu Val Ala Val
 195 200 205

Leu Gly Val Val Leu Ala Leu Gln Gln Gly Pro Glu Leu Gly Trp Gly
 210 215 220

Thr Leu Ile Trp Val Ser Leu Ala Val Gly Ile Ala Ala Ala Val Leu
 225 230 235 240

Phe Ile Trp Met Gln Thr Arg Ser Lys Ala Pro Leu Met Pro Leu Arg

245										250					255				
Ile	Phe	Lys	Thr	Arg	Asn	Phe	Ala	Ile	Gly	Ala	Phe	Ser	Il	Phe	Ser				
			260					265					270						
Leu	Gly	Phe	Thr	Val	Tyr	Ser	Val	Asn	Leu	Pro	Ile	Met	Leu	Tyr	Leu				
		275					280					285							
Gln	Thr	Ala	Gln	Gly	Met	Ser	Ser	Gln	Leu	Ala	Gly	Leu	Met	Leu	Val				
	290					295					300								
Pro	Met	Gly	Ile	Ile	Ser	Val	Val	Met	Ser	Pro	Val	Ile	Gly	Arg	Leu				
305					310				315						320				
Val	Asp	Arg	Leu	Ala	Pro	Gly	Met	Ile	Ser	Lys	Ile	Gly	Phe	Gly	Ala				
			325					330						335					
Leu	Ile	Phe	Ser	Met	Ala	Leu	Met	Ala	Val	Phe	Met	Ile	Ala	Asn	Leu				
		340					345						350						
Ser	Pro	Trp	Trp	Leu	Leu	Ile	Pro	Ile	Ile	Leu	Phe	Gly	Ser	Ser	Asn				
	355					360						365							
Ala	Met	Ser	Phe	Ala	Pro	Asn	Ser	Val	Ile	Ala	Leu	Arg	Asp	Val	Pro				
370						375					380								
Gln	Asp	Leu	Val	Gly	Ser	Ala	Ser	Gly	Phe	Tyr	Asn	Thr	Ser	Arg	Gln				
385					390				395						400				
Val	Gly	Ala	Val	Leu	Gly	Ala	Ala	Thr	Leu	Gly	Ala	Val	Met	Gln	Ile				
			405					410						415					
Gly	Val	Gly	Thr	Val	Ser	Phe	Gly	Val	Ala	Met	Gly	Ala	Ala	Ile	Leu				
		420					425					430							
Val	Thr	Leu	Val	Pro	Leu	Ile	Phe	Gly	Phe	Leu	Ala	Val	Thr	Gln	Phe				
	435					440					445								

Arg

<210> 261

<211> 1338

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1315)

<223> RXA02088

<400> 261

agagcaccca agcgacattg ttcgataata tgttctatta ttggtattaa tactgggtcag 60

ctagatataa aaggggcgca gggctagcct tgggtgtgaa atg tta act caa aaa 115
Met Leu Thr Gln Lys

	1	5	
ata gaa tta gag gct aaa cca aaa atc cca gag gag atc tgg gtg ctg			163
Ile Glu Leu Glu Ala Lys Pro Lys Ile Pro Glu Glu Ile Trp Val Leu			
	10	15	20
gtt gtg gct gcg ttt att att gcg ctg ggc tat ggc ctg att gcg ccg			211
Val Val Ala Ala Phe Ile Ile Ala Leu Gly Tyr Gly Leu Ile Ala Pro			
	25	30	35
att ttg cca cag ttt gtg gtc ggt ttt gat gta agt ttt gca gct gcc			259
Il Leu Pro Gln Phe Val Val Gly Phe Asp Val Ser Phe Ala Ala Ala			
	40	45	50
agt gcg gtg gtg tcc atc ttt gcg ggc gcc cgg ttg ttg ttt gcg ccg			307
Ser Ala Val Val Ser Ile Phe Ala Gly Ala Arg Leu Leu Phe Ala Pro			
	55	60	65
atg tcg ggg agt ttg atc gat aag atc ggt tcc cgt cgt gtg tat ctc			355
Met Ser Gly Ser Leu Ile Asp Lys Ile Gly Ser Arg Arg Val Tyr Leu			
	70	75	80
act ggt tta ctc acc gtg gct atc acc acg ggg ctt gtt gcg ttg gcg			403
Thr Gly Leu Leu Thr Val Ala Ile Thr Thr Gly Leu Val Ala Leu Ala			
	90	95	100
cag gaa tac tgg cag att ctg ctg ctt cgt ggc atc gca ggt att ggt			451
Gln Glu Tyr Trp Gln Ile Leu Leu Arg Gly Ile Ala Gly Ile Gly			
	105	110	115
tcc acc atg ttt acg gtc tct gcc atg ggc ctg atc gtg aag atg gcg			499
Ser Thr Met Phe Thr Val Ser Ala Met Gly Leu Ile Val Lys Met Ala			
	120	125	130
ccg gtg gag atc cgc ggg cgg tgt tcg tcg gta tat gcc agt tcg ttc			547
Pro Val Glu Ile Arg Gly Arg Cys Ser Ser Val Tyr Ala Ser Ser Phe			
	135	140	145
ctg ttt ggc aat att att ggc ccg gtt gtg ggt gct gcg atg tcc ggt			595
Leu Phe Gly Asn Ile Ile Gly Pro Val Val Gly Ala Ala Met Ser Gly			
	150	155	160
ttg ggc atg cgg tgg ccg ttc gcg att tat ggt gct tcc gtt ggc tta			643
Leu Gly Met Arg Trp Pro Phe Ala Ile Tyr Gly Ala Ser Val Gly Leu			
	170	175	180
gct gca ctt gtt gtg tgg tgg cgg atg ccg aaa acc aac gat tca ctt			691
Ala Ala Leu Val Val Trp Trp Arg Met Pro Lys Thr Asn Asp Ser Leu			
	185	190	195
cgg aag gct gat agc aat agt gtg ccg gcg ttg cgc ttt gct gag gca			739
Arg Lys Ala Asp Ser Asn Ser Val Pro Ala Leu Arg Phe Ala Glu Ala			
	200	205	210
att aag gat tct gcc tac cgc tcg gcg ttg ttt agt gct ttt gcc aat			787
Ile Lys Asp Ser Ala Tyr Arg Ser Ala Leu Phe Ser Ala Phe Ala Asn			
	215	220	225

ggt tgg tcg aac ttt ggt gtg cgt gtg gcg gtt ctt cca ctg ttt gcc 835
 Gly Trp Ser Asn Phe Gly Val Arg Val Ala Val Leu Pro Leu Phe Ala 245
 230 235 240

gca gct gca ttt agc aat ggc gga gct att gcg ggt ttt gcc atg gct 883
 Ala Ala Ala Phe Ser Asn Gly Gly Ala Ile Ala Gly Phe Ala Met Ala 260
 250 255

gcg ttc gcc gct gga aat gct ttg tgt ctg caa ttc gcg ggc gat ctc 931
 Ala Phe Ala Ala Gly Asn Ala Leu Cys Leu Gln Phe Ala Gly Asp Leu 275
 265 270

tca gat cgc att ggc cgt aaa ccg atg att att tcc ggg ctg atc gtc 979
 Ser Asp Arg Ile Gly Arg Lys Pro Met Ile Ile Ser Gly Leu Ile Val 290
 280 285

aat gca gtg ttc acg gca atg atc gga ttc ggc aca gaa gtg tgg atc 1027
 Asn Ala Val Phe Thr Ala Met Ile Gly Phe Gly Thr Glu Val Trp Ile 305
 295 300

ctg atc acg gta tct gcg ttg gca ggt gct ggt gcg ggc ttg ctt aat 1075
 Leu Ile Thr Val Ser Ala Leu Ala Gly Ala Gly Ala Gly Leu Leu Asn 325
 310 315 320

cca agt cag cag gcg gtg ctc gct gat gtt ata gat tcc cgc ccc ggc 1123
 Pro Ser Gln Gln Ala Val Leu Ala Asp Val Ile Asp Ser Arg Pro Gly 340
 330 335

gga aaa gtc tta gcg aat ttc caa atg gcg cag gat ttc ggt gcg att 1171
 Gly Lys Val Leu Ala Asn Phe Gln Met Ala Gln Asp Phe Gly Ala Ile 355
 345 350

gtt ggc ccg att ctc gta ggc atg atc gca gaa cag gca ggc ttc caa 1219
 Val Gly Pro Ile Leu Val Gly Met Ile Ala Glu Gln Ala Gly Phe Gln 370
 360 365

atc gga ttc atg ctg tgt ggt gtg atc agt ttg ctg gct gcg gtc gca 1267
 Ile Gly Phe Met Leu Cys Gly Val Ile Ser Leu Leu Ala Ala Val Ala 385
 375 380

tgg atc ttc ggc cgg gag acg ctg cca acg gcg aaa gtc gag cag gta 1315
 Trp Ile Phe Gly Arg Glu Thr Leu Pro Thr Ala Lys Val Glu Gln Val 405
 390 395 400

taaatgacgc caattgtgga gtc 1338

<210> 262

<211> 405

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Leu Thr Gln Lys Ile Glu Leu Glu Ala Lys Pro Lys Ile Pro Glu
 1 5 10 15

Glu Ile Trp Val Leu Val Val Ala Ala Phe Ile Il Ala Leu Gly Tyr
 20 25 30
 Gly Leu Ile Ala Pro Ile Leu Pro Gln Phe Val Val Gly Ph Asp Val
 35 40 45
 Ser Phe Ala Ala Ala Ser Ala Val Val Ser Ile Phe Ala Gly Ala Arg
 50 55 60
 Leu Leu Phe Ala Pro Met Ser Gly Ser Leu Ile Asp Lys Ile Gly Ser
 65 70 75 80
 Arg Arg Val Tyr Leu Thr Gly Leu Leu Thr Val Ala Ile Thr Thr Gly
 85 90 95
 Leu Val Ala Leu Ala Gln Glu Tyr Trp Gln Ile Leu Leu Leu Arg Gly
 100 105 110
 Ile Ala Gly Ile Gly Ser Thr Met Phe Thr Val Ser Ala Met Gly Leu
 115 120 125
 Ile Val Lys Met Ala Pro Val Glu Ile Arg Gly Arg Cys Ser Ser Val
 130 135 140
 Tyr Ala Ser Ser Phe Leu Phe Gly Asn Ile Ile Gly Pro Val Val Gly
 145 150 155 160
 Ala Ala Met Ser Gly Leu Gly Met Arg Trp Pro Phe Ala Ile Tyr Gly
 165 170 175
 Ala Ser Val Gly Leu Ala Ala Leu Val Val Trp Trp Arg Met Pro Lys
 180 185 190
 Thr Asn Asp Ser Leu Arg Lys Ala Asp Ser Asn Ser Val Pro Ala Leu
 195 200 205
 Arg Phe Ala Glu Ala Ile Lys Asp Ser Ala Tyr Arg Ser Ala Leu Phe
 210 215 220
 Ser Ala Phe Ala Asn Gly Trp Ser Asn Phe Gly Val Arg Val Ala Val
 225 230 235 240
 Leu Pro Leu Phe Ala Ala Ala Ala Phe Ser Asn Gly Gly Ala Ile Ala
 245 250 255
 Gly Phe Ala Met Ala Ala Phe Ala Ala Gly Asn Ala Leu Cys Leu Gln
 260 265 270
 Phe Ala Gly Asp Leu Ser Asp Arg Ile Gly Arg Lys Pro Met Ile Ile
 275 280 285
 Ser Gly Leu Ile Val Asn Ala Val Phe Thr Ala Met Ile Gly Phe Gly
 290 295 300
 Thr Glu Val Trp Ile Leu Ile Thr Val Ser Ala Leu Ala Gly Ala Gly
 305 310 315 320

Ala Gly Leu Leu Asn Pro Ser Gln Gln Ala Val Leu Ala Asp Val Ile
 325 330 335

Asp Ser Arg Pro Gly Gly Lys Val Leu Ala Asn Phe Gln Met Ala Gln
 340 345 350

Asp Phe Gly Ala Ile Val Gly Pro Ile Leu Val Gly Met Ile Ala Glu
 355 360 365

Gln Ala Gly Phe Gln Ile Gly Phe Met Leu Cys Gly Val Ile Ser Leu
 370 375 380

Leu Ala Ala Val Ala Trp Ile Phe Gly Arg Glu Thr Leu Pro Thr Ala
 385 390 395 400

Lys Val Glu Gln Val
 405

<210> 263
 <211> 1239
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1216)
 <223> RXA00764

<400> 263
 tactgcgtcg gatccgctga tgcttgcaga atcggacagt gatgggccgt ctgcgcctgc 60

acctgggacg actggattat taggggtgga attttcgctc atg aca ctc aag act 115
 Met Thr Leu Lys Thr
 1 5

agc gtt ttg gca cta ctc tta gat aac gtg cat gtt ctt ctg att gcg 163
 Ser Val Leu Ala Leu Leu Leu Asp Asn Val His Val Leu Leu Ile Ala
 10 15 20

aat cct gag tcg acc acg cag acg cag aaa ctt ttc cgt cgt gtg gtg 211
 Asn Pro Glu Ser Thr Thr Gln Thr Gln Lys Leu Phe Arg Arg Val Val
 25 30 35

cct gcg ttg atg gcg ctt gat ggt gtg tcg ctt gaa gcg agg ttt acg 259
 Pro Ala Leu Met Ala Leu Asp Gly Val Ser Leu Glu Ala Arg Phe Thr
 40 45 50

cac tat gga ggc cat gcg gag gaa atg gtt gcg ggt ttg acg gtg gat 307
 His Tyr Gly Gly His Ala Glu Glu Met Val Ala Gly Leu Thr Val Asp
 55 60 65

gat ttt gat gtg att atc ccc gcg ggt ggg gac ggc acc gtc aac gaa 355
 Asp Phe Asp Val Ile Ile Pro Ala Gly Gly Asp Gly Thr Val Asn Glu
 70 75 80 85

gtg ata aat ggg tta ctt ggg tcg gcg gaa ggt gat ttt aga aac ctt 403

365

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Thr Lys Val Val Leu Glu Ser Ile Thr Asp Ala Val Arg Val Tyr Ala				
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Pro Lys Thr His Pro Thr Pro Pro Ile Met Asn Trp Ala Val His Leu				
	345	350	355	
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Phe Lys His Val Arg Asp Phe Leu Arg Val Arg Thr Phe Gly Ile				
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Phe Arg Arg Val Val Pro Ala Leu Met Ala Leu Asp Gly Val Ser Leu				
	35	40	45	
Glu Ala Arg Phe Thr His Tyr Gly Gly His Ala Glu Glu Met Val Ala				
	50	55	60	
Gly Leu Thr Val Asp Asp Phe Asp Val Ile Ile Pro Ala Gly Gly Asp				
	65	70	75	80
Gly Thr Val Asn Glu Val Ile Asn Gly Leu Leu Gly Ser Ala Glu Gly				
	85	90	95	
Asp Phe Arg Asn Leu Glu Asp Leu Pro Ala Ile Ala Val Leu Pro Thr				
	100	105	110	
Gly Ser Ala Asn Val Phe Ala Arg Ala Leu Gly Tyr Pro Thr Asp Pro				
	115	120	125	
Tyr Ala Ala Ala Asp Ala Leu Val Glu Leu Ile Arg Lys Asn His Thr				
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Arg Thr Ile Thr Leu Gly Thr Trp Lys Gly Asp Asp Gln Gly Thr Arg				
	145	150	155	160
Trp Phe Ala Val Asn Ala Gly Phe Gly Ile Asp Ala Asp Val Ile Ala				
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                                   1           5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tqg qtc cca ttg atc gcg 163

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                                     Met Thr Val Gln Glu
                                     1                               5

ttc gac cgc gcg acc aaa ccc aca cca aaa ccc cca att gtt tct tgg 163
Phe Asp Arg Ala Thr Lys Pro Thr Pro Lys Pro Pro Ile Val Ser Trp
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gcg ttt tgg gat tgg ggt tcc gcc tct ttc aac gcg gtc ctc gtg acc 211

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Glu	Gly	Ser	Asn	Ala	Thr	Ser	Leu	Tyr	Ser	Met	Ala	Val	Ala	Ile	Ala		
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Gly	Val	Ile	Val	Ala	Val	Val	Ala	Pro	Val	Met	Gly	Arg	Arg	Ser	Asp		
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Ile	Lys	Gly	Thr	Arg	Arg	Arg	Ser	Leu	Arg	Met	Trp	Thr	Leu	Val	Thr		
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Val	Phe	Leu	Met	Phe	Cys	Leu	Phe	Thr	Val	Lys	Asn	Thr	Asp	Pro	Thr		
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Phe	Phe	Trp	Phe	Gly	Val	Ala	Ile	Met	Ala	Ile	Ala	Asn	Ile	Thr	Phe		
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gag	ttc	gct	gaa	gtt	cag	tac	tat	gcg	cag	ctc	tcc	caa	atc	tcg	acc	547	
Glu	Phe	Ala	Glu	Val	Gln	Tyr	Tyr	Ala	Gln	Leu	Ser	Gln	Ile	Ser	Thr		
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cgc	gaa	aac	gtg	ggc	cga	gtt	tct	ggt	ttc	ggc	tgg	tcc	atg	ggt	tac	595	
Arg	Glu	Asn	Val	Gly	Arg	Val	Ser	Gly	Phe	Gly	Trp	Ser	Met	Gly	Tyr		
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Phe	Gly	Gly	Ile	Val	Leu	Leu	Leu	Val	Cys	Tyr	Leu	Gly	Phe	Val	Ala		
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Gly	Asp	Gly	Asp	Thr	Arg	Gly	Phe	Leu	Asn	Leu	Pro	Ile	Glu	Asp	Gly		
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Met	Asn	Ile	Arg	Leu	Val	Ala	Val	Leu	Ala	Ala	Val	Trp	Phe	Leu	Val		
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tct	gcg	att	ccg	gca	ctt	ctt	cga	gtc	cca	gaa	att	gag	gca	cag	gta	787	
Ser	Ala	Ile	Pro	Ala	Leu	Leu	Arg	Val	Pro	Glu	Ile	Glu	Ala	Gln	Val		
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gct	gcc	gaa	gac	cac	ccc	aaa	ggc	ctc	ata	gct	gcc	tac	aag	gat	ctc	835	
Ala	Ala	Glu	Asp	His	Pro	Lys	Gly	Leu	Ile	Ala	Ala	Tyr	Lys	Asp	Leu		
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Thr	Phe	Gly	Ala	Ile	Leu	Ala	Val	Ser	Val	Tyr	Gly	Leu	Ser	Ala	Gly					
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Asp	Val	Leu	Leu	Phe	Gly	Val	Ala	Ala	Asn	Val	Val	Ser	Ala	Leu	Gly					
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Ala	Leu	Leu	Gly	Gly	Phe	Leu	Asp	Asp	Arg	Val	Gly	Pro	Lys	Pro	Ile					
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atc	ttg	att	tct	ctt	gcc	atc	atg	atc	gcc	gat	gct	gca	att	ctc	ttc	1123				
Ile	Leu	Ile	Ser	Leu	Ala	Ile	Met	Ile	Ala	Asp	Ala	Ala	Ile	Leu	Phe					
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Phe	Val	Glu	Gly	Pro	Thr	Asn	Phe	Trp	Ile	Phe	Gly	Leu	Ile	Leu	Cys					
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Ala	Phe	Val	Gly	Pro	Ala	Gln	Ser	Ala	Ser	Arg	Ser	Tyr	Leu	Thr	Arg					
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ctt	tcc	cca	gat	ggc	cag	gaa	ggc	cag	ctc	ttc	ggc	ctt	tat	gcc	act	1267				
Leu	Ser	Pro	Asp	Gly	Gln	Glu	Gly	Gln	Leu	Phe	Gly	Leu	Tyr	Ala	Thr					
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acc	ggc	cgt	gcc	gtg	agt	tgg	atg	gtg	ccg	tcg	ctg	ttt	ggt	gta	ttt	1315				
Thr	Gly	Arg	Ala	Val	Ser	Trp	Met	Val	Pro	Ser	Leu	Phe	Gly	Val	Phe					
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gtg	ggg	ctc	acc	ggc	gat	gac	cgc	act	ggt	att	ttg	gcc	atc	gcg	ctg	1363				
Val	Gly	Leu	Thr	Gly	Asp	Asp	Arg	Thr	Gly	Ile	Leu	Ala	Ile	Ala	Leu					
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Ile	Leu	Leu	Phe	Gly	Ile	Val	Leu	Leu	Ser	Met	Val	Lys	Pro	Pro	His					
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Lys	Val	Lys																		
			440																	

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<212> PRT

<213> Corynebacterium glutamicum

<400> 268

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 35 40 45
 Gly Ala Thr Leu Pro Glu Gly Ser Asn Ala Thr Ser Leu Tyr Ser Met
 50 55 60
 Ala Val Ala Ile Ala Gly Val Ile Val Ala Val Val Ala Pro Val Met
 65 70 75 80
 Gly Arg Arg Ser Asp Ile Lys Gly Thr Arg Arg Arg Ser Leu Arg Met
 85 90 95
 Trp Thr Leu Val Thr Val Phe Leu Met Phe Cys Leu Phe Thr Val Lys
 100 105 110
 Asn Thr Asp Pro Thr Phe Phe Trp Phe Gly Val Ala Ile Met Ala Ile
 115 120 125
 Ala Asn Ile Thr Phe Glu Phe Ala Glu Val Gln Tyr Tyr Ala Gln Leu
 130 135 140
 Ser Gln Ile Ser Thr Arg Glu Asn Val Gly Arg Val Ser Gly Phe Gly
 145 150 155 160
 Trp Ser Met Gly Tyr Phe Gly Gly Ile Val Leu Leu Leu Val Cys Tyr
 165 170 175
 Leu Gly Phe Val Ala Gly Asp Gly Asp Thr Arg Gly Phe Leu Asn Leu
 180 185 190
 Pro Ile Glu Asp Gly Met Asn Ile Arg Leu Val Ala Val Leu Ala Ala
 195 200 205
 Val Trp Phe Leu Val Ser Ala Ile Pro Ala Leu Leu Arg Val Pro Glu
 210 215 220
 Ile Glu Ala Gln Val Ala Ala Glu Asp His Pro Lys Gly Leu Ile Ala
 225 230 235 240
 Ala Tyr Lys Asp Leu Phe Gly Gln Ile Ala Glu Leu Trp Lys Gln Asp
 245 250 255
 Arg Asn Ser Val Tyr Phe Leu Ile Ala Ala Thr Val Phe Arg Asp Gly
 260 265 270
 Leu Ala Gly Val Phe Thr Phe Gly Ala Ile Leu Ala Val Ser Val Tyr
 275 280 285
 Gly Leu Ser Ala Gly Asp Val Leu Leu Phe Gly Val Ala Ala Asn Val
 290 295 300

Val Ser Ala Leu Gly Ala Leu Leu Gly Gly Phe Leu Asp Asp Arg Val
 305 310 315 320

Gly Pro Lys Pro Ile Ile Leu Ile Ser Leu Ala Ile Met Ile Ala Asp
 325 330 335

Ala Ala Ile Leu Phe Phe Val Glu Gly Pro Thr Asn Phe Trp Ile Phe
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Gly Leu Ile Leu Cys Ala Phe Val Gly Pro Ala Gln Ser Ala Ser Arg
 355 360 365

Ser Tyr Leu Thr Arg Leu Ser Pro Asp Gly Gln Glu Gly Gln Leu Phe
 370 375 380

Gly Leu Tyr Ala Thr Thr Gly Arg Ala Val Ser Trp Met Val Pro Ser
 385 390 395 400

Leu Phe Gly Val Phe Val Gly Leu Thr Gly Asp Asp Arg Thr Gly Ile
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Val Lys Pro Pro His Lys Val Lys
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 <223> RXN00535

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 Met Trp Trp Ala Gly
 1 5

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 Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln Thr Val Ala Leu Gly
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 Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu Val Leu Ser Leu Met
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ttc acg ctg ccg ctc tca gca cga ttc aat ggc tac cga cta cgc cga 259
 Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly Tyr Arg Leu Arg Arg
 40 45 50

act gaa atc ttc tgg gct acc ctc ctc acc gta gcc gtg ggc atc atg	307
Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val Ala Val Gly Ile Met	
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atc gtt ttg gga cgc ccc ctt ccc gga aac ccc cac ccc cca ctc gat	355
Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro His Pro Pro Leu Asp	
70 75 80 85	
cga tgg att cca gta ctt tta gtc ggc gtt gca gta atg ggt gga atg	403
Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala Val Met Gly Gly Met	
90 95 100	
tgg ctg ctt gcg gaa tac gta tta aag aag gac aaa gcc ctc atc ctt	451
Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp Lys Ala Leu Ile Leu	
105 110 115	
ggc ctt gtg acg ggt gca ttg ttt ggc tac gta gca gtg atg tcc aaa	499
Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val Ala Val Met Ser Lys	
120 125 130	
gcc gcg gtg gat ctt ttt gtc cat caa ggc ata acg gga ctc atc ttg	547
Ala Ala Val Asp Leu Phe Val His Gln Gly Ile Thr Gly Leu Ile Leu	
135 140 145	
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Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala Leu Leu Gly Thr Ile	
150 155 160 165	
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Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu Gln Lys Ser Leu Pro	
170 175 180	
gcc atg acc att gcc gaa cca att gtt gcc ttc agt ttg ggc tac ttg	691
Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe Ser Leu Gly Tyr Leu	
185 190 195	
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Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp Glu Trp Ile Ala Met	
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Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr Ile Ala Leu Ser Arg	
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Thr Ser Thr Met Pro Ala Gly Ser Lys Arg	
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<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

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 35 40 45
 Tyr Arg Leu Arg Arg Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val
 50 55 60
 Ala Val Gly Ile Met Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro
 65 70 75 80
 His Pro Pro Leu Asp Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala
 85 90 95
 Val Met Gly Gly Met Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp
 100 105 110
 Lys Ala Leu Ile Leu Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val
 115 120 125
 Ala Val Met Ser Lys Ala Ala Val Asp Leu Phe Val His Gln Gly Ile
 130 135 140
 Thr Gly Leu Ile Leu Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala
 145 150 155 160
 Leu Leu Gly Thr Ile Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu
 165 170 175
 Gln Lys Ser Leu Pro Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe
 180 185 190
 Ser Leu Gly Tyr Leu Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp
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<223> RXN00453

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Val Ile Ser Ala Trp 5
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cta ctt att ttg gcc att gtt ggt ggt ctg gcc ctg acg atg cag aag 163
Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala Leu Thr Met Gln Lys 20
10 15

ggg ttc agt aac tct ttc act att gaa gac acc cct tcg att gat gcc 211
Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr Pro Ser Ile Asp Ala 35
25 30

act gtt tct ctg gtt gaa aat ttc cct gat cag acg aac ccg gtg acg 259
Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln Thr Asn Pro Val Thr 50
40 45

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Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro Glu Gly Thr Thr Leu 65
55 60

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Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala Val Val Asp Tyr Ile 85
70 75 80

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Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu Arg Phe Gly Asn Pro 100
90 95

gtt gag gtg tct cct gcg ttg gaa gag atg gtc atc gag cag atg acc 451
Val Glu Val Ser Pro Ala Leu Glu Glu Met Val Ile Glu Gln Met Thr 115
105 110

agc atg ggg ctt cct gag gaa acc gct gca aag gat gct gcc aat ctg 499
Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys Asp Ala Ala Asn Leu 130
120 125

gcg gtg ttg agc gaa gac aaa acc att ggc tac acc tct ttc aac att 547
Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr Thr Ser Phe Asn Ile 145
135 140

gat gtt gag gcc gca gaa tat gtg gag caa aaa cac cgc gat gtg atc 595
Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys His Arg Asp Val Ile 165
150 155 160

aac gaa gcg atg caa atc ggt gaa gat tta ggt gtc cgg gtg gaa gcc 643
Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly Val Arg Val Glu Ala 180
170 175

ggt gga cct gct ttc ggt gat cca att cag att gaa acc acc agt gag 691
Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile Glu Thr Thr Ser Glu 195
185 190

atc atc ggt att ggc atc gcg ttc atc gtg ttg att ttc acc ttt ggt 739
Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu Ile Phe Thr Phe Gly 210
200 205

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cgc atg cca cgt gcc gat gct gcc gga atg gcg gtg ggc aca gct ggt Arg Met Pro Arg Ala Asp Ala Ala Gly Met Ala Val Gly Thr Ala Gly 280 285 290	979
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gga att ggt gga aac cca acg cca aag cag acg tgg gag caa gcg ctt Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr Trp Glu Gln Ala Leu 360 365 370	1219
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ccg ggt ctt gtg gtg gca gtg gtg gtc ttg ggt ctt ggt gcc ttg acc Pro Gly Leu Val Val Ala Val Val Val Leu Gly Leu Gly Ala Leu Thr 390 395 400 405	1315
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aat att gat acc act cag cgt cag tcg gct gat ttg atg gca gag ggc Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp Leu Met Ala Glu Gly 425 430 435	1411

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Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val Ile Val Asp Thr His	
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gag gtc aat gct gat tcc acc gca ttg cag cca ctg att gag gca cag	1507
Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro Leu Ile Glu Ala Gln	
455 460 465	
gag cct gaa gag ggc gag ttc gat cgg gag cag gcg gct cgt ttt gct	1555
Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln Ala Ala Arg Phe Ala	
470 475 480 485	
acc tat atg tat gtc acc cag acc tac aat tcc aac atc gat gtg aag	1603
Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser Asn Ile Asp Val Lys	
490 495 500	
aat gcg cag atc atc agc gtc aat gat gat ttc act gcg gcg cag att	1651
Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe Thr Ala Ala Gln Ile	
505 510 515	
ctc gtg act cca tac acc gga cct gcg gat aaa gag acc cct gag ttg	1699
Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys Glu Thr Pro Glu Leu	
520 525 530	
atg cac gtg ctg cgt gcg cag gaa gct cag att gag gat gtt acg gga	1747
Met His Val Leu Arg Ala Gln Glu Ala Gln Ile Glu Asp Val Thr Gly	
535 540 545	
act gaa ctg ggt acc act ggg ttt acg gcg gtt cag ttg gac att act	1795
Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val Gln Leu Asp Ile Thr	
550 555 560 565	
gag cag ctg gaa gac gca atg ccg gtt tac ctc gct gtg gtt gtt ggt	1843
Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu Ala Val Val Val Gly	
570 575 580	
ttg gct att ttc ctc ctc att ctg gtg ttc cgt tcc ctg ctt gtt ccg	1891
Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg Ser Leu Leu Val Pro	
585 590 595	
ctg gtt gct ggc ctt ggc ttc ttg ttg tct gtg ggt gcg gcc ttc ggt	1939
Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val Gly Ala Ala Phe Gly	
600 605 610	
gcg acg gtg ttg gtc tgg cag gag ggc ttc ggt ggc ttt gtg aac acc	1987
Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly Gly Phe Val Asn Thr	
615 620 625	
cct ggt ccg ctg att tcc ttc atg ccg atc ttc ctc atc ggc gtg acc	2035
Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe Leu Ile Gly Val Thr	
630 635 640 645	
ttc ggt ttg gcc atg gac tat cag gtg ttc ctt gtg act cgc atg cgc	2083
Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu Val Thr Arg Met Arg	
650 655 660	
gag cac tac acc cac cac aat ggc aag gga cag cct ggt tcc aag tac	2131

Glu His Tyr Thr His His Asn Gly Lys Gly Gln Pro Gly Ser Lys Tyr
 665 670 675

acc ccg gtt gag cag tca gtg att gaa ggc ttc acg cag ggc tcc cgc 2179
 Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe Thr Gln Gly Ser Arg
 680 685 690

gtg gtt aca gca gcg gca ctg atc atg att gcc gtg ttc gtg gcg ttt 2227
 Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala Val Phe Val Ala Phe
 695 700 705

att gat cag ccg ttg cca ttt att aag atc ttc ggt ttc gcg ttg ggt 2275
 Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe Gly Phe Ala Leu Gly
 710 715 720 725

gcg ggc gtg ttt ttc gat gct ttc ttc att cgc atg ggt ctg gtc ccc 2323
 Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg Met Gly Leu Val Pro
 730 735 740

gcg tcg atg ttc ctg atg ggc aag gcc acg tgg tgg atg cct aag tgg 2371
 Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp Trp Met Pro Lys Trp
 745 750 755

ctg gat cga att ctg cca agt ttg gac att gaa ggc acc gca ctg gag 2419
 Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu Gly Thr Ala Leu Glu
 760 765 770

aag gaa tgg gag gag aag cag gct gca cgt tagacttggc acctatgtca 2469
 Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg
 775 780

gat 2472

<210> 272

<211> 783

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Val Ile Ser Ala Trp Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala
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Leu Thr Met Gln Lys Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr
 20 25 30

Pro Ser Ile Asp Ala Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln
 35 40 45

Thr Asn Pro Val Thr Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro
 50 55 60

Glu Gly Thr Thr Leu Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala
 65 70 75 80

Val Val Asp Tyr Ile Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu
 85 90 95

Arg Phe Gly Asn Pro Val Glu Val Ser Pro Ala Leu Glu Glu Met Val
 100 105 110
 Ile Glu Gln Met Thr Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys
 115 120 125
 Asp Ala Ala Asn Leu Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr
 130 135 140
 Thr Ser Phe Asn Ile Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys
 145 150 155 160
 His Arg Asp Val Ile Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly
 165 170 175
 Val Arg Val Glu Ala Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile
 180 185 190
 Glu Thr Thr Ser Glu Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu
 195 200 205
 Ile Phe Thr Phe Gly Ser Leu Ile Ala Ala Gly Leu Pro Leu Ile Thr
 210 215 220
 Ala Val Ile Gly Val Gly Ile Gly Ala Leu Ala Ile Val Leu Ala Thr
 225 230 235 240
 Ala Phe Thr Asp Leu Asn Asn Val Thr Pro Val Leu Ala Val Met Ile
 245 250 255
 Gly Leu Ala Val Gly Ile Asp Tyr Ala Leu Phe Ile Leu Ser Arg Tyr
 260 265 270
 Arg Ala Glu Tyr Lys Arg Met Pro Arg Ala Asp Ala Ala Gly Met Ala
 275 280 285
 Val Gly Thr Ala Gly Ser Ala Val Val Phe Ala Gly Ala Thr Val Ile
 290 295 300
 Ile Ala Leu Val Ala Leu Ile Ile Ala Asp Ile Gly Phe Leu Thr Ala
 305 310 315 320
 Met Gly Ile Ser Ala Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala
 325 330 335
 Leu Thr Phe Ile Pro Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe
 340 345 350
 Lys Gly Lys Ile Pro Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr
 355 360 365
 Trp Glu Gln Ala Leu Asn Arg Arg Ser Lys Gly Arg Ser Trp Val Lys
 370 375 380
 Leu Val Gln Lys Ala Pro Gly Leu Val Val Ala Val Val Val Leu Gly
 385 390 395 400

Ala Leu Thr Ile Pro Ala Met Asn Leu Gln Leu Ser Leu Pro
 405 410 415
 Asp Ser Thr Ser Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp
 420 425 430
 Leu Met Ala Glu Gly Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val
 435 440 445
 Ile Val Asp Thr His Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro
 450 455 460
 Leu Ile Glu Ala Gln Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln
 465 470 475 480
 Ala Ala Arg Phe Ala Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser
 485 490 495
 Asn Ile Asp Val Lys Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe
 500 505 510
 Thr Ala Ala Gln Ile Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys
 515 520 525
 Glu Thr Pro Glu Leu Met His Val Leu Arg Ala Gln Glu Ala Gln Ile
 530 535 540
 Glu Asp Val Thr Gly Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val
 545 550 555 560
 Gln Leu Asp Ile Thr Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu
 565 570 575
 Ala Val Val Val Gly Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg
 580 585 590
 Ser Leu Leu Val Pro Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val
 595 600 605
 Gly Ala Ala Phe Gly Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly
 610 615 620
 Gly Phe Val Asn Thr Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe
 625 630 635 640
 Leu Ile Gly Val Thr Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu
 645 650 655
 Val Thr Arg Met Arg Glu His Tyr Thr His His Asn Gly Lys Gly Gln
 660 665 670
 Pro Gly Ser Lys Tyr Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe
 675 680 685
 Thr Gln Gly Ser Arg Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala
 690 695 700

Val Phe Val Ala Phe Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe
705 710 715 720

Gly Phe Ala Leu Gly Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg
725 730 735

Met Gly Leu Val Pro Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp
740 745 750

Trp Met Pro Lys Trp Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu
755 760 765

Gly Thr Ala Leu Glu Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg
770 775 780

<210> 273

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> RXN00932

<400> 273

cccaattaat ttatgcactt cggtagaggtt actcaciaaag agtagcgtgc aaagcccagc 60

aataaggtga tgtttcaacg attaggttac ggtaggggcc atg acg cca cag aaa 115
Met Thr Pro Gln Lys
1 5

ctt cac cgt ttt gca gcc ctt tta gaa atg ggt acc tgg acc ctg ctg 163
Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly Thr Trp Thr Leu Leu
10 15 20

atc atc ggc atg atc tta aaa tac agt gga gtg aca gac gcc gta acc 211
Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val Thr Asp Ala Val Thr
25 30 35

cct att gcc ggc ggt atc cac ggc ttt ggc ttc ctc tgt ttt gca gcc 259
Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe Leu Cys Phe Ala Ala
40 45 50

atc acc atc acc gtg tgg atc aat aat aag tgg aca ttc ccg cag ggt 307
Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp Thr Phe Pro Gln Gly
55 60 65

atc gca ggt ttg atc gtc tct gtt atc ccg tgg gct gca ttg cca ttt 355
Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp Ala Ala Leu Pro Phe
70 75 80 85

gca ttg tgg gca gac aag aag ggc ctc gtt gcc ggc gga tgg cgc ttt 403
Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala Gly Gly Trp Arg Phe
90 95 100

tca gat ccg tcc gaa aag cca cac act ttc ttt gac aag atc ttg gct 451
 Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe Asp Lys Ile Leu Ala
 105 110 115

caa ttg gtc agg cac cca atc cga tcc att tta att ctg ctg gtg att 499
 Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu Ile Leu Leu Val Ile
 120 125 130

atc gcc gtc gtc ttc tct atc ttg ctg gcg atg gga cca cct tat gat 547
 Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met Gly Pro Pro Tyr Asp
 135 140 145

cca gat gcc atc gca aac act gtg gat taaacaacag cctccttcac 594
 Pro Asp Ala Ile Ala Asn Thr Val Asp
 150 155

atg 597

<210> 274
 <211> 158
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 274
 Met Thr Pro Gln Lys Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly
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Thr Trp Thr Leu Leu Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val
 20 25 30

Thr Asp Ala Val Thr Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe
 35 40 45

Leu Cys Phe Ala Ala Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp
 50 55 60

Thr Phe Pro Gln Gly Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp
 65 70 75 80

Ala Ala Leu Pro Phe Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala
 85 90 95

Gly Gly Trp Arg Phe Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe
 100 105 110

Asp Lys Ile Leu Ala Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu
 115 120 125

Ile Leu Leu Val Ile Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met
 130 135 140

Gly Pro Pro Tyr Asp Pro Asp Ala Ile Ala Asn Thr Val Asp
 145 150 155

<210> 275
 <211> 534
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (65)..(511)
 <223> RXN03022

<400> 275
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 agcagtg atc atc acc gct ggc atc ttg gta gcg acc gcg acc gcc ctc 109
 Val Ile Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu
 1 5 10 15
 cta atg atc acc gcg gtc agc gag tca acg tac atc gtc atc tcc ctc 157
 Leu Met Ile Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu
 20 25 30
 gcc ggc ttc tcc ctt tat ggc ctt ggc ctc gga ctc ttc gcc acc cca 205
 Ala Gly Phe Ser Leu Tyr Gly Leu Gly Leu Gly Leu Phe Ala Thr Pro
 35 40 45
 gtc acc gat act gcg ctt gga aca ctt ccc aaa gac cgt acc ggc gct 253
 Val Thr Asp Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala
 50 55 60
 ggt gca ggt gta ttc aag atg tcc tct tcc ctc ggc gca gca ctc ggc 301
 Gly Ala Gly Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly
 65 70 75
 atc gca atc tcc act tca gtg ttc ctc gca ctt cgc gac ggc acc tcc 349
 Ile Ala Ile Ser Thr Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser
 80 85 90 95
 atc aac tcc gac gtc gca ctc gcc gga aca gtt tca ctt ggc atc aac 397
 Ile Asn Ser Asp Val Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn
 100 105 110
 gtt gta ttc gca gca aca gcc acc atc acc gca gca gtc ctt att cca 445
 Val Val Phe Ala Ala Thr Ala Thr Ile Thr Ala Ala Val Leu Ile Pro
 115 120 125
 aaa gcc gct ggc aaa gtc tca caa acc agc atc acc ctt cct gag cca 493
 Lys Ala Ala Gly Lys Val Ser Gln Thr Ser Ile Thr Leu Pro Glu Pro
 130 135 140
 gct atc gct gta aaa atc taaaacttca ccaggacaga taa 534
 Ala Ile Ala Val Lys Ile
 145

<210> 276
 <211> 149
 <212> PRT

<213> Corynebacterium glutamicum

<400> 276

Val Ile Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu Leu
 1 5 10 15

Met Ile Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu Ala
 20 25 30

Gly Phe Ser Leu Tyr Gly Leu Gly Leu Gly Leu Phe Ala Thr Pro Val
 35 40 45

Thr Asp Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala Gly
 50 55 60

Ala Gly Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly Ile
 65 70 75 80

Ala Ile Ser Thr Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser Ile
 85 90 95

Asn Ser Asp Val Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn Val
 100 105 110

Val Phe Ala Ala Thr Ala Thr Ile Thr Ala Ala Val Leu Ile Pro Lys
 115 120 125

Ala Ala Gly Lys Val Ser Gln Thr Ser Ile Thr Leu Pro Glu Pro Ala
 130 135 140

Ile Ala Val Lys Ile
 145

<210> 277

<211> 586

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(586)

<223> RXN03151

<400> 277

ccgaacttgg agctttgctg ttggaggcag ccaaatagtc ccaatgtaaa cgcaactgggt 60

agtatttggt taaccatcca cctcaaggag taaaacgcac gtg ctt tcc cac atc 115
 Val Leu Ser His Ile
 1 5

att gat gtc ctc gcc gac ccg atc gat ggc acc cca ctt gta ggc gcc 163
 Ile Asp Val Leu Ala Asp Pro Ile Asp Gly Thr Pro Leu Val Gly Ala
 10 15 20

gaa gat ttc tca cgg ttg gtg tct gaa tct ggg cat tcc tac gat gtt 211
 Glu Asp Phe Ser Arg Leu Val Ser Glu Ser Gly His Ser Tyr Asp Val

25										30					35					
gct	cgt	caa	ggg	tat	gtc	acc	ctg	gct	ggg	ggc	gca	ggg	ctg	cgc	tat	259				
Ala	Arg	Gln	Gly	Tyr	Val	Thr	Leu	Ala	Gly	Gly	Ala	Gly	Leu	Arg	Tyr					
40			45					50												
tca	ggc	gat	gat	gca	cag	atg	atc	gcg	gat	cgg	gaa	acc	ttc	ctt	tct	307				
Ser	Gly	Asp	Asp	Ala	Gln	Met	Ile	Ala	Asp	Arg	Glu	Thr	Phe	Leu	Ser					
55			60					65												
ggc	ggt	cac	ttc	gcg	ccc	ttc	gtg	gaa	gct	gtc	acc	gag	cat	gtt	caa	355				
Gly	Gly	His	Phe	Ala	Pro	Phe	Val	Glu	Ala	Val	Thr	Glu	His	Val	Gln					
70			75					80			85									
gat	gtc	gtt	gac	cag	gca	ggc	ctt	agc	gat	gac	gca	cag	cca	gtg	gtc	403				
Asp	Val	Val	Asp	Gln	Ala	Gly	Leu	Ser	Asp	Asp	Ala	Gln	Pro	Val	Val					
90				95					100											
tgc	gaa	atc	ggc	gcg	gga	acc	ggc	tac	tac	ttg	tcc	cat	acc	ctt	gat	451				
Cys	Glu	Ile	Gly	Ala	Gly	Thr	Gly	Tyr	Tyr	Leu	Ser	His	Thr	Leu	Asp					
105			110					115												
tct	gtt	gca	gga	tct	cgc	gga	att	ggc	att	gac	gtt	tcc	gtg	cac	gcc	499				
Ser	Val	Ala	Gly	Ser	Arg	Gly	Ile	Gly	Ile	Asp	Val	Ser	Val	His	Ala					
120			125					130												
gca	aag	cgt	ttg	gca	aag	tgt	cac	cct	cgc	gtc	ggc	gca	gtc	atc	gcg	547				
Ala	Lys	Arg	Leu	Ala	Lys	Cys	His	Pro	Arg	Val	Gly	Ala	Val	Ile	Ala					
135			140					145												
aac	gca	tgg	gca	cgc	ctg	ccg	att	gca	gat	aac	tcc	tcg				586				
Asn	Ala	Trp	Ala	Arg	Leu	Pro	Ile	Ala	Asp	Asn	Ser	Ser								
150			155					160												

<210> 278

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

Val	Leu	Ser	His	Ile	Ile	Asp	Val	Leu	Ala	Asp	Pro	Ile	Asp	Gly	Thr
1				5					10					15	

Pro	Leu	Val	Gly	Ala	Glu	Asp	Phe	Ser	Arg	Leu	Val	Ser	Glu	Ser	Gly
		20						25					30		

His	Ser	Tyr	Asp	Val	Ala	Arg	Gln	Gly	Tyr	Val	Thr	Leu	Ala	Gly	Gly
		35					40					45			

Ala	Gly	Leu	Arg	Tyr	Ser	Gly	Asp	Asp	Ala	Gln	Met	Ile	Ala	Asp	Arg
	50					55					60				

Glu	Thr	Phe	Leu	Ser	Gly	Gly	His	Phe	Ala	Pro	Phe	Val	Glu	Ala	Val
65					70					75					80

Thr	Glu	His	Val	Gln	Asp	Val	Val	Asp	Gln	Ala	Gly	Leu	Ser	Asp	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	85	90	95
Ala Gln Pro Val Val Cys Glu Ile Gly Ala Gly Thr Gly Tyr Tyr Leu			
100	105	110	
Ser His Thr Leu Asp Ser Val Ala Gly Ser Arg Gly Ile Gly Ile Asp			
115	120	125	
Val Ser Val His Ala Ala Lys Arg Leu Ala Lys Cys His Pro Arg Val			
130	135	140	
Gly Ala Val Ile Ala Asn Ala Trp Ala Arg Leu Pro Ile Ala Asp Asn			
145	150	155	160
Ser Ser			

<210> 279
 <211> 543
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(543)
 <223> RXN02832

<400> 279

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Arg Gly Pro Val Met Asp Tyr Thr Asn Gln Ser Leu Val Ala Phe Phe	
1 5 10 15	
ttt aaa gca tta acg tca tat tta aag aaa cac aat tgt tta tat gtc	96
Phe Lys Ala Leu Thr Ser Tyr Leu Lys Lys His Asn Cys Leu Tyr Val	
20 25 30	
ctt gta gat cca tat tta att gaa aat tta cgc aat gca gac ggt gaa	144
Leu Val Asp Pro Tyr Leu Ile Glu Asn Leu Arg Asn Ala Asp Gly Glu	
35 40 45	
att gtt aaa tct tat gat aac cga gca ttt gtt aga aca atg gat aaa	192
Ile Val Lys Ser Tyr Asp Asn Arg Ala Phe Val Arg Thr Met Asp Lys	
50 55 60	
tta ggt tat aaa cac caa ggt ttc cct gta ggt tat gat tca atg agc	240
Leu Gly Tyr Lys His Gln Gly Phe Pro Val Gly Tyr Asp Ser Met Ser	
65 70 75 80	
caa atc cgt tgg ctg tca gtg tta gat tta aaa gat aag act gaa gac	288
Gln Ile Arg Trp Leu Ser Val Leu Asp Leu Lys Asp Lys Thr Glu Asp	
85 90 95	
caa ctt tta aaa gaa atg gat tat caa acg aga cgt aat att aaa aaa	336
Gln Leu Leu Lys Glu Met Asp Tyr Gln Thr Arg Arg Asn Ile Lys Lys	
100 105 110	

aca tat gat att ggt gtc aaa act aaa acg tta acg att gat gaa acg 384
 Thr Tyr Asp Ile Gly Val Lys Thr Lys Thr Leu Thr Ile Asp Glu Thr
 115 120 125

 caa act ttt ttc gac tta ttc cat atg gct gag gaa aag cac ggt ttc 432
 Gln Thr Phe Phe Asp Leu Phe His Met Ala Glu Glu Lys His Gly Phe
 130 135 140

 aaa ttc cgt gag tta cca tac ttt gaa gaa atg caa aag tta tac gat 480
 Lys Phe Arg Glu Leu Pro Tyr Phe Glu Glu Met Gln Lys Leu Tyr Asp
 145 150 155 160

 gac cac gcc atg tta aag ttg gcg tat att gat tta aac gag tat tta 528
 Asp His Ala Met Leu Lys Leu Ala Tyr Ile Asp Leu Asn Glu Tyr Leu
 165 170 175

 aaa acg ttg caa tta 543
 Lys Thr Leu Gln Leu
 180

<210> 280
 <211> 181
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 280
 Arg Gly Pro Val Met Asp Tyr Thr Asn Gln Ser Leu Val Ala Phe Phe
 1 5 10 15

 Phe Lys Ala Leu Thr Ser Tyr Leu Lys Lys His Asn Cys Leu Tyr Val
 20 25 30

 Leu Val Asp Pro Tyr Leu Ile Glu Asn Leu Arg Asn Ala Asp Gly Glu
 35 40 45

 Ile Val Lys Ser Tyr Asp Asn Arg Ala Phe Val Arg Thr Met Asp Lys
 50 55 60

 Leu Gly Tyr Lys His Gln Gly Phe Pro Val Gly Tyr Asp Ser Met Ser
 65 70 75 80

 Gln Ile Arg Trp Leu Ser Val Leu Asp Leu Lys Asp Lys Thr Glu Asp
 85 90 95

 Gln Leu Leu Lys Glu Met Asp Tyr Gln Thr Arg Arg Asn Ile Lys Lys
 100 105 110

 Thr Tyr Asp Ile Gly Val Lys Thr Lys Thr Leu Thr Ile Asp Glu Thr
 115 120 125

 Gln Thr Phe Phe Asp Leu Phe His Met Ala Glu Glu Lys His Gly Phe
 130 135 140

 Lys Phe Arg Glu Leu Pro Tyr Phe Glu Glu Met Gln Lys Leu Tyr Asp
 145 150 155 160

Asp His Ala Met Leu Lys Leu Ala Tyr Ile Asp Leu Asn Glu Tyr Leu
 165 170 175

Lys Thr Leu Gln Leu
 180

<210> 281

<211> 1539

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1516)

<223> RXN00165

<400> 281

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gactctcaaa gtggcgttgt cgcagcggcc gtggagcttt gtg gcg tct gct ggc 115
 Val Ala Ser Ala Gly
 1 5

atg gcg gcg tct ttt atc tgc aat ggg tta acg cct gtg att gtg ggt 163
 Met Ala Ala Ser Phe Ile Cys Asn Gly Leu Thr Pro Val Ile Val Gly
 10 15 20

aag gcg gtg gat gag gct att ggc acg agc gat ctg cag cga ttg tgg 211
 Lys Ala Val Asp Glu Ala Ile Gly Thr Ser Asp Leu Gln Arg Leu Trp
 25 30 35

ttc tgg att gcc atg ttg gcg gtt ctt ttc tta acg gcg atg acg gtg 259
 Phe Trp Ile Ala Met Leu Ala Val Leu Phe Leu Thr Ala Met Thr Val
 40 45 50

aac tgg att gct cgg tac atg ttg gtg cgg agc cag cag ttg gtc agc 307
 Asn Trp Ile Ala Arg Tyr Met Leu Val Arg Ser Gln Gln Leu Val Ser
 55 60 65

cat gat ttg cgc atg ttg gtg act gat cgg att caa gat ccg cgt ggt 355
 His Asp Leu Arg Met Leu Val Thr Asp Arg Ile Gln Asp Pro Arg Gly
 70 75 80 85

ttt gct gga aaa gag cgc act gcg ggt gga ttg ttg tcg att gcg tca 403
 Phe Ala Gly Lys Glu Arg Thr Ala Gly Gly Leu Leu Ser Ile Ala Ser
 90 95 100

tcg gat acg cag cgg gtg ggc gat atc gtc atg atg acg gtg ttc ccg 451
 Ser Asp Thr Gln Arg Val Gly Asp Ile Val Met Met Thr Val Phe Pro
 105 110 115

gtg gcg gaa ttg gcg tcg att att tat ggc gcc gtg gtg atg tac agc 499
 Val Ala Glu Leu Ala Ser Ile Ile Tyr Gly Ala Val Val Met Tyr Ser
 120 125 130

att aat ccg tgg ttg agt gtg gct gtg ctg att ggt gga ccg ctg ctg 547

Ile Asn Pro Trp Leu Ser Val Ala Val Leu Ile Gly Gly Pro Leu Leu 135 140 145	
gtt gtg gtg gct att cag gtc tca aag ccg ttg cag aag cgt tcg ggt Val Val Val Ala Ile Gln Val Ser Lys Pro Leu Gln Lys Arg Ser Gly 150 155 160 165	595
gct cgt cag cag gcg gtg gca cag gct gcg gct act gca act gat gtg Ala Arg Gln Gln Ala Val Ala Gln Ala Ala Ala Thr Ala Thr Asp Val 170 - 175 180	643
gtg cag ggc ttg aga att ttg aag ggt ttg ggc gcg att gtc acg gtg Val Gln Gly Leu Arg Ile Leu Lys Gly Leu Gly Ala Ile Val Thr Val 185 190 195	691
cgc cgt cgg tac gag gcg att tct ggt gag gct tat cgg aag acg gtt Arg Arg Arg Tyr Glu Ala Ile Ser Gly Glu Ala Tyr Arg Lys Thr Val 200 205 210	739
cat gcg gat gct gcg gaa gct cgc ttg aat ggt gtc acc gat gcg gcg His Ala Asp Ala Ala Glu Ala Arg Leu Asn Gly Val Thr Asp Ala Ala 215 220 225	787
ggc gcc atc ttt gtg tcc gcg ttg ggt att gga gca gga ttt ttg gcg Gly Ala Ile Phe Val Ser Ala Leu Gly Ile Gly Ala Gly Phe Leu Ala 230 235 240 245	835
ctg caa ggt cag atg agt att ggt gat ttg atc acg gtt gtg gga ctc Leu Gln Gly Gln Met Ser Ile Gly Asp Leu Ile Thr Val Val Gly Leu 250 255 260	883
aca cag ttt ttg atc atg ccg atg acc atg ctt ggt cga aat gtg gca Thr Gln Phe Leu Ile Met Pro Met Thr Met Leu Gly Arg Asn Val Ala 265 270 275	931
tcg cgc tgg gca tcg gcg gag gcg tcg gca aag cgt att agg gga gtg Ser Arg Trp Ala Ser Ala Glu Ala Ser Ala Lys Arg Ile Arg Gly Val 280 285 290	979
ctc ggt gct gat ttt gag aga gtg tct gcg cat gat gcg gac aag gct Leu Gly Ala Asp Phe Glu Arg Val Ser Ala His Asp Ala Asp Lys Ala 295 300 305	1027
gag gag att atc caa caa ctt gcc aaa ggt ttg acg gtt att cga ggc Glu Glu Ile Ile Gln Gln Leu Ala Lys Gly Leu Thr Val Ile Arg Gly 310 315 320 325	1075
act gat gag cag ctc gtt gag gta tta gag cag ttg cca cgt act cgg Thr Asp Glu Gln Leu Val Glu Val Leu Glu Gln Leu Pro Arg Thr Arg 330 335 340	1123
gtg att gtg gct cct cat gcg gcg gat ctt ttt gat caa agt gtc agg Val Ile Val Ala Pro His Ala Ala Asp Leu Phe Asp Gln Ser Val Arg 345 350 355	1171
gac aat gtg cat ccc gtg gca gag gtc gcg gag aaa gcc att gaa gtt Asp Asn Val His Pro Val Ala Glu Val Ala Glu Lys Ala Ile Glu Val 1219	

360	365	370	
gcc tcc tgt gac gat att cca ggt ggt agt tcc aag att gtg ggc gag			1267
Ala Ser Cys Asp Asp Ile Pro Gly Gly Ser Ser Lys Ile Val Gly Glu			
375	380	385	
ggt gga cgg ttg ctc tcg ggt ggt cag cgt cag cgc gtt gca ctg gct			1315
Gly Gly Arg Leu Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Leu Ala			
390	395	400	405
cgg gcg att gct ttt gat cca gag gtg ttg gtg ctt caa gat ccc aca			1363
Arg Ala Ile Ala Phe Asp Pro Glu Val Leu Val Leu Gln Asp Pro Thr			
410	415		420
acg gca gtg gat tct gtg acg gag caa aac att gct cag caa gtg gca			1411
Thr Ala Val Asp Ser Val Thr Glu Gln Asn Ile Ala Gln Gln Val Ala			
425	430		435
gca cac cgt gca gga aaa gtg acc att gtg ttt agt gag gca ccc gcg			1459
Ala His Arg Ala Gly Lys Val Thr Ile Val Phe Ser Glu Ala Pro Ala			
440	445		450
tgg agt gcg gtg gct gat caa cac gtt gag gca gct gct ttg cgg gag			1507
Trp Ser Ala Val Ala Asp Gln His Val Glu Ala Ala Ala Leu Arg Glu			
455	460		465
gtt atg aaa tgagtgggga gacgtcgaaa agc			1539
Val Met Lys			
470			

<210> 282

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

Val Ala Ser Ala Gly Met Ala Ala Ser Phe Ile Cys Asn Gly Leu Thr			
1	5	10	15
Pro Val Ile Val Gly Lys Ala Val Asp Glu Ala Ile Gly Thr Ser Asp			
20	25		30
Leu Gln Arg Leu Trp Phe Trp Ile Ala Met Leu Ala Val Leu Phe Leu			
35	40		45
Thr Ala Met Thr Val Asn Trp Ile Ala Arg Tyr Met Leu Val Arg Ser			
50	55		60
Gln Gln Leu Val Ser His Asp Leu Arg Met Leu Val Thr Asp Arg Ile			
65	70		75
Gln Asp Pro Arg Gly Phe Ala Gly Lys Glu Arg Thr Ala Gly Gly Leu			
85	90		95
Leu Ser Ile Ala Ser Ser Asp Thr Gln Arg Val Gly Asp Ile Val Met			
100	105		110

Met Thr Val Phe Pro Val Ala Glu Leu Ala Ser Ile Ile Tyr Gly Ala
 115 120 125
 Val Val Met Tyr Ser Ile Asn Pro Trp Leu Ser Val Ala Val Leu Ile
 130 135 140
 Gly Gly Pro Leu Leu Val Val Val Ala Ile Gln Val Ser Lys Pro Leu
 145 150 155 160
 Gln Lys Arg Ser Gly Ala Arg Gln Gln Ala Val Ala Gln Ala Ala Ala
 165 170 175
 Thr Ala Thr Asp Val Val Gln Gly Leu Arg Ile Leu Lys Gly Leu Gly
 180 185 190
 Ala Ile Val Thr Val Arg Arg Arg Tyr Glu Ala Ile Ser Gly Glu Ala
 195 200 205
 Tyr Arg Lys Thr Val His Ala Asp Ala Ala Glu Ala Arg Leu Asn Gly
 210 215 220
 Val Thr Asp Ala Ala Gly Ala Ile Phe Val Ser Ala Leu Gly Ile Gly
 225 230 235 240
 Ala Gly Phe Leu Ala Leu Gln Gly Gln Met Ser Ile Gly Asp Leu Ile
 245 250 255
 Thr Val Val Gly Leu Thr Gln Phe Leu Ile Met Pro Met Thr Met Leu
 260 265 270
 Gly Arg Asn Val Ala Ser Arg Trp Ala Ser Ala Glu Ala Ser Ala Lys
 275 280 285
 Arg Ile Arg Gly Val Leu Gly Ala Asp Phe Glu Arg Val Ser Ala His
 290 295 300
 Asp Ala Asp Lys Ala Glu Glu Ile Ile Gln Gln Leu Ala Lys Gly Leu
 305 310 315 320
 Thr Val Ile Arg Gly Thr Asp Glu Gln Leu Val Glu Val Leu Glu Gln
 325 330 335
 Leu Pro Arg Thr Arg Val Ile Val Ala Pro His Ala Ala Asp Leu Phe
 340 345 350
 Asp Gln Ser Val Arg Asp Asn Val His Pro Val Ala Glu Val Ala Glu
 355 360 365
 Lys Ala Ile Glu Val Ala Ser Cys Asp Asp Ile Pro Gly Gly Ser Ser
 370 375 380
 Lys Ile Val Gly Glu Gly Gly Arg Leu Leu Ser Gly Gly Gln Arg Gln
 385 390 395 400
 Arg Val Ala Leu Ala Arg Ala Ile Ala Phe Asp Pro Glu Val Leu Val
 405 410 415

Leu Gln Asp Pro Thr Thr Ala Val Asp Ser Val Thr Glu Gln Asn Ile
 420 425 430

Ala Gln Gln Val Ala Ala His Arg Ala Gly Lys Val Thr Ile Val Phe
 435 440 445

Ser Glu Ala Pro Ala Trp Ser Ala Val Ala Asp Gln His Val Glu Ala
 450 455 460

Ala Ala Leu Arg Glu Val Met Lys
 465 470

<210> 283

<211> 1470

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1447)

<223> RXN01190

<400> 283

cagggttttg atgagaacaa cacacaccgc ttcaagcatt ctgcgaagaa tgatcaggcg 60

gcagcggggc aaggttgcggt ttggcgcatt ctttttgggg atg tgg cag ctg tcg 115
 Met Trp Gln Leu Ser
 1 5

gaa gca ttg gtg ccg att gcg att ggt ttg atc gtt gat cat gcg gtt 163
 Glu Ala Leu Val Pro Ile Ala Ile Gly Leu Ile Val Asp His Ala Val
 10 15 20

ctc aca aaa gat ctc cgc cga tta gtg gtc ggg ctt gtc gct ttt gtt 211
 Leu Thr Lys Asp Leu Arg Arg Leu Val Val Gly Leu Val Ala Phe Val
 25 30 35

gtg ctg ttt gtg gtg ttg agt ttt tct aat cgt ttc ggt tcg cgc gcg 259
 Val Leu Phe Val Val Leu Ser Phe Ser Asn Arg Phe Gly Ser Arg Ala
 40 45 50

ttg aat agg gcc gtg aac ttt gaa tcc cat gcg ctc cgc gta gag gta 307
 Leu Asn Arg Ala Val Asn Phe Glu Ser His Ala Leu Arg Val Glu Val
 55 60 65

gcc gat cat gcg ttg aag aat ctg gat ccg cgc aat ttg gtg cct ggc 355
 Ala Asp His Ala Leu Lys Asn Leu Asp Pro Arg Asn Leu Val Pro Gly
 70 75 80 85

gag gtg atg tcg cgg tcc acc gca gat gcg gat tct tcg acg cgt att 403
 Glu Val Met Ser Arg Ser Thr Ala Asp Ala Asp Ser Ser Thr Arg Ile
 90 95 100

ttc ggg cag atc gga acc ggt gtt tcg gct gcg acg gga ttt ctt ggt 451
 Phe Gly Gln Ile Gly Thr Gly Val Ser Ala Ala Thr Gly Phe Leu Gly

105	110	115	
gca gcg acc tac ctg ttg atc agt gac tgg ctg gtc ggg ttg ttg gtg Ala Ala Thr Tyr Leu Leu Ile Ser Asp Trp Leu Val Gly Leu Leu Val 120 125 130			499
ctt gtg ctg gta ccg atc att tcg gga gtg gtt gca ctg gct agc aag Leu Val Leu Val Pro Ile Ile Ser Gly Val Val Ala Leu Ala Ser Lys 135 140 145			547
ggc att tct aaa agg agt gtc acc cag cag gag aag ttg gcg gag tct Gly Ile Ser Lys Arg Ser Val Thr Gln Gln Glu Lys Leu Ala Glu Ser 150 155 160 165			595
ggc gcg cag gca agt gac atc atg atg ggg ctg cgc gtg atc aag gcg Gly Ala Gln Ala Ser Asp Ile Met Met Gly Leu Arg Val Ile Lys Ala 170 175 180			643
atc ggt ggc gag cgt tgg gcc gtg aag act ttt gaa aag gcg tcg cag Ile Gly Gly Glu Arg Trp Ala Val Lys Thr Phe Glu Lys Ala Ser Gln 185 190 195			691
gca tca gcg aga gcg gcg gtt gat act gca gtt gct tcg ggc aaa gtc Ala Ser Ala Arg Ala Ala Val Asp Thr Ala Val Ala Ser Gly Lys Val 200 205 210			739
gct ggt att ggt gag ttg tcc att gcg gtg aat ttg gct gcg gtg ttg Ala Gly Ile Gly Glu Leu Ser Ile Ala Val Asn Leu Ala Ala Val Leu 215 220 225			787
ttg ctt gct ggt tgg cgg gtc acc acg ggg gag ttg ggg cct ggc cag Leu Leu Ala Gly Trp Arg Val Thr Thr Gly Glu Leu Gly Pro Gly Gln 230 235 240 245			835
ttg atc gca att gtg ggt gtg gcg gtg tat ttg tca gag ccg att cgc Leu Ile Ala Ile Val Gly Val Ala Val Tyr Leu Ser Glu Pro Ile Arg 250 255 260			883
ttg ctg agc aac tcg att aat gcc tca gct att gcg cac ggt gca gcg Leu Leu Ser Asn Ser Ile Asn Ala Ser Ala Ile Ala His Gly Ala Ala 265 270 275			931
gag cgg gtg gct aat ttc tta aac ctc gac gaa tct cag gca cag tac Glu Arg Val Ala Asn Phe Leu Asn Leu Asp Glu Ser Gln Ala Gln Tyr 280 285 290			979
gaa agc agc gaa aca atc aat gac ggc gaa ttc ctc gtc atc gtg ccc Glu Ser Ser Glu Thr Ile Asn Asp Gly Glu Phe Leu Val Ile Val Pro 295 300 305			1027
cca gcc agc acg ctt cca cac ggc gac aat atc ttg gct aca cct cat Pro Ala Ser Thr Leu Pro His Gly Asp Asn Ile Leu Ala Thr Pro His 310 315 320 325			1075
gct gcc gac att ttc gaa ggt acc ttg cgg tca aat att tcc atg aat Ala Ala Asp Ile Phe Glu Gly Thr Leu Arg Ser Asn Ile Ser Met Asn 330 335 340			1123

cat gag gac aac gtg cca att gat ccg cag gta att cgc gct tct ggt 1171
 His Glu Asp Asn Val Pro Ile Asp Pro Gln Val Ile Arg Ala Ser Gly
 345 350 355

ctg act gac atc att gag gtg gac gga ctt gat gcg ccg gtg cgc gat 1219
 Leu Thr Asp Ile Ile Glu Val Asp Gly Leu Asp Ala Pro Val Arg Asp
 360 365 370

acg gga agc aat tta tcg ggt ggg cag cgt cag cga gtg gct ttg gcc 1267
 Thr Gly Ser Asn Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Leu Ala
 375 380 385

agg gcg ttg cat gca gac gcg gaa gta ctg gtg ctg atg gat cca acc. 1315
 Arg Ala Leu His Ala Asp Ala Glu Val Leu Val Leu Met Asp Pro Thr
 390 395 400 405

agc gcg gtg gat tca gtg acg gag gtg tct atc gcg cag ggg att aag 1363
 Ser Ala Val Asp Ser Val Thr Glu Val Ser Ile Ala Gln Gly Ile Lys
 410 415 420

cag ctg cga gca ggc aaa acc acc att gtg gtg agt tct tcg ccc gcg 1411
 Gln Leu Arg Ala Gly Lys Thr Thr Ile Val Val Ser Ser Ser Pro Ala
 425 430 435

ttt tac aac ttg gcg gat cgg gtg att tca cat gtc taatttgatg 1457
 Phe Tyr Asn Leu Ala Asp Arg Val Ile Ser His Val
 440 445

gcacatcatcga cac 1470

<210> 284

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

Met Trp Gln Leu Ser Glu Ala Leu Val Pro Ile Ala Ile Gly Leu Ile
 1 5 10 15

Val Asp His Ala Val Leu Thr Lys Asp Leu Arg Arg Leu Val Val Gly
 20 25 30

Leu Val Ala Phe Val Val Leu Phe Val Val Leu Ser Phe Ser Asn Arg
 35 40 45

Phe Gly Ser Arg Ala Leu Asn Arg Ala Val Asn Phe Glu Ser His Ala
 50 55 60

Leu Arg Val Glu Val Ala Asp His Ala Leu Lys Asn Leu Asp Pro Arg
 65 70 75 80

Asn Leu Val Pro Gly Glu Val Met Ser Arg Ser Thr Ala Asp Ala Asp
 85 90 95

Ser Ser Thr Arg Ile Phe Gly Gln Ile Gly Thr Gly Val Ser Ala Ala

100	105	110
Thr Gly Phe Leu Gly Ala Ala	Thr Tyr Leu Leu Ile	Ser Asp Trp Leu
115	120	125
Val Gly Leu Leu Val Leu Val	Leu Val Pro Ile Ile	Ser Gly Val Val
130	135	140
Ala Leu Ala Ser Lys Gly Ile Ser Lys Arg Ser Val Thr Gln Gln Glu		
145	150	155
Lys Leu Ala Glu Ser Gly Ala Gln Ala Ser Asp Ile Met Met Gly Leu		
165	170	175
Arg Val Ile Lys Ala Ile Gly Gly Glu Arg Trp Ala Val Lys Thr Phe		
180	185	190
Glu Lys Ala Ser Gln Ala Ser Ala Arg Ala Ala Val Asp Thr Ala Val		
195	200	205
Ala Ser Gly Lys Val Ala Gly Ile Gly Glu Leu Ser Ile Ala Val Asn		
210	215	220
Leu Ala Ala Val Leu Leu Leu Ala Gly Trp Arg Val Thr Thr Gly Glu		
225	230	235
Leu Gly Pro Gly Gln Leu Ile Ala Ile Val Gly Val Ala Val Tyr Leu		
245	250	255
Ser Glu Pro Ile Arg Leu Leu Ser Asn Ser Ile Asn Ala Ser Ala Ile		
260	265	270
Ala His Gly Ala Ala Glu Arg Val Ala Asn Phe Leu Asn Leu Asp Glu		
275	280	285
Ser Gln Ala Gln Tyr Glu Ser Ser Glu Thr Ile Asn Asp Gly Glu Phe		
290	295	300
Leu Val Ile Val Pro Pro Ala Ser Thr Leu Pro His Gly Asp Asn Ile		
305	310	315
Leu Ala Thr Pro His Ala Ala Asp Ile Phe Glu Gly Thr Leu Arg Ser		
325	330	335
Asn Ile Ser Met Asn His Glu Asp Asn Val Pro Ile Asp Pro Gln Val		
340	345	350
Ile Arg Ala Ser Gly Leu Thr Asp Ile Ile Glu Val Asp Gly Leu Asp		
355	360	365
Ala Pro Val Arg Asp Thr Gly Ser Asn Leu Ser Gly Gly Gln Arg Gln		
370	375	380
Arg Val Ala Leu Ala Arg Ala Leu His Ala Asp Ala Glu Val Leu Val		
385	390	395
Leu Met Asp Pro Thr Ser Ala Val Asp Ser Val Thr Glu Val Ser Ile		

405

410

415

Ala Gln Gly Ile Lys Gln Leu Arg Ala Gly Lys Thr Thr Ile Val Val
 420 425 430

Ser Ser Ser Pro Ala Phe Tyr Asn Leu Ala Asp Arg Val Ile Ser His
 435 440 445

Val

<210> 285

<211> 1368

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1345)

<223> RXN01102

<400> 285

attctatggt tgttgggaga gatgacttaa tttggaatca cgggctttaa cacgcgctga 60

cattgagcaa cttcccagca tgtggaaaag cccaggtttc gtg gct gtc ctc gtg 115
 Val Ala Val Leu Val
 1 5

gcg gtt gca gca gcg ttc ggc agt tgg tca ctc ctt ctt ccc gtc gta 163
 Ala Val Ala Ala Ala Phe Gly Ser Trp Ser Leu Leu Leu Pro Val Val
 10 15 20

ccg cta gcg gtc ctc aac aac ggc gga tca agc gct gtc gcc ggt gcc 211
 Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser Ala Val Ala Gly Ala
 25 30 35

acc act ggc atc ttc atg gca gct aca gtg atc act cag att ttc act 259
 Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile Thr Gln Ile Phe Thr
 40 45 50

ccc gct gcg ctg cgg aaa att ggc tac acc cca gtg atg gct ttc gcc 307
 Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro Val Met Ala Phe Ala
 55 60 65

gca ttc atg ctg ggt gtg cca gcc atc ggg tac atc ttc agc gtc gag 355
 Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr Ile Phe Ser Val Glu
 70 75 80 85

cca att cca gtg ctg gta gtg tcc gca ctt cga gga att ggg ttc ggt 403
 Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg Gly Ile Gly Phe Gly
 90 95 100

gcg ctc acc gtc gca gaa tct gcg ttg gtg gct gaa ctc gtt ccc gta 451
 Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala Glu Leu Val Pro Val
 105 110 115

cgc ttc ttg ggc aaa gct tct gga atg ttg ggc gta ttt att ggc ctt	499
Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly Val Phe Ile Gly Leu	
120 125 130	
tcc caa atg ctt ttc ctg cct gcc ggg ttg gcg tta ggt gac caa ttt	547
Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala Leu Gly Asp Gln Phe	
135 140 145	
ggc tac aac gtg gtc tat gtt tta ggt gcc gtt atc gca cta gtt gca	595
Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val Ile Ala Leu Val Ala	
150 155 160 165	
gcg gtg atg tgt ctg cgt att ccg cag gtt aag gca gcg gca aag cag	643
Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys Ala Ala Ala Lys Gln	
170 175 180	
caa cca cag gtg agc gaa cag gag cgt tct gtt tcc acc tgg aag ttg	691
Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val Ser Thr Trp Lys Leu	
185 190 195	
gtg ctg gtt ccc tcc ttg gct gtt acc agt ttg tca atg act ttt ggc	739
Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu Ser Met Thr Phe Gly	
200 205 210	
gca gtg tct tca ttc ctt cca gct gca gtc att gag tta gat cca gga	787
Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile Glu Leu Asp Pro Gly	
215 220 225	
tta ggt gct gca tta gcg ggt att att tta tcc att acc ggt ggt tct	835
Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser Ile Thr Gly Gly Ser	
230 235 240 245	
tca atg gtg ttc cgc tac ctg tcc ggc gtt atc gct gac cgc cgc ggt	883
Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile Ala Asp Arg Arg Gly	
250 255 260	
gtg cct ggt acc acg atg att cct gct cag atc att ggg ttc tta ggt	931
Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile Ile Gly Phe Leu Gly	
265 270 275	
gtc gtt tta atc acc gtc aca atc ttc caa ggc tgg tcc gtg tgg ctt	979
Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly Trp Ser Val Trp Leu	
280 285 290	
ttg att ata ggt gca gtg atg ttt ggt ggt gct ttt ggc atg gtg caa	1027
Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala Phe Gly Met Val Gln	
295 300 305	
aac gaa gcg ttg ctt tca atg ttt ttc cgg ctt cct cgc act aga gtc	1075
Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu Pro Arg Thr Arg Val	
310 315 320 325	
tcc gaa gcc tcc gcc atc tgg aat atc gcc ttt gat tcg gga aca gga	1123
Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe Asp Ser Gly Thr Gly	
330 335 340	
atc gga agc ttc ctg ctt ggc ata gtt gcc gca tcg ctt gct tac agt	1171

Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala Ser Leu Ala Tyr S r
 345 350 355

ggt gct ttt ggt tcc gga gcc gtg gtg att ttg ttt gga atc gtt ttg 1219
 Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu Phe Gly Ile Val Leu
 360 365 370

acc acc gcc gat cga atc att ggg cgg cac cgc att act gaa tac aac 1267
 Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg Ile Thr Glu Tyr Asn
 375 380 385

aac acc cgc gcg cgt ttg cgc cag gtg cca gtc gct cgg cgt gca gtg 1315
 Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val Ala Arg Arg Ala Val
 390 395 400 405

caa ggg ctg cgc aac agg cgc aaa gat cgc taaaacgctt ttcgacgcca 1365
 Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
 410 415

ccc 1368

<210> 286
 <211> 415
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 286
 Val Ala Val Leu Val Ala Val Ala Ala Ala Phe Gly Ser Trp Ser Leu
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Leu Leu Pro Val Val Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser
 20 25 30

Ala Val Ala Gly Ala Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile
 35 40 45

Thr Gln Ile Phe Thr Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro
 50 55 60

Val Met Ala Phe Ala Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr
 65 70 75 80

Ile Phe Ser Val Glu Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg
 85 90 95

Gly Ile Gly Phe Gly Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala
 100 105 110

Glu Leu Val Pro Val Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly
 115 120 125

Val Phe Ile Gly Leu Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala
 130 135 140

Leu Gly Asp Gln Phe Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val
 145 150 155 160

Ile Ala Leu Val Ala Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys
 165 170 175
 Ala Ala Ala Lys Gln Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val
 180 185 190
 Ser Thr Trp Lys Leu Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu
 195 200 205
 Ser Met Thr Phe Gly Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile
 210 215 220
 Glu Leu Asp Pro Gly Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser
 225 230 235 240
 Ile Thr Gly Gly Ser Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile
 245 250 255
 Ala Asp Arg Arg Gly Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile
 260 265 270
 Ile Gly Phe Leu Gly Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly
 275 280 285
 Trp Ser Val Trp Leu Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala
 290 295 300
 Phe Gly Met Val Gln Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu
 305 310 315 320
 Pro Arg Thr Arg Val Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe
 325 330 335
 Asp Ser Gly Thr Gly Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala
 340 345 350
 Ser Leu Ala Tyr Ser Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu
 355 360 365
 Phe Gly Ile Val Leu Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg
 370 375 380
 Ile Thr Glu Tyr Asn Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val
 385 390 395 400
 Ala Arg Arg Ala Val Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
 405 410 415

<210> 287

<211> 348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(325)

<223> RXN00788

<400> 287

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ttgatccagc actgcttgca gtgaggcctc attagttggc atg gcc tcc tcc atc 115
 Met Ala Ser Ser Ile
 1 5

aac atc gga gtg ttc aac ctt gga aat gct gtt gct gcc tgg ctt gct 163
 Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val Ala Ala Trp Leu Ala
 10 15 20

ggt gca acc atc acc act tcc ctt gga ctc aca tca gcc gga tta gtt 211
 Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr Ser Ala Gly Leu Val
 25 30 35

ggc ggt ttg atg acg tcc ctc gga cta gtg ttg gcc atc gtg gct gtg 259
 Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu Ala Ile Val Ala Val
 40 45 50

gtt ttg cgt cga aaa gcg caa ggc acc caa gcg acc atc agc gtt gtg 307
 Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala Thr Ile Ser Val Val
 55 60 65

gag cac cag ccc gcc caa taaataattt ctctcttcta att 348
 Glu His Gln Pro Ala Gln
 70 75

<210> 288

<211> 75

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

Met Ala Ser Ser Ile Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val
 1 5 10 15

Ala Ala Trp Leu Ala Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr
 20 25 30

Ser Ala Gly Leu Val Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu
 35 40 45

Ala Ile Val Ala Val Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala
 50 55 60

Thr Ile Ser Val Val Glu His Gln Pro Ala Gln
 65 70 75

<210> 289

<211> 1764

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1741)

<223> RXN02119

<400> 289

ttcgggtccgc tctggcaaaa atggctggct gccacctcgg cgcagcagct taagggctgg 60

gcttaaattg cttgtcgacg cctagtgcc caatggagac atg acc gaa aca ctt 115
 Met Thr Glu Thr Leu
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gtg gtg aat ggc ctt gca ggc ggc tat ggg cac cgc aca tta ttt aac 163
 Val Val Asn Gly Leu Ala Gly Gly Tyr Gly His Arg Thr Leu Phe Asn
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gat gtg aat ctc acc gta gct gcc ggc gat gtc gtg ggc gtt gtc ggc 211
 Asp Val Asn Leu Thr Val Ala Ala Gly Asp Val Val Gly Val Val Gly
 25 30 35

gtc aat ggc gct ggt aaa tcc aca ttt cta aaa att ctg gcg ggc gtg 259
 Val Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys Ile Leu Ala Gly Val
 40 45 50

gaa aag cca ctg gct gga act atc gcg ctt tcg cca gcc gat gct ttt 307
 Glu Lys Pro Leu Ala Gly Thr Ile Ala Leu Ser Pro Ala Asp Ala Phe
 55 60 65

gtg ggc tac ttg cca cag gaa cac acc cgc acg tct gga gag acg atc 355
 Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr Ser Gly Glu Thr Ile
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gca gtt tac att gct cgt cga acc ggc tgc caa gct gca aca act gcc 403
 Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln Ala Ala Thr Thr Ala
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atg gat gac acc gcc gaa gcg ttt ggt gcg gat cca gac aac gct gcc 451
 Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp Pro Asp Asn Ala Ala
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ttg gcc gat gca tac gcc gag gcg ctg gat cgg tgg atg gcc agt ggc 499
 Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg Trp Met Ala Ser Gly
 120 125 130

gca gcc gat ttg gat gaa cgc atc ccc atc gtg ctc gct gat ttg ggc 547
 Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val Leu Ala Asp Leu Gly
 135 140 145

ttt gag ctt ccc acc tcg acg ctg atg gaa gga ctt tca gcc ggc cag 595
 Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly Leu Ser Gly Gly Gln
 150 155 160 165

gca gcc cgg gtc ggg ctg gcg gcg tta ctg ttg tca cgt ttt gac att 643
 Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu Ser Arg Phe Asp Ile
 170 175 180

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ctc gat ctg cac caa aat tcc cac cat gtt tat ggc ggt gga tat gat Leu Asp Leu His Gln Asn Ser His His Val Tyr Gly Gly Gly Tyr Asp 230 235 240 245	835
tcc tac ctt gag gaa cgc gca gtg cta cgc cag cac gcc cgt gac caa Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln His Ala Arg Asp Gln 250 255 260	883
tat gag gaa ttt gcg gaa aag aag aag gac ctt gtg gca cgt gct cga Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu Val Ala Arg Ala Arg 265 270 275	931
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gca cct gac aac gac aaa ctt cgg aag aaa gcc gct gcg gaa tcc agt Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala Ala Ala Glu Ser Ser 295 300 305	1027
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ggg act gcc acg atg ggc acg agc gtg gcg atc gga gaa atc gat cag	1363

Gly	Thr	Ala	Thr	Met	Gly	Thr	Ser	Val	Ala	Ile	Gly	Glu	Ile	Asp	Gln		
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gca	cga	gcg	tta	ctt	gat	cca	cag	ttg	cca	ctg	att	tct	gcg	ttt	gaa	1411	
Ala	Arg	Ala	Leu	Leu	Asp	Pro	Gln	Leu	Pro	Leu	Ile	Ser	Ala	Phe	Glu		
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Lys	His	Val	Pro	Asp	Leu	Pro	Ile	Ser	Glu	Val	Arg	Thr	Leu	Leu	Ala		
		440					445					450					
aaa	ttt	ggg	ctg	aat	gat	aat	cat	gtg	gaa	cgg	gac	gtc	gaa	aag	cta	1507	
Lys	Phe	Gly	Leu	Asn	Asp	Asn	His	Val	Glu	Arg	Asp	Val	Glu	Lys	Leu		
	455					460					465						
tct	cct	ggc	gag	cgc	acg	cgc	gcc	gga	ctt	gcg	ctg	cta	cag	gtg	cgg	1555	
Ser	Pro	Gly	Glu	Arg	Thr	Arg	Ala	Gly	Leu	Ala	Leu	Leu	Gln	Val	Arg		
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ggc	gtc	aac	gtg	ctt	gtt	ctt	gat	gag	ccc	acc	aac	cac	ctt	gac	ctg	1603	
Gly	Val	Asn	Val	Leu	Val	Leu	Asp	Glu	Pro	Thr	Asn	His	Leu	Asp	Leu		
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gag	gcc	atc	gag	caa	ttg	gag	caa	gcg	ttg	gcc	tcg	tat	gat	ggg	gtg	1651	
Glu	Ala	Ile	Glu	Gln	Leu	Glu	Gln	Ala	Leu	Ala	Ser	Tyr	Asp	Gly	Val		
			505					510					515				
ttg	ctg	ctg	gtc	acg	cac	gat	cgt	cgc	atg	ttg	gac	gct	gtg	cag	acc	1699	
Leu	Leu	Leu	Val	Thr	His	Asp	Arg	Arg	Met	Leu	Asp	Ala	Val	Gln	Thr		
		520					525					530					
aat	cgt	cgt	tgg	cat	gtc	gag	gct	ggc	gaa	gtt	agg	gag	cta			1741	
Asn	Arg	Arg	Trp	His	Val	Glu	Ala	Gly	Glu	Val	Arg	Glu	Leu				
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<211> 547

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

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Arg	Thr	Leu	Phe	Asn	Asp	Val	Asn	Leu	Thr	Val	Ala	Ala	Gly	Asp	Val
			20					25					30		

Val	Gly	Val	Val	Gly	Val	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Phe	Leu	Lys
		35					40					45			

Ile	Leu	Ala	Gly	Val	Glu	Lys	Pro	Leu	Ala	Gly	Thr	Ile	Ala	Leu	Ser
	50					55					60				

Pro Ala Asp Ala Phe Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr

65	70	75	80
Ser Gly Glu Thr Ile Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln	85	90	95
Ala Ala Thr Thr Ala Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp	100	105	110
Pro Asp Asn Ala Ala Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg	115	120	125
Trp Met Ala Ser Gly Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val	130	135	140
Leu Ala Asp Leu Gly Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly	145	150	155
Leu Ser Gly Gly Gln Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu	165	170	175
Ser Arg Phe Asp Ile Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp	180	185	190
Leu Asp Gly Leu Glu Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly	195	200	205
Gly Val Val Leu Val Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val	210	215	220
Thr Thr Val Leu Glu Leu Asp Leu His Gln Asn Ser His His Val Tyr	225	230	235
Gly Gly Gly Tyr Asp Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln	245	250	255
His Ala Arg Asp Gln Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu	260	265	270
Val Ala Arg Ala Arg Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg	275	280	285
Asn Ala Ile Lys Arg Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala	290	295	300
Ala Ala Glu Ser Ser Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu	305	310	315
Ser Arg Ile Ala Arg Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp	325	330	335
Lys Leu Gln Phe Ser Val Gly Lys Ala Ser Arg Ser Ser Ser Val Val	340	345	350
Ser Thr Leu Asn Asp Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly	355	360	365
Pro Val Ser Ile Gln Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly			

370

375

380

Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn
 385 390 395 400

Gln Glu Pro Thr Ser Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile
 405 410 415

Gly Glu Ile Asp Gln Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu
 420 425 430

Ile Ser Ala Phe Glu Lys His Val Pro Asp Leu Pro Ile Ser Glu Val
 435 440 445

Arg Thr Leu Leu Ala Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg
 450 455 460

Asp Val Glu Lys Leu Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala
 465 470 475 480

Leu Leu Gln Val Arg Gly Val Asn Val Leu Val Leu Asp Glu Pro Thr
 485 490 495

Asn His Leu Asp Leu Glu Ala Ile Glu Gln Leu Glu Gln Ala Leu Ala
 500 505 510

Ser Tyr Asp Gly Val Leu Leu Leu Val Thr His Asp Arg Arg Met Leu
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Arg Glu Leu
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<222> (101)..(1615)

<223> RXN01605

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 Val Thr Ser Asp Ser
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ccc gcg cca gca acc gtc aac gcg gta ttc aac aac agc aac ggc ttc 163
 Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn Asn Ser Asn Gly Phe
 10 15 20

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Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn Thr Val Val Glu Thr	
25 30 35	
atg gac acg gaa ttc ggc gtc cgc att gtg gat aac atg ctc gtc ggt	259
Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp Asn Met Leu Val Gly	
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Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala Ala Glu Gly Ala Thr	
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Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp Gly Ala Val Gln Leu	
70 75 80 85	
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Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile Ala Ser Ala Asn Glu	
90 95 100	
ggt gcg caa tcg ctt gcc gac ggc gcc agc cag ctc gac acc ggc ctc	451
Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln Leu Asp Thr Gly Leu	
105 110 115	
ggc tcc gcg gct aca ggc agc caa acg ctc gcc gac ggt cta tcc agc	499
Gly Ser Ala Ala Thr Gly Ser Gln Thr Leu Ala Asp Gly Leu Ser Ser	
120 125 130	
ctg tct gcg ggc acc gcc caa cta ggc caa ggc gca acc cag gtt tca	547
Leu Ser Ala Gly Thr Ala Gln Leu Gly Gln Gly Ala Thr Gln Val Ser	
135 140 145	
gat ggc gtg ggc caa ctt gtc gac caa gta gca cca ctg acc gcc tat	595
Asp Gly Val Gly Gln Leu Val Asp Gln Val Ala Pro Leu Thr Ala Tyr	
150 155 160 165	
gtt cca gac atc aac tct cag ttg atc acc ctg cgc gac ggc gca gcc	643
Val Pro Asp Ile Asn Ser Gln Leu Ile Thr Leu Arg Asp Gly Ala Ala	
170 175 180	
acc att gcc tct gaa cta tct gat ccc tcc agc acc tac cgc tcc ggc	691
Thr Ile Ala Ser Glu Leu Ser Asp Pro Ser Ser Thr Tyr Arg Ser Gly	
185 190 195	
gtg gac tcc gct gtg agc gca tcc cag caa cta gca gcc ggc ctg caa	739
Val Asp Ser Ala Val Ser Ala Ser Gln Gln Leu Ala Ala Gly Leu Gln	
200 205 210	
acc ctg aaa gac gga tcc agc caa ctc agc atc ggt gca cgc acc ctc	787
Thr Leu Lys Asp Gly Ser Ser Gln Leu Ser Ile Gly Ala Arg Thr Leu	
215 220 225	
gct gat ggc acc agc caa ttg gcc gca ggt tcc gaa cag cta gtt gtt	835
Ala Asp Gly Thr Ser Gln Leu Ala Ala Gly Ser Glu Gln Leu Val Val	
230 235 240 245	
ggc gca caa gca ctg cgc gac ggc acc gtc cag ctt gat gaa ggc tcc	883

Gly	Ala	Gln	Ala	Leu	Arg	Asp	Gly	Thr	Val	Gln	Leu	Asp	Glu	Gly	Ser		
				250					255					260			
agc	gaa	ctc	gcc	ctc	aaa	ctc	acc	gac	ggc	gca	agc	caa	gta	cca	acc	931	
Ser	Glu	Leu	Ala	Leu	Lys	Leu	Thr	Asp	Gly	Ala	Ser	Gln	Val	Pro	Thr		
			265					270				275					
ttc	gct	gac	ggc	gca	gac	acc	acc	atc	gca	acc	cca	gtt	gaa	aca	gaa	979	
Phe	Ala	Asp	Gly	Ala	Asp	Thr	Thr	Ile	Ala	Thr	Pro	Val	Glu	Thr	Glu		
		280					285				290						
caa	gca	gga	gac	acc	aca	ccg	ctc	ttc	ggc	att	ggc	ctc	gca	cca	ttc	1027	
Gln	Ala	Gly	Asp	Thr	Thr	Pro	Leu	Phe	Gly	Ile	Gly	Leu	Ala	Pro	Phe		
	295					300					305						
ttc	atg	gct	gtc	ggc	ctg	ttc	atg	gga	gca	acc	gtt	gcc	tgg	atg	atc	1075	
Phe	Met	Ala	Val	Gly	Leu	Phe	Met	Gly	Ala	Thr	Val	Ala	Trp	Met	Ile		
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Leu	His	Pro	Ile	Ser	Arg	Arg	Ala	Leu	Asp	Ser	Arg	Met	Gly	Gly	Phe		
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cga	ggc	acc	ctg	gca	agc	tac	ctt	cca	tca	aca	gtc	tta	ggc	ctt	ggc	1171	
Arg	Gly	Thr	Leu	Ala	Ser	Tyr	Leu	Pro	Ser	Thr	Val	Leu	Gly	Leu	Gly		
		345					350					355					
caa	gca	acc	atc	atg	tgg	gca	gta	ctg	tac	ttc	ctg	ctc	gac	ctc	aat	1219	
Gln	Ala	Thr	Ile	Met	Trp	Ala	Val	Leu	Tyr	Phe	Leu	Leu	Asp	Leu	Asn		
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cca	gct	cac	cca	gct	gga	ctg	tgg	atg	gcg	atg	gtc	gcc	atc	tca	tgg	1267	
Pro	Ala	His	Pro	Ala	Gly	Leu	Trp	Met	Ala	Met	Val	Ala	Ile	Ser	Trp		
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gta	ttc	atc	tcc	att	acc	cat	atg	ttc	aac	aac	gtg	gca	gga	ccc	tcc	1315	
Val	Phe	Ile	Ser	Ile	Thr	His	Met	Phe	Asn	Asn	Val	Ala	Gly	Pro	Ser		
390				395				400						405			
gca	ggc	cgt	gtg	ctg	tcc	atc	gtg	atg	atg	tcc	ttc	cag	cta	gtc	tcc	1363	
Ala	Gly	Arg	Val	Leu	Ser	Ile	Val	Met	Met	Ser	Phe	Gln	Leu	Val	Ser		
			410				415					420					
tcc	ggt	ggc	cta	tac	cca	cca	gaa	acc	cag	cca	gca	ttc	ttc	cac	tgg	1411	
Ser	Gly	Gly	Leu	Tyr	Pro	Pro	Glu	Thr	Gln	Pro	Ala	Phe	Phe	His	Trp		
		425					430					435					
ttc	cac	acc	tac	gac	ccg	atc	acc	tac	gca	gtc	aac	ctc	gtg	cgc	caa	1459	
Phe	His	Thr	Tyr	Asp	Pro	Ile	Thr	Tyr	Ala	Val	Asn	Leu	Val	Arg	Gln		
	440					445					450						
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	455					460				465							
atc	tgg	gta	ctg	ctc	ttc	atc	tgg	gca	ctg	atg	ctc	gcc	atc	tcc	acc	1555	
Ile	Trp	Val	Leu	Leu	Phe	Ile	Trp	Ala	Leu	Met	Leu	Ala	Ile	Ser	Thr		

470 475 480 485

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 Glu Leu Lys Val
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Thr Val Val Glu Thr Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp
 35 40 45

Asn Met Leu Val Gly Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala
 50 55 60

Ala Glu Gly Ala Thr Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp
 65 70 75 80

Gly Ala Val Gln Leu Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile
 85 90 95

Ala Ser Ala Asn Glu Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln
 100 105 110

Leu Asp Thr Gly Leu Gly Ser Ala Ala Thr Gly Ser Gln Thr Leu Ala
 115 120 125

Asp Gly Leu Ser Ser Leu Ser Ala Gly Thr Ala Gln Leu Gly Gln Gly
 130 135 140

Ala Thr Gln Val Ser Asp Gly Val Gly Gln Leu Val Asp Gln Val Ala
 145 150 155 160

Pro Leu Thr Ala Tyr Val Pro Asp Ile Asn Ser Gln Leu Ile Thr Leu
 165 170 175

Arg Asp Gly Ala Ala Thr Ile Ala Ser Glu Leu Ser Asp Pro Ser Ser
 180 185 190

Thr Tyr Arg Ser Gly Val Asp Ser Ala Val Ser Ala Ser Gln Gln Leu
 195 200 205

Ala Ala Gly Leu Gln Thr Leu Lys Asp Gly Ser Ser Gln Leu Ser Ile

210

215

220

Gly Ala Arg Thr Leu Ala Asp Gly Thr Ser Gln Leu Ala Ala Gly Ser
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Glu Gln Leu Val Val Gly Ala Gln Ala Leu Arg Asp Gly Thr Val Gln
 245 250 255

Leu Asp Glu Gly Ser Ser Glu Leu Ala Leu Lys Leu Thr Asp Gly Ala
 260 265 270

Ser Gln Val Pro Thr Phe Ala Asp Gly Ala Asp Thr Thr Ile Ala Thr
 275 280 285

Pro Val Glu Thr Glu Gln Ala Gly Asp Thr Thr Pro Leu Phe Gly Ile
 290 295 300

Gly Leu Ala Pro Phe Phe Met Ala Val Gly Leu Phe Met Gly Ala Thr
 305 310 315 320

Val Ala Trp Met Ile Leu His Pro Ile Ser Arg Arg Ala Leu Asp Ser
 325 330 335

Arg Met Gly Gly Phe Arg Gly Thr Leu Ala Ser Tyr Leu Pro Ser Thr
 340 345 350

Val Leu Gly Leu Gly Gln Ala Thr Ile Met Trp Ala Val Leu Tyr Phe
 355 360 365

Leu Leu Asp Leu Asn Pro Ala His Pro Ala Gly Leu Trp Met Ala Met
 370 375 380

Val Ala Ile Ser Trp Val Phe Ile Ser Ile Thr His Met Phe Asn Asn
 385 390 395 400

Val Ala Gly Pro Ser Ala Gly Arg Val Leu Ser Ile Val Met Met Ser
 405 410 415

Phe Gln Leu Val Ser Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro
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Ala Phe Phe His Trp Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val
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Asn Leu Val Arg Gln Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro
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Arg Phe Ile Gln Ala Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met
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 <222> (101)..(664)
 <223> RXN01091

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              Met Val Pro Asn Thr
              1 5

gtc ctt atc cat gac gaa acc gcc gat ctg gcg acg cag atc cag cgg 163
Val Leu Ile His Asp Glu Thr Ala Asp Leu Ala Thr Gln Ile Gln Arg
              10 15 20

ctg gaa cat atc atg gcg tgc ctg cgc gat ccg gtc agc gga tgc ccg 211
Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro Val Ser Gly Cys Pro
              25 30 35

tgg gat att gaa cag acc ttt gcc agc atc gcg ccc cac acg att gag 259
Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala Pro His Thr Ile Glu
              40 45 50

gaa ggc tac gag gtt gcc gac gcc atc gcg cag gaa gac tgg ccc gag 307
Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln Glu Asp Trp Pro Glu
              55 60 65

cta cgc ggc gag ttg ggc gat ttg ctg ttt cag acc gtg ttt cac gcc 355
Leu Arg Gly Glu Leu Gly Asp Leu Leu Phe Gln Thr Val Phe His Ala
              70 75 80 85

caa atg gcg cgc gag gca ggc cat ttc gct ttg gtt gac gtg gtg aag 403
Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu Val Asp Val Val Lys
              90 95 100

gca att tcg gac aag atg gtt ttg cgc cat ccg cac gtg ttc ggc gcg 451
Ala Ile Ser Asp Lys Met Val Leu Arg His Pro His Val Phe Gly Ala
              105 110 115

cag tcg aac gcg aaa tcc gcc gac cag cag gtg gaa gat tgg gaa gtc 499
Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val Glu Asp Trp Glu Val
              120 125 130

atc aag gcg ccc gag cgc gcg ggc aaa gcg caa aag ggc gtt ttg gat 547
Ile Lys Ala Pro Glu Arg Ala Gly Lys Ala Gln Lys Gly Val Leu Asp
              135 140 145

ggc gtc gcg ctg gga ctg cct gcc ctg atg cgc gcg acg aag ctg caa 595
Gly Val Ala Leu Gly Leu Pro Ala Leu Met Arg Ala Thr Lys Leu Gln
              150 155 160 165
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Pro His Thr Ile Glu Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln
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Glu Asp Trp Pro Glu Leu Arg Gly Glu Leu Gly Asp Leu Leu Phe Gln
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Thr Val Phe His Ala Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu
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Val Asp Val Val Lys Ala Ile Ser Asp Lys Met Val Leu Arg His Pro
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His Val Phe Gly Ala Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val
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Glu Asp Trp Glu Val Ile Lys Ala Pro Glu Arg Ala Gly Lys Ala Gln
 130 135 140

Lys Gly Val Leu Asp Gly Val Ala Leu Gly Leu Pro Ala Leu Met Arg
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 Met Asn Ala Asp Lys
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 Lys Met Cys Gly Met Asn Pro Asp Ser Gln Tyr Val Glu Leu Ala Val
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 gaa gtt ttc gga ctc ctc gcg gac gcc act cga gtt cgc atc atc ttg 211
 Glu Val Phe Gly Leu Leu Ala Asp Ala Thr Arg Val Arg Ile Ile Leu
 25 30 35
 gca ctt cga aac agt ggt gaa ctt tcc gta aac cac ctc gcg gac atc 259
 Ala Leu Arg Asn Ser Gly Glu Leu Ser Val Asn His Leu Ala Asp Ile
 40 45 50
 gtc gat aaa tcc ccc gca gca gtt tcc caa cac ctc gcc cgg ctg cgc 307
 Val Asp Lys Ser Pro Ala Ala Val Ser Gln His Leu Ala Arg Leu Arg
 55 60 65
 atg gcc cga atc gtg tcc acc cgt caa gaa ggt caa cga gtt ttc tac 355
 Met Ala Arg Ile Val Ser Thr Arg Gln Glu Gly Gln Arg Val Phe Tyr
 70 75 80 85
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 Lys Leu Thr Asn Glu His Ala Ser Gln Leu Val Ser Asp Ala Ile Phe
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 Gln Ala Glu His Thr Ile Ala Asp Gly Gln Thr Pro Pro His His His
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 35 40 45

His Leu Ala Asp Ile Val Asp Lys Ser Pro Ala Ala Val Ser Gln His
 50 55 60

Leu Ala Arg Leu Arg Met Ala Arg Ile Val Ser Thr Arg Gln Glu Gly
 65 70 75 80

Gln Arg Val Phe Tyr Lys Leu Thr Asn Glu His Ala Ser Gln Leu Val
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